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Socio-Demographic, Clinical, and Household Environmental Profiles of Visceral and Cutaneous Leishmaniasis Cases in Keekonyokie Ward, Kajiado West Sub-County, Kenya

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Abstract

Purpose: To describe the socio-demographic and clinical profile of patients diagnosed with visceral (VL) and cutaneous leishmaniasis (CL) in Keekonyokie Ward, Kajiado West Sub-County, Kenya, and to determine the household-level environmental and behavioural determinants associated with disease occurrence.

Methodology: A retrospective hospital-based descriptive study supplemented by a cross-sectional household survey was conducted in Keekonyokie Ward, Kajiado West Sub-County, Kenya. Cases were ascertained from facility registers, active community case-finding by Community Health Promoters, and the ICIPE KaLaAzar Mapper dataset. Village-level environmental and behavioural determinants of CL case counts were examined using negative binomial regression.

Findings: A total of 174 confirmed cases were enrolled: 159 CL (91.4%) and 15 VL (8.6%). Median age was 13 years, with the 5–14 age group accounting for 40.6% of cases; students were the largest occupational group (47.9%). Proximity to termite mounds (94.8%), dog ownership (91.4%), and mud-walled housing (63.8%) were the most prevalent household exposures. Land surface temperature and elevation were significant univariate village-level predictors of CL case counts, although neither retained significance after multivariable adjustment.

Unique Contribution to Theory, Practice and Policy: This study provides the first systematic characterization of cutaneous and visceral leishmaniasis in Keekonyokie Ward, applying the socio-ecological systems framework in a semi-arid pastoral setting. Findings affirm that transmission risk arises from interacting multi-level determinants rather than single predictors. For practice, the findings identify priority villages and the 5–14 years age group for targeted surveillance, and highlight mud-walled housing as a modifiable risk factor. For policy, the study supports incorporating environmental and behavioural risk monitoring into routine surveillance and strengthening community-based treatment follow-up through Community Health Promoters.

Keywords: *Cutaneous Leishmaniasis, Visceral Leishmaniasis, Environmental Determinants, Household Risk Factors, Kajiado*

JEL Classification: *I15, I18, Q54, C21*

INTRODUCTION

Leishmaniasis re-emerged in Keekonyokie, Kajiado, Kenya in 2021, following an approximately three-decade period during which no further local cases were documented after an isolated 1993 report of three paediatric VL cases in the same area (Johnson et al., 1993, as cited in Matoke-Muhia et al., 2026). Leishmaniasis is a vector-borne parasitic disease caused by protozoa of the genus *Leishmania* and transmitted through the bites of infected female phlebotomine sandflies. The disease presents a broad clinical spectrum, ranging from self-limiting cutaneous lesions to severe visceral disease, commonly known as kala-azar, which can be fatal if left untreated. Human leishmaniasis occurs primarily in three clinical forms: cutaneous, visceral, and mucosal leishmaniasis (CDC, 2024b). CL is the most common form globally, responsible for an estimated 600,000 to 1,000,000 new cases annually, and is caused by multiple *Leishmania* species including *L. tropica* and *L. major* in the Old World (Kumar et al., 2026). VL, caused predominantly by *L. donovani* in East Africa, is the most severe form, with 50,000 to 90,000 new cases annually and near-universal fatality if left untreated (Alvar et al., 2012). The WHO 2021–2030 roadmap for neglected tropical diseases targets a reduction of VL mortality to below 1% across 56 endemic countries by 2025 (WHO, 2023).

While VL has historically dominated the leishmaniasis research agenda, CL imposes a substantial and underappreciated burden of its own. Despite its public health significance, CL remains understudied in sub-Saharan Africa, with limited data on its true incidence, transmission dynamics, and the *Leishmania* species, vectors, and reservoir hosts involved in disease transmission (Blaizot et al., 2024). A 2025 systematic review and meta-analysis confirmed that CL is a major public health and social problem across East Africa, with its disfiguring visible lesions leading to social rejection, stigma, and discrimination among affected populations (Ahmed et al., 2025). In Kenya specifically, WHO classifies the country as endemic for CL, yet published data on its true extent, burden, and risk factors remain comparatively scarce relative to VL (Ngere et al., 2020).

East Africa carries approximately 75% of the global VL burden (Matoke-Muhia et al., 2026). Kenya is among the highest-burden priority countries, with VL endemic in 11 counties in arid and semi-arid regions and more than 1,000 new VL cases reported annually since 2017 (WHO, 2025). The national burden of VL in Kenya has increased sharply in recent years, with reported cases rising from 1,575 in 2024 to 3,577 in 2025, indicating a more than twofold increase in disease incidence (Beacon Project, 2026). This surge reflects a widening public health concern, with the disease spreading beyond traditionally endemic areas into new regions. Contributing factors are believed to include environmental and climatic changes that favor sandfly vector proliferation, as well as expanding human settlements into previously uninhabited ecological zones (O'Brien et al., 2024). The increasing incidence highlights ongoing challenges in surveillance, early case detection, and disease control in endemic counties.

The re-emergence of leishmaniasis in Kajiado County represents a dual-disease public health crisis involving both CL and VL. Entomological investigations across eight villages in Keekonyokie Ward identified 22 suspected CL cases, of whom eight were laboratory-confirmed with *Leishmania tropica*, alongside 10 confirmed VL patients predominantly in children under 15 years of age (Matoke-Muhia et al., 2026). Co-circulation of both parasite species with high human blood indices indicates sustained, concurrent transmission of CL and VL within the same community (Hassaballa et al., 2021). The broader VL burden in Kajiado West Sub-County has continued to intensify, with at least 150 patients treated for kala-azar in the six months preceding March 2025, the majority being boys aged 9–11 years engaged in livestock herding (Beacon Project, 2026).

In Gilgil, Nakuru County, recurrent CL epidemics have established the disease as a persistent public health concern; *Phlebotomus guggisbergi* is the confirmed vector of *L. tropica*, with *Ph. saevus s.l.* and *Ph. aculeatus* identified as additional potential vectors, while molecular detection of *L. major* in *Ph. guggisbergi* suggests it may also act as a permissive vector for this species, pending further confirmation (Owino et al., 2019).

The co-circulation of distinct *Leishmania* species within a single focus, as observed for *L. donovani* and *L. tropica* in Keekonyokie Ward, has been documented elsewhere and is increasingly attributed to environmental and land-use change rather than to two entirely separate, spatially isolated vector systems. In central Tunisia, *L. major* and *L. tropica* co-circulated in a mixed focus of zoonotic and chronic CL, where the two parasites shared partial vector overlap through *Phlebotomus longicuspis*, driven primarily by the proximity of human settlements to the biotopes of each parasite's respective rodent reservoir hosts (Abbas et al., 2022). This pattern reflects a broader mechanism increasingly reported across leishmaniasis-endemic settings: land-use fragmentation and human encroachment into forest, rangeland, or reservoir habitat either newly exposes human populations to previously sylvatic pathogen pools, or perturbs pathogen-vector-host dynamics in ways that enhance cross-species transmission (Purse et al., 2017). A comparable phenomenon has recently been described in Nepal and Sudan, where *L. donovani*, classically associated with VL, has been documented causing CL in sympatry with VL cases, a pattern interpreted as reflecting environmentally and diagnostically driven geographic expansion of a known parasite rather than the emergence of a genuinely new transmission system (Sereno, 2026). The Kajiado entomological data, in which both *L. donovani* and *L. tropica* DNA were detected in *Phlebotomus saevus*, fit this same broader pattern (Matoke-Muhia et al., 2026), suggesting that the co-circulation observed in Keekonyokie Ward most plausibly reflects a broader environmental and ecological shift, driven by pastoral land-use change and expanding human-livestock settlement, that has brought previously distinct sylvatic and peridomestic transmission cycles into overlapping contact, consistent with global patterns linking land-use and climatic change to multi-species leishmaniasis transmission.

Environmental and socioeconomic factors critically shape this transmission. In Keekonyokie Ward, the semi-arid pastoral landscape is characterised by acacia woodland, termite mounds, mud-walled housing with cracked surfaces, and a livelihood system centred on livestock herding-conditions collectively conducive to sandfly breeding and sustained human-vector contact (Abdullahi et al., 2024; Lotukoi et al., 2017). Abdullahi et al. (2024) identifies dog ownership, malnutrition, and low educational attainment as significant risk factors in comparable East African settings.

Statement of the Problem

Despite the escalating dual burden of cutaneous and visceral leishmaniasis, key epidemiological evidence required to guide targeted control in Keekonyokie Ward remains limited. No study has systematically described the socio-demographic or clinical characteristics of patients with confirmed VL or CL in this re-emergent focus, leaving key attributes such as age, sex, occupation, nutritional status, and clinical presentation insufficiently quantified at the local level. In addition, household-level environmental and behavioural exposures among confirmed cases have not been comprehensively assessed, limiting understanding of the contextual drivers of transmission in this pastoral setting, despite entomological evidence demonstrating co-circulation of *Leishmania donovani* and *Leishmania tropica* within the ward (Matoke-Muhia et al., 2026). This study therefore addresses these gaps by describing the socio-demographic and clinical profiles of VL and CL patients and by determining the household-level environmental and behavioural determinants influencing disease occurrence in Keekonyokie Ward.

Objectives

The general objective of this study was to generate evidence on the socio-demographic, clinical, and environmental-behavioural profile of visceral and cutaneous leishmaniasis in Keekonyokie Ward, Kajiado West Sub-County, Kenya, to inform targeted outbreak response. The specific objectives were:

i. To describe the socio-demographic and clinical profile of patients diagnosed with visceral and cutaneous leishmaniasis in Keekonyokie Ward, Kajiado West Sub-County.

ii. To determine environmental and behavioral determinants influencing the occurrence of visceral and cutaneous leishmaniasis in Keekonyokie Ward, Kajiado West Sub-County.

LITERATURE REVIEW

Theoretical Framework

This study is grounded in the socio-ecological systems framework for vector-borne disease transmission, which conceptualises disease risk as the result of interactions between biological, environmental, and social determinants operating at household and landscape scales. The framework guides examination of how pastoral land use, housing characteristics, and human behavioural practices interact with environmental factors such as temperature, elevation, and vegetation to influence sandfly habitat suitability and human exposure risk (Geto et al., 2024; Grifferty et al., 2023). Rather than treating these as independently categorised risk factors, the framework explicitly conceptualises human behaviour as actively reshaping the ecological niches that sustain sandfly populations: livestock enclosure placement and mud-walled housing construction create microhabitats favourable to sandfly breeding and resting (Hassaballa et al., 2021), with cracked mud walls, damp housing, and termite mounds consistently identified as key drivers of vector density in East African settings, including Baringo County, Kenya (O'Brien et al., 2024). Conversely, community-level modification of these same structures, such as sealing wall cracks or clearing termite mounds, illustrates how human behaviour can also actively reduce ecological suitability for sandflies, underscoring the bidirectional nature of this human-niche interaction. Pastoral mobility and outdoor occupational exposure further determine the frequency and location of human-vector contact within these niches. Disease risk in this framework therefore emerges from the dynamic feedback between human land-use practices and the ecological suitability they generate, rather than from the additive influence of separately measured variables.

Conceptual Framework

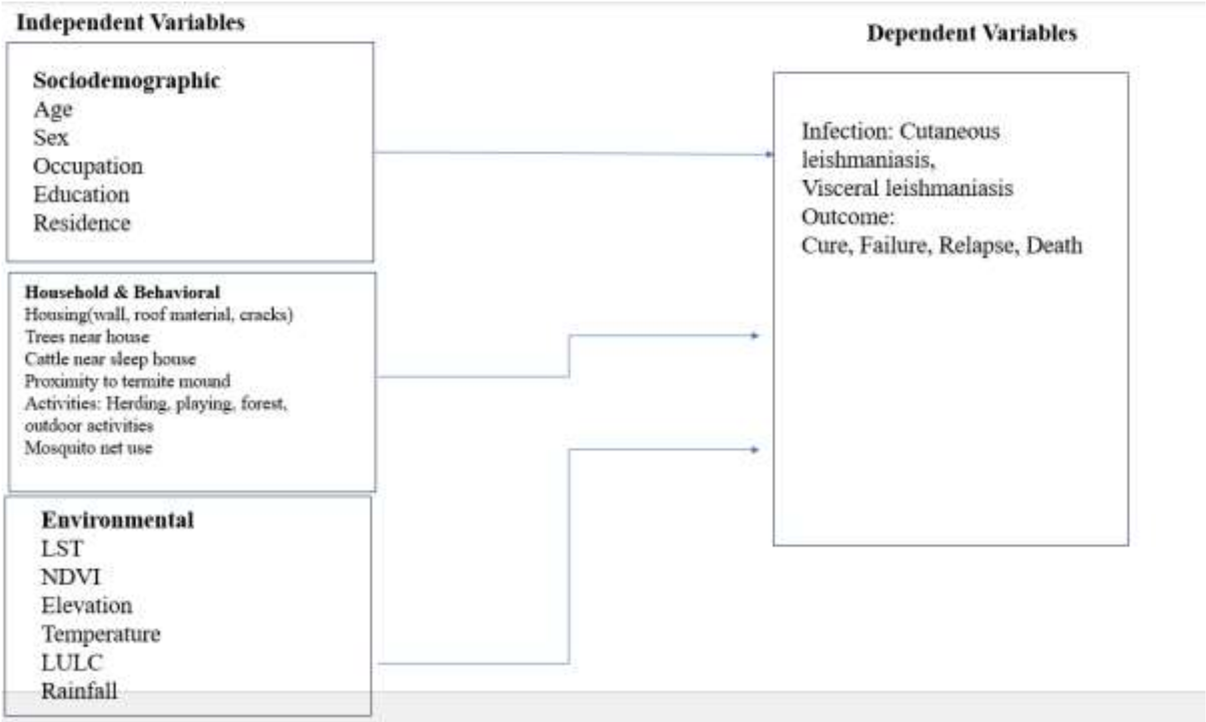


Figure 1: Conceptual Framework Illustrating the Hypothesized Relationships between Sociodemographic, Household/Behavioral, And Environmental Factors and Leishmaniasis Outcomes in Kenya, 2025.

The conceptual framework (Figure 1) illustrates the hypothesized pathways through which sociodemographic, household and behavioral, environmental, and clinical factors influence the occurrence and outcomes of cutaneous and visceral leishmaniasis. These factors are hypothesized to affect disease risk both directly and indirectly through increased exposure to infected sandflies and treatment adherence. While Figure 1 depicts these determinants at a categorical level, the framework further hypothesizes a specific directional distinction among them: environmental and behavioural exposures (e.g., proximity to termite mounds, housing structure, occupational activity) are treated as mediators lying on the causal pathway between sociodemographic risk factors and sandfly contact, whereas nutritional status is hypothesized to function primarily as a moderator of disease severity and treatment response rather than a mediator of infection risk. This distinction is supported by evidence that nutritional status shows no significant community-level association with VL infection itself (Sagaki et al., 2025), while experimental and clinical evidence indicates that it alters disease progression and reduces treatment efficacy once infection has occurred (Ferreira-Paes et al., 2025; Gashaw et al., 2025). This directional hypothesis guided the analytic approach, in which nutritional status was evaluated as a modifier of clinical severity and treatment outcomes rather than as an intermediate step in the infection pathway. Guided by this framework, descriptive and multivariable analyses were conducted to evaluate the independent and combined effects of these determinants on leishmaniasis epidemiology.

Empirical Review

Socio-demographic and Clinical Profiles of Leishmaniasis

The socio-demographic profile of leishmaniasis patients in East Africa reflects the intersection of biological susceptibility and occupational exposure. VL predominantly affects children and adolescents, with studies consistently reporting that over 50–60% of confirmed cases occur in those under 15 years of age, and a male-to-female ratio of approximately 3:1, attributed to greater outdoor exposure among boys engaged in livestock herding and agricultural labour (Geto et al., 2024; Cloots et al., 2020). A 2024 systematic review and meta-analysis of VL in Eastern Africa confirmed that male sex, younger age, larger family size, and presence of a VL-infected household member were all significantly associated with infection (Geto et al., 2024). In active outbreak settings such as Keekonyokie Ward, this demographic skew is particularly pronounced, with the majority of kala-azar patients being boys aged 9–11 years engaged in livestock herding (Beacon Project, 2026).

The clinical presentation of VL in East Africa follows a well-established pattern of prolonged fever, progressive splenomegaly, hepatomegaly, weight loss, and pallor, with anaemia-reflected in markedly reduced haemoglobin values-among the most consistent laboratory findings (Nail & Imam, 2013). Occupations involving outdoor activities, particularly livestock herding, forest visits, and stone masonry, have been associated with significantly elevated odds of CL acquisition, reflecting the peridomestic and landscape-level exposure dynamics of *L. tropica* transmission (O'Brien et al., 2024).

CL commonly manifests as single or multiple skin lesions that vary in severity, ranging from localized lesions to large, destructive ulcers. Following an incubation period of approximately 2–8 months, CL typically presents as a painless erythematous papule on exposed body parts such as the face, forearms, and lower legs (CDC, 2024a). These lesions gradually enlarge into nodules or plaques over several months. Transmission often occurs during summer, with clinical symptoms appearing later in winter. Although lesions may heal spontaneously, recovery usually results in lifelong immunity (Bilgic-Temel et al., 2019).

Leishmaniasis recidivans-a chronic relapsing form characterised by treatment-unresponsive lesions-has been specifically documented in *L. tropica* foci in the Kenyan Rift Valley, adding to the clinical complexity and burden of CL in the region (Gitari et al., 2018).

Household Environmental and Behavioural Risk Factors

Evidence from East African leishmaniasis foci consistently identifies peridomestic environmental conditions as key drivers of sandfly density and human-vector contact. Proximity to termite mounds is among the most consistently reported risk factors for VL in Kenya and Ethiopia, as these structures provide humid, sheltered microhabitats ideal for *Phlebotomus* breeding and resting (Geto et al., 2024; Hassaballa et al., 2021). Dog ownership and proximity to domestic animal enclosures have been associated with increased sandfly density, as animals serve as blood-meal hosts that sustain vector populations in and around homesteads (Hassaballa et al., 2021). Environmental and behavioral factors, including outdoor sleeping, vegetation surrounding homes, and poor housing conditions such as cracked walls, have been identified as important risk factors for *Leishmania* infection. Conversely, the use of bed nets has been associated with a reduced risk of infection in some settings (Belay et al., 2026).

A study from Khyber District reported a higher burden of cutaneous leishmaniasis among males and observed seasonal peaks in disease occurrence. In univariate analysis, several sociodemographic, household, and behavioral factors (including education level, household size, housing type, prior family history of leishmaniasis, and knowledge of sandfly behavior) were associated with infection; however, none remained statistically significant in multivariable models, suggesting complex and interrelated transmission dynamics(Lu et al., 2024).

The reemergence of CL has been linked to sociodemographic changes such as rapid urbanization, deforestation, migration, and social instability, which alter vector habitats and facilitate disease transmission (Tapias Rivera et al., 2025). Rock hyraxes and wild rodents in the peridomestic environment have been implicated as potential zoonotic reservoirs for *L. tropica* in some East African foci, with patients in Kenyan CL clusters significantly more likely to report sighting rock hyraxes near their homes (Ngere et al., 2020).

Nutritional status is an important cross-cutting determinant for both forms. Experimental evidence from murine models further demonstrates that marasmic malnutrition reduces the efficacy of standard VL treatment with meglumine antimoniate, with refeeding partially but not fully reversing these effects, underscoring the need for integrated nutritional and therapeutic management in malnourished patients (Ferreira-Paes et al., 2025).However, a cross-sectional study in the pastoral Karamoja region of Uganda found no statistically significant association between nutritional status and VL infection at the community level, suggesting that malnutrition may suppress health-seeking behaviour and reduce detection of asymptomatic cases rather than simply elevating apparent risk (Sagaki et al., 2025). For CL, evidence from Ethiopia found that over one-fifth of CL patients were malnourished, with malnutrition disproportionately prevalent among those with recurrent and relapsing disease, suggesting that nutritional status shapes both clinical manifestation and treatment responsiveness in cutaneous disease (Gashaw et al., 2025).

Environmental Predictors of Leishmaniasis Occurrence

For CL, environmental factors including temperature, slope, and proximity to livestock sheds have been significantly associated with disease occurrence in emerging *L. tropica* foci (Ghatee et al., 2018). Beyond East Africa, comparable elevation-driven patterns have been documented elsewhere: a study in Khyber District found CL cases concentrated at elevations between 294 and 1,916 metres, occurring predominantly in agricultural and rangeland areas, underscoring the broader role of elevation and land-use type in shaping environmental suitability for transmission (Lu et al., 2024).

Research Gaps

Despite the re-emergence of both VL and CL in Kajiado County, there remains limited evidence describing the clinical, socio-demographic, and household-level exposure profile of the current outbreak. Most epidemiological studies in Kenya have focused on established endemic regions in northern counties such as Turkana, Baringo, and West Pokot, with little attention to emerging foci in semi-arid pastoral communities in southern Kenya. This gap is not merely one of missing surveillance data; it reflects a more fundamental problem of ecological non-stationarity. Environmental and land-use conditions are known to actively reshape disease-environment relationships over time, meaning that risk models and epidemiological patterns derived under one set of ecological conditions cannot be reliably assumed to hold as those conditions change (Purse et al., 2017). Kajiado's pastoral landscape is itself undergoing rapid land-use intensification, expanding livestock settlement, and encroachment into previously undisturbed terrain; epidemiological and environmental-suitability data drawn from long-established northern foci may therefore no longer accurately represent the drivers of transmission in this newly active, ecologically distinct focus, rather than simply being extrapolated southward. Published data on CL specifically, its burden and risk factors, remain comparatively scarce across Kenya (O'Brien et al., 2024; Blaizot et al., 2024), and the concurrent circulation of *L. donovani* and *L. tropica* in the same community, as confirmed in Keekonyokie Ward, represents an epidemiologically unusual situation for which no local characterisation exists. Furthermore, no study has systematically examined the environmental and behavioural determinants of case occurrence in this re-emergent focus, limiting the evidence base available to target vector control and case-finding resources.

METHODOLOGY

Research Design

This study was a retrospective, hospital-based descriptive study supplemented by a cross-sectional household survey among traced cases conducted in Keekonyokie Ward, Kajiado West Sub-County, Kenya.

Study Site

Keekonyokie Ward covers approximately 807 km² and is characterized by a semi-arid savannah landscape with extensive Acacia woodlands and termite mound networks. The local economy is predominantly based on pastoralism.

Sampling Technique

Cases were identified through a systematic review of paper-based patient registers covering the period from January 2022 to June 2025, drawing on facility records from Oltepesi Health Centre (113 cases) and the KaLaAzar Mapper dataset maintained by ICIPE, which identified 13 additional confirmed VL cases who had sought care at other facilities. This combined list of 126 cases was provided to Community Health Promoters (CHPs) for household-level field retracing. In the field, CHPs successfully retraced 66 of the listed cases and additionally identified 51 further cases known to them through community contact but not captured in any facility register, bringing the combined case pool to 177. Three cases were subsequently excluded during data reconciliation due to duplicate entries and missing village identifiers required for data verification, yielding a final analytical sample of 174 confirmed leishmaniasis cases, comprising 159 CL and 15 VL cases. No VL cases was retraced back in the community hence analyses involving household environmental and behavioural characteristics were restricted to CL cases, while VL cases were included only in the descriptive summaries.

Sample Size

The descriptive dataset comprised 174 confirmed leishmaniasis cases (159 CL and 15 VL). Household follow-up was conducted only for CL cases because most VL patients had been referred to higher-level facilities and could not be reliably traced for household assessment. Household environmental and behavioural analyses were conducted using the final household dataset of 116 unique CL cases identified through community tracing and verification by CHPs.

Data Collection Procedure

Data collection involved three components: health facility records review, household surveys, and environmental data extraction.

Household Survey – Household surveys were conducted using a structured, interviewer-administered questionnaire administered by trained CHPs. The questionnaire captured data on housing characteristics (wall and roof materials, presence of wall cracks), animal contact (dogs, cattle, goats), behavioural factors (herding activities, sleeping location, and kitchen sleeping practices), ecological proximity (termite mounds, water bodies, and surrounding vegetation), and use of personal protective measures (mosquito net ownership and usage). CHPs conducted direct household observations to validate selected environmental and housing characteristics. All data collectors underwent standardized training prior to fieldwork.

Environmental Data Extraction – Environmental variables were extracted at each geocoded household location using Google Earth Engine. For each household point, spatially matched values were obtained from global geospatial datasets, including land surface temperature (MODIS MOD11A2), NDVI (MODIS MOD13Q1), precipitation (CHIRPS), mean air temperature (ERA5-Land), elevation and slope (SRTM 30 m), population density (WorldPop 2020), land cover (ESA WorldCover v100), water bodies (JRC Global Surface Water), and soil properties (OpenLandMap). All spatial datasets were preprocessed and standardized to ensure consistency in spatial resolution and projection prior to extraction.

Ethical Consideration

Ethical approval was obtained from the Kenyatta National Hospital–University of Nairobi Ethics and Research Committee (KNH-UoN ERC) (Reference No. KNH/ERC/R/204). A research permit was subsequently obtained from the National Commission for Science, Technology and Innovation (NACOSTI) (Reference No. NACOSTI/P/25/4179924). Permission to access health facility records was granted by the relevant county health authorities and the management of Oltepesi Health Centre. Written informed consent was obtained from all adult participants. For participants under 18 years of age, consent was obtained from a parent or legal guardian, and assent was obtained from children capable of providing it. Participation was voluntary, and confidentiality and anonymity of participant information were maintained throughout the study.

Statistical Analysis

Statistical analyses were conducted using R statistical software (Version 4.5.1; R Foundation for Statistical Computing, Vienna, Austria). Data were first cleaned and checked for missing values, outliers, and inconsistencies prior to analysis. Missing data are reported explicitly throughout; no imputation was performed.

Descriptive statistics were used to summarize demographic, clinical, behavioural, and environmental variables. Categorical variables were presented as frequencies and proportions, while continuous variables were summarized using means and standard deviations or medians and interquartile ranges, depending on data distribution. Bivariate associations between categorical variables and CL status were assessed using the Chi-square test or Fisher's exact test, where appropriate. Continuous variables were compared between groups using independent t-tests or Mann–Whitney U tests based on normality assumptions.

Environmental predictors were assessed for multicollinearity using Pearson correlation matrices prior to regression modelling. Variables with pairwise correlations $|r| > 0.7$ were considered collinear; where collinearity was identified, the variable with the strongest biological plausibility was retained. Mean air temperature was excluded from multivariable modelling due to collinearity with both LST ($r = 0.63$) and elevation ($r = -0.79$). Negative binomial regression was used to model village-level CL case counts across 21 villages to account for overdispersion in the outcome variable. Univariate negative binomial models were fitted for each environmental predictor individually. Variables with $p < 0.20$ in univariate analysis were entered into a multivariable model. Given that cases were identified through active tracing and facility records rather than a defined at-risk cohort, no population offset was applied; exponentiated coefficients are therefore presented as count ratios (CR) with 95% confidence intervals. Statistical significance was assessed at a 5% level ($p < 0.05$). All regression analyses were conducted using the MASS package in R.

Seasonal analysis was performed on individual case-level data using enrolment date as a proxy for date of presentation. To account for the known incubation period of *Leishmania tropica* (range 2–8 months; median approximately 4 months), estimated infection dates were calculated by subtracting four months from each patient's enrolment date. Monthly case counts are presented by both enrolment date and estimated infection date to illustrate the relationship between observed presentation patterns and probable transmission timing.

Missing Data

Missing data were observed for several sociodemographic and clinical variables. This was mainly attributable to incomplete documentation in routine paper-based health facility registers, particularly for occupation and education. Household-level exposure data were only obtained for cases successfully traced and consenting to household visits. No data imputation was performed, and analyses were based on available data, with denominators reported for each variable in the respective tables.

RESULTS

Study Population

A total of 174 confirmed leishmaniasis cases were included in the analysis, comprising 159 (91.4%) CL and 15 (8.6%) VL cases. The median age was 13 years (IQR: 6–29). Among cases with available age data (n = 171), the 5–14 years age group accounted for 40.6% (70/171). Students represented the most common occupation category among cases with available data (57/119, 47.9%), while Oltepesi was the most affected village (48/174, 27.6%). Sociodemographic characteristics of the study population are summarised in Table 1.

Case Ascertainment and Community Tracing

For the household survey, Community Health Promoters (CHPs) were provided with 126 cases identified from health facility records and the KaLaAzar mapper dataset for community tracing. During fieldwork, CHPs identified 117 individuals with a history of leishmaniasis. Of these, 66 corresponded to cases listed in the health facility records, while 51 were previously treated cases known to the CHPs but absent from the facility registers. Following data cleaning, one duplicate record was removed, resulting in a final household dataset of 116 unique CL cases for the behavioural and household environmental analyses.

Table 1: Sociodemographic and Anthropometric Characteristics by Diagnosis Type

Variable	Category	CL (n = 159)	VL (n = 15)	Overall (n = 174)
Sex	Female	80 (50.3%)	7 (46.7%)	87 (50.0%)
	Male	79 (49.7%)	8 (53.3%)	87 (50.0%)
Age (years)	Median (IQR)	13 (7–29)	6 (6–12)	13 (6–29)
Age group	0–4	24 (15.1%)	1 (6.7%)	25 (14.4%)
	5–14	61 (38.4%)	9 (60.0%)	70 (40.2%)
	15–24	24 (15.1%)	1 (6.7%)	25 (14.4%)
	25–44	29 (18.2%)	2 (13.3%)	31 (17.8%)
	45+	20 (12.6%)	0 (0.0%)	20 (11.5%)
	Missing	1 (0.6%)	2 (13.3%)	3 (1.7%)
Occupation	Student	55 (34.6%)	2 (13.3%)	57 (32.8%)
	Livestock keeping	24 (15.1%)	0 (0.0%)	24 (13.8%)
	None	32 (20.1%)	1 (6.7%)	33 (19.0%)
	Other	5 (3.1%)	0 (0.0%)	5 (2.9%)
	Missing	43 (27.0%)	12 (80.0%)	55 (31.6%)
Education	None	48 (30.2%)	10 (66.7%)	58 (33.3%)
	Primary+	69 (43.4%)	2 (13.3%)	71 (40.8%)
	Missing	42 (26.4%)	3 (20.0%)	45 (25.9%)
Village	Oltepesi	45 (28.3%)	3 (20.0%)	48 (27.6%)
	Esonorua	20 (12.6%)	9 (60.0%)	29 (16.7%)
	Embolei	17 (10.7%)	0 (0.0%)	17 (9.8%)
	Other	77 (48.4%)	3 (20.0%)	80 (46.0%)

Clinical Characteristics

Visceral Leishmaniasis

Of the 15 VL patients, fever lasting more than two weeks and splenomegaly were each present in 11 patients (84.6%). Severe undernutrition was prevalent, with 12 of 14 patients with BMI data (85.7%) classified as underweight, and a median BMI of 14.2 kg/m² (IQR 12.6–14.6). The majority of VL patients (10/14, 71.4%) received the first-line combination regimen of sodium stibogluconate (SSG) plus paromomycin for 17 days.

Cutaneous Leishmaniasis

Among CL patients, median BMI was 16.3 kg/m² (IQR 14.1–22.2), with 53 of 87 patients with BMI data (60.9%) classified as underweight. The arms were the most common lesion site (46/116, 39.7%), followed by legs (42/116, 36.2%) and face (25/116, 21.6%). The majority of patients presented with a single lesion (85/102, 83.3%). Most CL cases had acute disease with lesion duration of 12 months or less (106/116, 91.4%). Intravenous SSG was the most frequently used treatment regimen (82/133, 61.7%). Initial cure was achieved in 88.5% of CL patients; however, treatment completion was incomplete in 25.9% and six-month follow-up was unavailable for 12.1%. Full clinical characteristics are presented in Table 2.

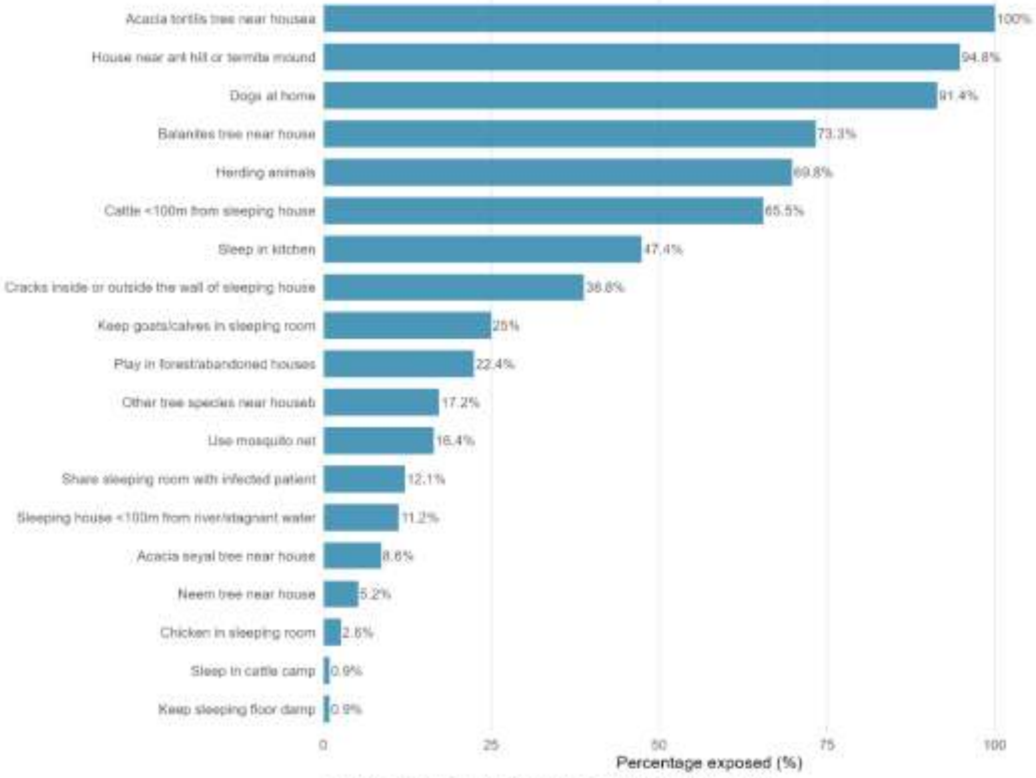
Table 2: Clinical Characteristics by Diagnosis Type

Variable	Categories	Frequency n (%)
Visceral Leishmaniasis (VL), N = 15		
Fever > 2 weeks	Yes	11 (84.6%)
	No	2 (15.4%)
Splenomegaly	Yes	11 (84.6%)
	No	2 (15.4%)
BMI category (n = 14)	Underweight	12 (85.7%)
	Normal	1 (7.1%)
	Overweight	1 (7.1%)
Treatment received (n = 14)	SSG + Paromomycin	10 (71.4%)
	Amphotericin B	3 (21.4%)
	Other	1 (7.1%)
Treatment duration (n = 13)	17 days	9 (69.2%)
	6–10 days	3 (23.1%)
	30 days	1 (7.7%)
Cutaneous Leishmaniasis (CL), N = 159		
BMI category (n = 87)	Underweight	53 (60.9%)
	Normal	22 (25.3%)
	Overweight/Obese	12 (13.8%)
Lesion location (n = 116)	Arms	46 (39.7%)
	Legs	42 (36.2%)
	Face	25 (21.6%)
	Other	3 (2.6%)
Number of lesions (n = 102)	Single	85 (83.3%)
	Multiple	17 (16.7%)
Lesion duration (n = 116)	Acute (≤12 months)	106 (91.4%)
	Chronic (>12 months)	10 (8.6%)
Treatment received (n = 133)	IV SSG	82 (61.7%)
	Intralesional SSG	50 (37.6%)
	Other	1 (0.8%)

SSG = Sodium Stibogluconate. Lesion duration classified as acute (≤12 months) or chronic (>12 months).

Environmental and Behavioural Exposures

Complete household questionnaire data were available for 116 patients. Dogs were present in 91.4% of homes and proximity to termite mounds was reported by 94.8%. Herding was the most common behavioural exposure (69.8%). Only 16.4% of patients used any mosquito net. Regarding housing structure, the majority of patients resided in mud-walled dwellings (74/116, 63.8%), with grass-thatched roofing being the most common roof type (65/116, 56.0%). The most prevalent combined housing structure was mud walls with grass-thatched roofing (62/116, 53.4%). Key exposure frequencies are presented in Figure 1.



a Acacia tortilis: recorded as a checkbox (presence only); absence was not captured,
so 100% reflects the recording method, not universal exposure
b Other tree species: Mathenge (n=2), Oil (n=17), Olangoingoroi (n=1)

Figure 2: Key Household Environmental and Behavioural Exposures among Confirmed CL Cases, Keekonyokie Ward (N = 116)

Environmental Determinants of CL Case Distribution

Village-level negative binomial regression was performed using data from 21 villages. In univariate analysis, daytime land surface temperature (LST) was positively and significantly associated with higher village-level CL case counts (CR 1.300, 95% CI 1.094–1.544, p=0.0028). Mean air temperature showed a similar but non-significant positive association (CR 1.177, 95% CI 0.941–1.472, p=0.154) and was excluded from multivariable modelling due to collinearity with LST. Elevation was inversely and significantly associated with case counts (CR 0.997, 95% CI 0.995–0.999, p=0.0080). NDVI, average monthly precipitation, slope, and population density were not significantly associated with village-level case counts in univariate analysis. In the multivariable model, none of LST (CR 1.180, 95% CI 0.928–1.50, p=0.176), elevation (CR 0.999, 95% CI 0.996–1.00, p=0.432), or population density (CR 0.940, 95% CI 0.656–1.35, p=0.735) reached statistical significance, likely reflecting residual collinearity between LST and elevation (r=−0.69) and limited statistical power (n=21 villages). Full regression results are presented in Table 3.

Table 3: Association between Environmental Variables and CL Case Counts at Village Level Using Negative Binomial Regression (n = 21 Villages)

Environmental Variable	CR	95% CI	p-value
A. Univariate Models (n = 21 villages)			
NDVI	2.576	0.029 – 231.875	0.680
Land surface temperature, day (°C)	1.300	1.094 – 1.544	0.0028**
Mean air temperature (°C)	1.177	0.941 – 1.472	0.154
Average monthly precipitation (mm)	1.000	0.997 – 1.003	0.911
Elevation (m)	0.997	0.995 – 0.999	0.0080**
Slope	0.826	0.557 – 1.224	0.340
Population density (per km²)	0.797	0.580 – 1.095	0.162
B. Multivariable Model – Final (LST + Elevation + Population density)			
Land surface temperature, day (°C)	1.180	0.928 – 1.50	0.176
Elevation (m)	0.999	0.996 – 1.00	0.432
Population density (per km²)	0.940	0.656 – 1.35	0.735

*CR = Count Ratio. Values above 1 indicate positive association with higher case counts; values below 1 indicate inverse association. * p<0.05; ** p<0.01.*

Summary

This study describes the epidemiological, clinical, and environmental characteristics of 174 confirmed leishmaniasis cases in Keekonyokie Ward, Kajiado West Sub-County, Kenya over a four-year period. The outbreak is dominated by cutaneous leishmaniasis (91.4%), disproportionately affects school-age children and students, and is geographically concentrated in the Oltepesi–Esonorua corridor. Household-level exposures are near-universal, including proximity to termite mounds (94.8%), dog ownership (91.4%), and mud-walled housing (63.8%), reflecting the pastoral socioecological context. Treatment completion gaps (25.9% incomplete) and very limited follow-up data represent important programmatic weaknesses. Environmental analysis identified daytime land surface temperature and elevation as the strongest univariate predictors of village-level case counts, consistent with the role of temperature in sandfly biology.

Discussion

This study provides the first integrated socio-demographic, clinical, and environmental characterisation of the ongoing leishmaniasis outbreak in Keekonyokie Ward. Two findings stand out and merit discussion in relation to existing evidence.

First, the marked demographic divergence between CL and VL cases is notable. While CL cases were evenly distributed by sex and skewed toward school-age and young adult patients (median age 13 years), VL cases were considerably younger (median age 6 years), more likely to have no formal education (83.3% vs. 41.0% for CL), and disproportionately concentrated in Esonorua village (60.0% of VL cases vs. 12.6% of CL cases). This pattern is broadly consistent with East African evidence linking VL to younger children with limited outdoor protective behaviour and greater household-level exposure (Geto et al., 2024), but the degree of geographic concentration in a single village suggests a highly localised VL transmission focus distinct from the more dispersed CL distribution across the ward. This divergence supports treating CL and VL as epidemiologically distinct, co-circulating processes within the same ecological setting, consistent with confirmed entomological co-transmission of *L. donovani* and *L. tropica* (Matoke-Muhia et al., 2026), rather than assuming shared risk pathways.

Second, the high prevalence of underweight status among both VL (85.7%) and CL (60.9%) patients indicates that nutritional vulnerability is a shared feature across both disease forms. Among CL patients specifically, this nutritional vulnerability co-occurred with near-universal environmental exposure (termite mounds, 94.8%; dog ownership, 91.4%) and minimal protective behaviour (mosquito net use, 16.4%), illustrating the layered, mutually reinforcing nature of risk in this population. This is consistent with experimental evidence that malnutrition impairs immune competence and increases susceptibility to progression to clinical VL (Ferreira-Paes et al., 2025), and with findings elsewhere in East Africa that nutritional status shapes both disease risk and treatment response in CL (Gashaw et al., 2025). The co-occurrence of high nutritional vulnerability with minimal protective behaviour among CL patients suggests that single-factor interventions are unlikely to be sufficient, reinforcing this study's theoretical framing of transmission as a product of interacting determinants rather than independent risk factors. This interpretation is further supported by the significant univariate associations observed between land surface temperature, elevation, and CL case counts at the village level, which, although attenuated after multivariable adjustment, are consistent with environmental conditions acting alongside behavioural and nutritional factors rather than independently of them.

Limitations

This study has several limitations. First, the retrospective use of routine health facility records was affected by incomplete documentation, which may have introduced information bias in selected sociodemographic and clinical variables. Second, household-level environmental and behavioural exposure data were only available for cutaneous leishmaniasis cases, limiting comparison of exposure profiles across disease forms. Third, the cross-sectional design precludes causal inference between identified risk factors and leishmaniasis occurrence. Finally, referral of visceral leishmaniasis patients to higher-level facilities limited the completeness of follow-up and outcome ascertainment. Despite these limitations, the integration of facility-based data and community household surveys provides a robust description of the epidemiology and environmental determinants of leishmaniasis in the study area.

Conclusion

Persistent leishmaniasis transmission in Keekonyokie Ward disproportionately affects school-age children and is underpinned by near-universal sandfly habitat exposure, very high dog ownership, widespread livestock herding in the absence of protective measures, and poorly sealed housing. Transmission peaks during and immediately following the short rains season (October–December), as inferred from estimated infection dates adjusted for the median incubation period of *L. tropica*. The concentration of cases in a small number of villages, together with the significant association between land surface temperature, elevation, and case counts, supports a geographically and environmentally targeted rather than uniform ward-wide intervention approach.

Recommendations

Theory: These findings support the socio-ecological systems framework by demonstrating that leishmaniasis transmission in Keekonyokie Ward arises from the interaction of host, environmental, and behavioural determinants rather than from any single risk factor in isolation. The attenuation of land surface temperature and elevation after multivariable adjustment, together with the coexistence of widespread environmental exposure and limited adoption of protective behaviours, suggests that future theoretical models should explicitly account for interactions among environmental, household, and behavioural factors instead of considering them as independent pathways.

Practice: Four evidence-based interventions are recommended. First, fine-mesh insecticide-treated bed nets should be prioritised for households in Oltepesi, Esonorua, and Embolei, the three villages accounting for over half of all identified cases. Second, community health promoters should conduct active case-finding in high-burden villages, with particular emphasis on children aged 5–14 years, who represented the most affected age group. Third, community-based health education should target school-aged children and their caregivers, promoting behaviours that reduce exposure to sandfly bites during livestock herding and other outdoor activities, while encouraging early recognition of symptoms and prompt healthcare seeking. Fourth, health facilities should strengthen leishmaniasis surveillance through standardised recording of diagnosis, treatment outcomes, referral status, and follow-up information to improve data completeness and continuity of care.

Policy: County and national health authorities should incorporate environmental risk monitoring, particularly land surface temperature and elevation, into routine leishmaniasis surveillance to enable geographically targeted allocation of prevention and control resources. Community-based treatment follow-up and defaulter tracing should be integrated into county neglected tropical disease (NTD) programmes to improve treatment completion and outcome monitoring. Given the low household ownership of mosquito nets observed in this study, Keekonyokie Ward should be prioritised during future long-lasting insecticidal net (LLIN) distribution campaigns. In addition, a formal referral and feedback mechanism between Oltepesi Health Centre and referral hospitals should be established to ensure complete documentation of treatment outcomes for patients referred for visceral leishmaniasis management.

Future Research: Future studies should include matched community controls and prospective cohort designs to strengthen causal inference regarding household, behavioural, and environmental risk factors for leishmaniasis. Further investigation of the epidemiological role of domestic dogs as potential reservoirs of visceral leishmaniasis through canine serosurveillance is warranted, given the high prevalence of dog ownership observed in the study area. Entomological investigations incorporating sandfly sampling across environmental gradients, together with parasite genotyping, would improve understanding of local transmission dynamics. Formal spatial cluster analysis and ecological niche modelling of case locations, building on the environmental associations identified here, would further help identify fine-scale transmission hotspots and refine geographically targeted intervention strategies. Finally, prospective linkage of community, primary healthcare, and referral facility data should be undertaken to evaluate treatment adherence, referral completion, relapse, and long-term clinical outcomes, thereby strengthening surveillance and informing more effective control strategies.

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