

# The geographical distribution patterns of human *Leishmania* species detected within molecular methods in Iraq: a systematic review and meta-analysis.

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#### **Abstract**

The aim of this reference study on the spread and distribution of various parasites was to aid in the control and treatment of these parasites and save researchers time and effort by providing them with essential and valuable information. This systematic review includes articles related to the detection of Leishmania species through molecular diagnostic methods published in Arabic and English from 2009 to 2021. From five international and local databases Google Scholar, PubMed, Science Direct, Scopus and Iraqi Academic Journals, we extracted 35 papers that satisfied the inclusion criteria and were eligible for systematic review and meta-analysis. This systematic review attempted to answer the following question: Did Leishmania species follow a specific pattern in its geographical distribution in Iraq? The systematic review results show that *Leishmania major* is distributed from the northern provinces (the least prevalent) to the southern provinces (the highest prevalence). On the other hand, L. tropica follows a heterogeneous distribution pattern, which is the highest in the northern and the lowest in the southern regions. The meta-analysis shows the presence of *L.major* in 1226/2542 (48.23%; 95%CI 09.60-101.21) and L.tropica in 1313/2542 (51.65%; 95%CI 29.87-119.56). As a diagnostic method, most articles reported the use of conventional polymerase chain reaction (PCR) or nested-PCR. Most of these used ITS-1 and KDNA as genetic markers. In conclusion, However, the movement of populations (immigration and displacement) among different governorates can sometimes change this distribution curve. The distribution of Leishmania species follows a specific pattern influenced by the presence of the parasite vector and climatic conditions. This pattern maintains *L.tropica* prevalence in the northern regions and *L.major* superiority in the southern regions.

#### **Keywords**

Cutaneous leishmania; visceral leishmania; systematic review; molecular detection; Iraq.

High light

The geographical distribution of Leishmania species is subject to climate factors and the presence of vectors and does not differ from the global geographical distribution.

ACL is prevalent in southern Iraq, while ZCL is more common in central and northern Iraq.

Wasit is the governorate with the most cases of ACL, and Baghdad recorded more cases of ZCL.

The use of molecular detection methods is the best and most appropriate method for parasite diagnosis. Also, the use of ITS1 and kDNA parameters gives more accurate results.

#### Introduction

Leishmaniasis is an epidemic that has infected pupils in over 90 countries. The annual infection rate is 1500000 (1). There are now three types of Leishmaniasis: cutaneous (CL), visceral (VL) and mucocutaneous (MCL). In the old world,

leishmaniasis resulted from one of three species: *Leishmania major, L.tropica* and *L.infantum* (2). Although humans are the common parasite carriers and reservoir hosts, the parasite can also be transmitted by wild animals such as rodents and dogs, which are more common in rural and forested areas (zoonotic infections) (3). The parasite cycle includes two phases: the infective phase (promastigote), which resides in the stomach and salivary glands of the sand fly (*Phlebotomus* spp.), and the amastigote phase, which resides in the definitive host (human) and is later transmitted to mosquitoes after a blood meal (4).

The epidemic geographical distribution and transmission are associated with several factors, including the vector's (sandfly) presence and the migration of people from rural into suburbs or urban (5). In infected pools, mammals constitute a reservoir of parasite-infected animals (6). Rescue changes in environmental conditions and human migration are factors that lead to advance the spread of the epidemic, leading to spatial and temporal changes (7). For example, 40,000 people were infected in Delhi during the early 1940s, but there are rarely any infections in Delhi today (8).

The prevalence of cutaneous leishmaniasis is often underestimated because most official statistics are obtained through an approximate expected survey based solely on the number of patients who visit official health institutions (9). In addition, multiple factors lead to the diagnosis of a faulty or undiagnosed infection, including limited or absent access to diagnostic services to medical facilities (10), epidemiological expansion and the slow progression of the disease. *L.major* produces ulcers near the bite site only, so the spread of these infections is usually late and only into the adjacent skin (causing accompanying lesions). However, these morphological characteristics must be unique to *L. major*, since *L.tropica* have been reported to cause visceral infections (far from bit site) (11).

The presence of an infection is primarily confirmed via optical and microscopic diagnoses. Serology or cultures are also used to detect parasites (12). Although the presence of the parasite can be revealed by all these methods, they cannot be used to identify the species. Precise geographical and epidemiological maps for these species are thus difficult to establish. However, the diagnosis of species and sub-species has produced a genetic tree for this parasite(13).

This systematic review aims to identify the factors affecting the distribution and transmission of Leishmania species in Iraq that are diagnosed by molecular methods.

#### Methods

#### **Search Methodology:**

This systematic review assesses the extent of *Leishmania* spp. distribution in the various provinces of Iraq and attempts to answer the following question: can the geographical location in Iraq influence the distribution of *Leishmania* spp.? We scanned all the articles published in various scientific databases (Google Scholar, PubMed, Science Direct, Scopus and Iraqi Academic Journals) between the years 2009 and 2021. We searched for Medical Subject Heading (MeSH) terms such as Baghdad boil, visceral leishmaniasis, cutaneous leishmaniasis, genotyping, and molecular diagnosis in Iraq using Arabic and English.

#### **Inclusion Criteria:**

Articles discussing Leishmania spp. and meeting the following conditions were included: use of epidemiological and molecular detection methods sole focus on *Leishmania spp.*, no discussion of approaches to therapy or pathology, and published from 2009 to 2021. All documents not fulfilling these conditions were excluded (Fig. 1).





#### **Data Extraction:**

Each of the selected 35 articles was divided into one of two categories: (1 the spread of cutaneous leishmaniasis and (2) the spread of visceral leishmaniasis. From these articles, the following information was extracted: the year of publication, governorate, sample size, infection rate, Leishmania species, the molecular detection method and gene marker.

#### **Statistical Analysis**

To conduct the meta-analysis, we used GraphPad Prism Version 7.

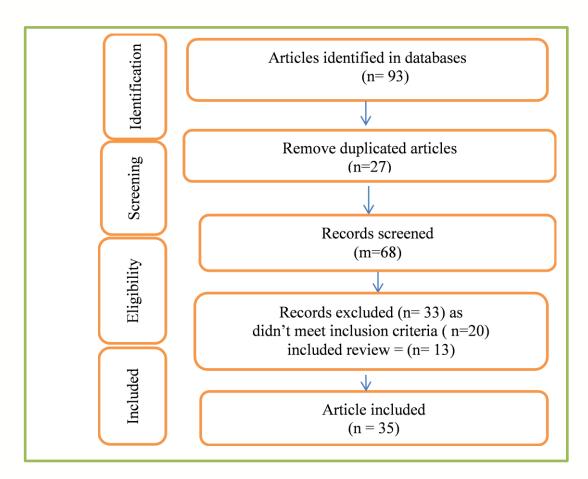


Fig.1 summary diagram of systematic flowing.

#### **Results**

Scanning five scientific databases yielded 93 research papers and 58 articles not meeting the criteria of the study were excluded. A total of 35 studies were evaluated, 33 of which focused on the prevalence of cutaneous leishmaniasis (CL) and two of which dealt with visceral leishmaniasis only (Fig. 1).

In total, 7,842 subjects were examined. Of these, 2,542/7,205 (35.28%) were confirmed to be infected with cutaneous leishmaniasis (Tab. 1) and 190/637 (29.28%) with visceral leishmaniasis (Tab. 2). In the cutaneous leishmaniasis group, patients infected with *L.tropica* were 1,313/2,542 (51.65%, %95CI: 29.87-119.56) with *L.major* were 1,226/2,542 (48.23%, %95CI: 09.60-101.21) (Tab. 5, Fig. 2). In the visceral leishmaniasis group, *L. tropica* was found in 148/190 (77.89%) patients, whereas L. *Infantum* was found in 42/190 (22.11%) patients (Tab. 2).

In Baghdad and the middle provinces, the prevalence of *L. tropica* was higher, whereas L. *major* was more common in the southern and middle - Euphrates (Tab. 3). Wasit had the highest *L.* major prevalence at 262/332 (%95 CI: 0.29-0.354), whereas

Baghdad had the highest *L.tropica* prevalence at 303/426 (%95 CI: 0.13-0.18). *L. aethiopica* was only detected in Tikrit province (3/117) (Tab. 3, Fig. 3). The year 2018 recorded the highest prevalence of 1,071/1,400 (76.5%). Of these, 518 (%95 CI 0.37-0.43) were infected with *L. tropica* and 553 (% 95 CI: 0.42-0.47) with *L. major*. (Fig. 4, Tab. 4).

Skin biopsy was the most common detection procedure, whereas blood samples were used as a detection method in only two research papers. Commercial PCR was used in 11 papers (752 patients) (495 were *L. tropica*: 254 were *L. major*), real-time PCR and RFLP were used twice for all one method, and nested-PCR was used in 17 papers (1,457 patients) (648 were *L. tropica*: 827 were L. *major*)(Tab. 1). The genetic marker ITS-1 was used in 11 papers, the KDNA in 18 papers, and the protein kinase in one paper (Tab. 1).

#### **Discussion**

Leishmaniasis has spread significantly in Iraq in recent years, a total of 8691 cases of infections were reported by the World Health Organization(WHO) in 2020 (14). The reason for this significant increase in infections is the great population growth (15), the presence of vectors and climatic temperature and humidity conditions (16). There are two types of Leishmaniasis (cutaneous and visceral) in Iraq (17). Various methods can be used to detect Leishmania spp. but, it is not possible to differentiate between the types that cause the disease except with the use of the molecular method (18). The goal of this systematic and meta-analysis review was to determine the geographic distribution of *Leishmania* species and to confirm whether this distribution follows a specific pattern.

In Iraq, there have been very few epidemiological studies using molecular methods. The number of papers examined clearly shows this. Perhaps this is because parasitologists depend on the dermatologist's initial diagnosis and rely on cases that reach hospitals without performing a comprehensive survey of the entire region(10). Most of the previous studies aimed to find ways to treat or determine the immunological or physiological effect of the presence of the parasite in the patient's body.

According to the findings of the study, cutaneous leishmaniasis is more common than visceral leishmaniasis in Iraqi provinces. Although the study included 15 out of 18 governorates, the data show that cutaneous leishmaniasis has spread further, while visceral leishmaniasis has been limited because the sand fly (*P. alexandri*) which transmits *L. infantum* is rare in Iraq (19), or the occurrence of the parasite must be transmitted through the blood to infect areas far from the site of the bite for the disease to occur (20). The efforts of the Iraqi Ministry of Health and the World Health Organization, on the other hand, have played a significant role in reducing the prevalence of visceral leishmaniasis (21).

The current systematic review found that the prevalence of *L. tropica* (ZCL) is greater than that of *L. major* (ACL). This is due to the displacement of many people from the northern governorates and their movement to the southern and central regions after the ISIS invasion of Iraq, with many living in unhygienic conditions in the camps, and the proximity of the transmission foci of *L. tropica* on the Iraq\_Iran border, in addition to the presence of parasite vectors (rodents and rats) (22).

The presence of the sandfly is the primary cause of the increase in the rate and spread of the foci of ACL(23). Sandfly species (*P. papatasi*, *P. sergenti and Sergentomiya sentoni*) have been confirmed in southern Iraq by Al-Mayali and Al-Hassani (24). Moreover, a study by Al-Bajalan *et al.* reported that, in addition to other mammalian hosts and vectors, the propagation of the sand fly species *P. papatasi* is



only present in the northern regions (25). All of these factors have influenced the spatial and geographical distribution of cutaneous leishmaniasis in Iraq. The ACL spread is also affected by certain climate factors such as humidity and temperature, which effectively contribute to the vitality and spread rate of the parasite (26).

Even in a single province, the distribution of cutaneous leishmaniasis continues geographically and spatially. The prevalence rate of ACL is higher in each of the southern provinces than that of ZCL, and vice versa in the central and northern provinces. The growing population and the displacement of many residents in other provinces is the cause of the high infection rate in Baghdad (27) and of the surging waves after the ISIS invasion. Wasit province (southeast of Baghdad) exhibits the highest number of ACL infections due to the presence of parasite vectors (28). Most of the governorate's areas border on Iran (29). In addition, studies in this governorate examined large numbers of infected people. The highest prevalence rate of leishmaniasis was in 2018, because we adopted only molecular studies and the number of research papers in this year was more, this finding does not agree with what was published by the World Health Organization (2).

In systemic testing, two genetic markers, ITS1 and kDNA have been reported in the majority of previous studies, with a tendency to use KDNA more often. Previous studies indicated that the sensitivity of kDNA is higher than that of ITS-1 and that it can detect fewer than 200 DNA copies. Therefore, the use of either primer gives a better diagnostic result(30).

#### Conclusion

The present review concluded that the Leishmania species' spatial and geographical distribution is a result of climate change and parasite vector presence. This distribution does not differ in the prevalence of Leishmania species from the general distribution. The review is a database allowing the number of infections in Iraqi regions over several years to be estimated by researchers and by epidemiological studies interested. It's not new to say that molecular diagnosis is the best approach. The most suitable diagnosis is the use of genetic markers ITS1 and kDNA.

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Tab.1 Characteristics of the cutaneous leishmania species identified in systematic review from 2009 – 20121.

Hassan Z. I. (31)				,	rom 200	)9 – 20121					
Hassan Z. I. (31)   2018   Erbil   Skin biopsy   58   58   58   0   0   PCR   ITS-1	Author	Year	Province	type of	total	infected	L.	L.	L.	method	Gene
Hassan Z. I. (31)   2018   Erbit   Skin biopsy   58   58   58   0   0   PCR   ITS-1   Vaulini and Al-   2020   Balybind   Skin biopsy   275   68   42   26   0   PCR   BDNA   Vousir (41)   Rasheed et al. (35)   2018   Baghdad   Skin biopsy   75   68   42   26   0   Real-time   PCR   PCR				sample			tropica	major	aethio		marker
Hassan Z. I. (31)   2018				-			•		pica		s
Rashlim and Al- Qualish (20)   Babylon   Skin biopsy   215   178   141   37   0   Nested.   FCR   Quarish (32)   Qualer, stul. (33)   2009   Baghdad   Skin biopsy   27   2   0   2   0   PCR   KDNA   Younis and Al- 2018   Baghdad   Skin biopsy   75   68   42   26   0   Real-Time   KDNA   FCR   KDNA   Thwani (34)   2018   Baghdad   Skin biopsy   75   68   42   26   0   Real-Time   KDNA   FCR	Hassan Z. I. (31)	2018	Erbil	Skin biopsy	58	58	58	0	_	PCR	
Quarishit(32)											
Description   Color		2020	Daoyion	Skin olopsy	213	170	141	37			115 2
Vounis and Al-	` ` ` `	2000	Doobdod	Clain biomara	27	2	0	2	0		1-DNIA
Rasheed et al. (35)   2018   Baghdad   Blood samples   90   82   63   19   0   Nested-Rahamed (37)   Noori, et al., (36)   2020   Baghdad   Skin biopsy   88   82   57   25   0   PCR   mm   PCR   P											
Rasheed et al. (35)   2018   Baghdad   Blood samples   Skin biopsy   90   82   63   19   0   Nested-Rando   PCR   Muhammed (37)   2020   Baghdad   Skin biopsy   88   82   57   25   0   PCR   ITS-1   Muhammed (37)   2021   Baghdad   Skin biopsy   88   82   57   25   0   PCR   ITS-1   Muhammed (37)   2020   Baghdad   Skin biopsy   44   42   30   12   0   Nested-PCR   Rando   PCR   Muhammed (37)   2020   Baghdad   Skin biopsy   44   42   30   12   0   Nested-PCR   Rando   PCR   Muhammed (37)   2020   Baghdad   Skin biopsy   50   40   26   14   0   Nested-PCR   Rando   PCR   Muhammed (37)   PCR   ITS-1   PCR		2018	Baghdad	Skin biopsy	75	68	42	26	0		kDNA
Yousif, et al., (36)   2020   Baghdad   Skin biopsy   90   82   63   19   0   Nested-PCR   m	` /										
Younis and Muhammed (37)	Rasheed et al. (35)	2018	Baghdad		150	150	120	30	0	PCR	KDNA
Muhammed (37)	Yousif, et al., (36)	2020	Baghdad	Skin biopsy	90	82	63	19	0		Rando m
Muhammed (37)	Younis and	2021	Baghdad	Skin biopsy	88	82	57	25	0	PCR.	ITS-1
Noori, et al., (38)   2017   Baghdad   Skin biopsy   44   42   30   12   0   Nested-   FCR			$\mathcal{C}$	1 3						· ·	
Hawas, et al., (39)   2020   Baghdad (displaced)*   Skin biopsy   50   40   26   14   0   Nested-PCR	` ′	2017	Raghdad	Skin biopsy	44	42	30	12	0		KDNA
Hawas, et al., (39)   2020   Baghdad (displaced)*   Skin biopsy   50   40   26   14   0   Nested-PCR   ITS-1	1,0011, et al., (50)	2017	Bugildud	Skin olopsy	7-7	72	30	12			INDIVI
Al-Jubori, et al., (40)   2019   Baghdad and Tikrit   Skin biopsy   117   117   87   27   3   PCR   ITS-1	Hawas at al. (20)	2020	Doobdod	Clain biomera	50	40	26	1.4	0		ITC 1
Al-Jubori, et al., (40)   2019   Baghdad and Tikrit   2020   Diyala   Skin biopsy   30   30   17   13   0   Nested-PCR   TIS-1	Hawas, et al., (39)	2020		Skin biopsy	50	40	26	14	U		112-1
Al-Ghabban, et al.,   2020   Diyala   Skin biopsy   30   30   17   13   0   Nested-PCR	11 1 1 1 (10)	2010		G1 : 1 :	445	445	0.7	25			TERM 4
Canal.   C	Al-Jubori, et al., (40)	2019		Skin biopsy	117	117	87	27	3	PCR	ITS-1
Seaad, et al., (42)   2017   Qadisiyah (displaced)   Qadisiyah (displaced)   Qadisiyah (displaced)   Qadisiyah   Blood samples   Seaamples   Seaampl		2020	Diyala	Skin biopsy	30	30	17	13	0		ITS-1
Al-Difaie and Jasim (43)		2017	Oadicivah	Skin bioney	4007	62	41	21	Λ		Pando
Al-Difaic and Jasim (43)	Seaau, et al., (42)	2017		Skill blopsy	4007	02	41	21	U	rck	
Mohammad and Hmood (44)	ALDIC: LT	2017		D1 1		40	22	27	0	DCD	
Mohammad and Hmood (44)		2017	Qadisiyah		55	49	22	27	0	PCR	KDNA
Hmood (44)	` ,										
Bablkadhim, S.J. (45)   2018   Qadisiyah   Skin biopsy   145   38   10   28   0   Nested-PCR   KDNA		2018	Qadisiyah	Skin biopsy	50	42	7	35	0		Rando
Jabbar, et al., (46)   2019   Thi Qar   Skin biopsy   50   48   0   48   0   Nested-PCR   KDNA   PCR   Flaih, et al., (47)   2021   Thi Qar   Skin biopsy   80   65   46   19   0   Nested-PCR   KDNA   PCR   Al-Fahdawi, et al.,   2018   Anbar   Skin biopsy   122   62   42   20   0   RFLP   TTS-1   (48)   Al-Bajalan, et al.,   2018   Sulaimaniyah   Skin biopsy   30   15   0   15   0   PCR   TTS-1   (49)   Hamza, et al., (50)   2019   Karbala   Skin biopsy   92   92   0   92   0   PCR   TTS-2   Hassan, et al., (51)   2020   Kirkuk   Skin biopsy   200   143   143   0   0   PCR   KDNA   Al-Lamy and Al-Lamy and Al-Abady (52)   AL-Hucheimi, et al.,   2015   Najaf   Skin biopsy   80   40   25   15   0   Nested-PCR   KDNA   (53)   AL-Hucheimi, et al.,   2009   Najaf   Skin biopsy   83   52   7   45   0   Nested-PCR   KDNA   PCR   Ali and Al-Hadrawy   2019   Najaf   Skin biopsy   57   37   16   21   0   Nested-PCR   KDNA   PCR   (54)   Ali and Al-Hadrawy   2019   Najaf   Skin biopsy   60   33   10   23   0   Nested-PCR   KDNA   PCR   Ali, et al., (56)   2018   Different**   Skin biopsy   60   33   233   350   0   Nested-PCR   Rahi, et al., (57)   2013   Wasit   Skin biopsy   64   44   16   28   0   PCR   TTS-1   Rahi, AA. (58)   2014   Wasit   Skin biopsy   60   53   11   42   0   Real-Time   RCNA   PCR   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR	Hmood (44)									PCR	m
Jabbar, et al., (46)   2019   Thi Qar   Skin biopsy   50   48   0   48   0   Nested- RDNA	abdlkadhim, S.J. (45)	2018	Qadisiyah	Skin biopsy	145	38	10	28	0	Nested-	KDNA
Jabbar, et al., (46)   2019   Thi Qar   Skin biopsy   50   48   0   48   0   Nested-PCR	, , ,			1 3							
Flaih, et al., (47)   2021   Thi Qar   Skin biopsy   80   65   46   19   0   Nested-PCR	Jabbar et al. (46)	2019	Thi Oar	Skin biopsy	50	48	0	48	0		KDNA
Flaih, et al., (47)   2021   Thi Qar   Skin biopsy   80   65   46   19   0   Nested-PCR	340041, et al., (10)	2017	Till Qui	Skin olopsy	30	10	O	10			INDIVI
Al-Fahdawi, et al.,   2018   Anbar   Skin biopsy   122   62   42   20   0   RFLP   ITS-1	Elaib at al. (47)	2021	Thi Oan	Clain biomer	90	65	16	10	0		KDMA
Al-Fahdawi, et al., (48)	Frain, et al., (47)	2021	1 m Qar	Skin biopsy	80	65	46	19	U		KDNA
Al-Bajalan, et al.,   2018   Sulaimaniyah   Skin biopsy   30   15   0   15   0   PCR   ITS-1											
Al-Bajalan, et al., (49)	, ,	2018	Anbar	Skin biopsy	122	62	42	20	0	RFLP	ITS-1
Hamza, et al., (50)   2019   Karbala   Skin biopsy   92   92   0   92   0   PCR   ITS-2	(48)										
Hamza, et al., (50)   2019   Karbala   Skin biopsy   92   92   0   92   0   PCR   ITS-2	Al-Bajalan, et al.,	2018	Sulaimaniyah	Skin biopsy	30	15	0	15	0	PCR	ITS-1
Hassan, et al., (51)   2020   Kirkuk   Skin biopsy   200   143   143   0   0   PCR   KDNA	(49)		•								
Hassan, et al., (51)   2020   Kirkuk   Skin biopsy   200   143   143   0   0   PCR   KDNA	Hamza, et al., (50)	2019	Karbala	Skin biopsy	92	92	0	92	0	PCR	ITS-2
Al-Lamy and Al-Abady (52)  AL- Hucheimi, et al., (53)  AL- Hucheimi, et al., (55)  Ali and Al-Hadraawy (55)  Ali, et al., (57)  Rahi, AA. (58)  Al-Hucheimi, et al., (2015)  Al-Hucheimi, et al., (2015)  Ali maysan  Skin biopsy  Skin biopsy  Skin biopsy  Skin biopsy  Skin biopsy  Skin biopsy  Ali and Al-Hadraawy  Ali, et al., (56)  Ali, et al., (57)  Ali and Al-Hadraawy  Ali, et al., (57)  Ali and Al-Hadraawy  Ali and Al-Hadraawy											KDNA
Abady (52)											
AL- Hucheimi, et al., (53)         2015         Najaf (53)         Skin biopsy (53)         83         52         7         45         0         Nested-PCR (50)         KDNA PCR (53)           AL- Hucheimi, et al., (54)         2009         Najaf (54)         Skin biopsy (57)         37         16         21         0         Nested-PCR (50)         KDNA PCR (54)           Ali and Al-Hadraawy (55)         2019         Najaf (55)         Skin biopsy (58)         60         33         10         23         0         Nested-PCR (50)         KDNA PCR (50)           Ali, et al., (56)         2018         Different**         Skin biopsy (58)         233         350         0         Nested-PCR (50)         Nested-PCR	-	2021	Maysan	Skill blopsy	80	40	23	13	U		KDNA
AL- Hucheimi, et al.,   2009   Najaf   Skin biopsy   57   37   16   21   0   Nested-PCR   KDNA   (54)   Ali and Al-Hadraawy   2019   Najaf   Skin biopsy   60   33   10   23   0   Nested-PCR   KDNA   (55)   Ali, et al., (56)   2018   Different**   Skin biopsy   700   583   233   350   0   Nested-PCR   ITS-1   Rahi, et al., (57)   2013   Wasit   Skin biopsy   64   44   16   28   0   PCR   ITS-1   Rahi, AA. (58)   2014   Wasit   Skin biopsy   60   53   11   42   0   Real-Time   KDNA   PCR   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Rahi, AA. (59)   2015   Wasit   Skin biopsy   46   20   8   12   0   PCR   KDNA   Candidate   Candida		2015	N. C	C1: 1:	02	<b>50</b>	7	4.5	0		IZDALA
AL- Hucheimi, et al., (54)         2009         Najaf (54)         Skin biopsy (57)         37         16         21         0 Nested PCR         KDNA PCR           Ali and Al-Hadraawy (55)         2019         Najaf Skin biopsy (55)         60         33         10         23         0 Nested KDNA PCR           Ali, et al., (56)         2018         Different**         Skin biopsy (700)         583         233         350         0 Nested PCR           Rahi, et al., (57)         2013         Wasit         Skin biopsy (64)         44         16         28         0 PCR         ITS-1 PCR           Rahi, AA. (58)         2014         Wasit         Skin biopsy (60)         53         11         42         0 Real-Time KDNA PCR           Rahi, AA. (59)         2015         Wasit         Skin biopsy (46)         20         8         12         0 PCR         KDNA		2015	Najat	Skin biopsy	83	52	/	45	U		KDNA
(54)         PCR           Ali and Al-Hadraawy (55)         2019         Najaf         Skin biopsy (50)         33         10         23         0         Nested- KDNA PCR           Ali, et al., (56)         2018         Different**         Skin biopsy (700)         583         233         350         0         Nested- PCR           Rahi, et al., (57)         2013         Wasit         Skin biopsy (64)         44         16         28         0         PCR         ITS-1           Rahi, AA. (58)         2014         Wasit         Skin biopsy (60)         53         11         42         0         Real-Time KDNA PCR           Rahi, AA. (59)         2015         Wasit         Skin biopsy (46)         20         8         12         0         PCR KDNA											
Ali and Al-Hadraawy (55)         2019         Najaf (55)         Skin biopsy (55)         60         33         10         23         0         Nested-PCR (KDNA)           Ali, et al., (56)         2018         Different**         Skin biopsy (700)         583         233         350         0         Nested-PCR (ITS-1)           Rahi, et al., (57)         2013         Wasit         Skin biopsy (64)         44         16         28         0         PCR (ITS-1)           Rahi, AA. (58)         2014         Wasit         Skin biopsy (60)         53         11         42         0         Real-Time (KDNA)           Rahi, AA. (59)         2015         Wasit         Skin biopsy (46)         20         8         12         0         PCR (KDNA)	AL- Hucheimi, et al.,	2009	Najaf	Skin biopsy	57	37	16	21	0		KDNA
(55)         PCR           Ali, et al., (56)         2018         Different**         Skin biopsy         700         583         233         350         0         Nested-PCR           Rahi, et al., (57)         2013         Wasit         Skin biopsy         64         44         16         28         0         PCR         ITS-1           Rahi, AA. (58)         2014         Wasit         Skin biopsy         60         53         11         42         0         Real-Time KDNA PCR           Rahi, AA. (59)         2015         Wasit         Skin biopsy         46         20         8         12         0         PCR         KDNA	(54)									PCR	
(55)         PCR           Ali, et al., (56)         2018         Different**         Skin biopsy         700         583         233         350         0         Nested-PCR           Rahi, et al., (57)         2013         Wasit         Skin biopsy         64         44         16         28         0         PCR         ITS-1           Rahi, AA. (58)         2014         Wasit         Skin biopsy         60         53         11         42         0         Real-Time KDNA PCR           Rahi, AA. (59)         2015         Wasit         Skin biopsy         46         20         8         12         0         PCR         KDNA	Ali and Al-Hadraawy	2019	Najaf	Skin biopsy	60	33	10	23	0	Nested-	KDNA
Ali, et al., (56)         2018         Different**         Skin biopsy         700         583         233         350         0         Nested-PCR           Rahi, et al., (57)         2013         Wasit         Skin biopsy         64         44         16         28         0         PCR         ITS-1           Rahi, AA. (58)         2014         Wasit         Skin biopsy         60         53         11         42         0         Real-Time KDNA PCR           Rahi, AA. (59)         2015         Wasit         Skin biopsy         46         20         8         12         0         PCR         KDNA	· · · · · · · · · · · · · · · · · · ·		3								
Rahi, et al., (57)   2013   Wasit   Skin biopsy   64   44   16   28   0   PCR   ITS-1	` '	2018	Different**	Skin biopsy	700	583	233	350	0		ITS-1
Rahi, et al., (57)       2013       Wasit       Skin biopsy       64       44       16       28       0       PCR       ITS-1         Rahi, AA. (58)       2014       Wasit       Skin biopsy       60       53       11       42       0       Real-Time KDNA PCR         Rahi, AA. (59)       2015       Wasit       Skin biopsy       46       20       8       12       0       PCR       KDNA	7111, 61 al., (56)	2010	Different	Skin cropsy	, 00	505	233	330			115 1
Rahi, AA. (58)       2014       Wasit       Skin biopsy       60       53       11       42       0       Real-Time PCR       KDNA         Rahi, AA. (59)       2015       Wasit       Skin biopsy       46       20       8       12       0       PCR       KDNA	Dah: at al. (57)	2012	Wesit	Claire Initiation	C 1	4.4	1.0	20	0		ITC 1
Rahi, AA. (59)         2015         Wasit         Skin biopsy         46         20         8         12         0         PCR         KDNA											
Rahi, AA. (59) 2015 Wasit Skin biopsy 46 20 8 12 0 PCR KDNA	Kanı, AA. (58)	2014	wasit	Skin biopsy	60	53	11	42	0		KDNA
										PCR	KDNA
Al-Tamemy and Al-   2017   Wasit   Skin biopsy   80   68   7   61   0   Nested-   KDNA	Al-Tamemy and Al-	2017	Wasit	Skin biopsy	80	68	7	61	0	Nested-	KDNA

Winta / College									- Will	
Qurashi (60)									PCR	
Al-Khanaq, MN (61)	2018	Wasit	Skin biopsy	70	55	6	49	0	Nested-	KDNA
									PCR	
Rahi, et al., (62)	2019	Wasit	Skin biopsy	60	42	4	38	0	Nested-	KDNA
									PCR	
Faieq, ZA(63)	2019	Wasit	Skin biopsy	70	50	18	32	0	RT-PCR	KDNA

<sup>\*</sup> from Ninawa and salahalddin provinces.

Tab.2. Characteristics of the vescieral leishmania species identified in systematic review.

Author	Year	Province	type of	total	Infected	L.	L.	method	Gene
			sample			tropica	infantum		markers
Al-Mishry, et	2013	Basrah	Blood	50	42	0	42	PCR	KDNA
al. (64)									
Al-Hussaini,	2017	Najaf	Blood	587	148	148	0	Nested-	KDNA
et al. (65)								PCR	

Tab.3 Meta-analysis of cutaneous leishmania species in different provinces.

Province	Total	infected	L. tropica	%95 CI	L. major	595 CI
Erbil	58	58	58	0.05 -	0	0 –
				0.083		0.004
Babylon	215	178	141	0.134 -	37	0.033 -
				0.18		0.062
Baghdad	474	426	303	0.307 -	114	0.117 -
				0.37		0.165
Diyala	30	30	17	0.011 -	13	0.009 -
				0.03		0.027
Qadisiyah	250	129	19	0.013 -	90	0.09 -
				0.033		0.134
Thi Qar	130	113	46	0.038 -	67	0.065 -
				0.067		0.103
Anbar	122	62	42	0.034 -	20	0.015 -
				0.063		0.037
Sulaimaniyah	30	15	0	0 -	15	0.011 -
				0.004		0.030
Karbala	92	92	0	0 -	92	0.093 -
				0.004		0.136
Kirkuk	200	143	143	0.136 -	0	0 -
				0.184		0.005
Maysan	80	40	25	0.018 -	15	0.011 -
				0.040		0.030
Najaf	200	122	33	0.026 -	89	0.089 -
				0.051		0.132
Wasit	450	332	70	0.062 -	262	0.290 -
				0.097		0.354
			P.valu<0.001	1.256 -	P.valu<0.001	0.857 -
				1.167		0.796

<sup>\*\*</sup> Qadisiyah 88, Wasit 85, Najaf 79, Thi-Qar76, Basrah 67, Baghdad 65, Diyala 63, and Tikrit 60.





Tab. 4. Meta-analysis of cutaneous leishmania species among study years.

				<u> </u>	<u> </u>	
Year	Total	infected	L.tropica	%95CI	L. major	%95CI
2009	84	39	16	0.007 - 0.0201	23	0.012 - 0.028
2013	64	44	16	0.007 - 0.0201	28	0.015 - 0.032
2014	60	53	11	0.004 - 0.0152	42	0.025 - 0.045
2015	129	72	15	0.007 - 0.0191	57	0.036 - 0.059
2017	4186	221	80	0.050 - 0.0768	121	0.083 - 0.116
2018	1400	1071	518	0.376 - 0.4305	553	0.423 - 0.479
2019	449	382	119	0.078 - 0.1097	260	0.190 - 0.235
2020	585	473	381	0.272 - 0.3222	83	0.054 - 0.083
2021	248	187	128	0.084 - 0.1172	59	0.037 - 0.061
			P. value < 0.0001	2.61 - 2.67	P.value	1.023 - 1.044
					< 0.0001	

Tab.5 Meta-analysis publication bias of cutaneous leishmania species.

140.	1 ab. 5 Wicta analysis publication bias of cutaneous leisimaina species.									
Parameters	Total	Rate (%95 CI)		Het	Egger's test					
			df	P.	Cochran	I2	E.	p.		
				value	Q		bias	value		
L. tropica	1313	51.65%(29.87-	32	1.00	.00	0.00%	2.574	<		
		119.56)						0.0001		
L. major	1226	48.23%(09.60-	32	1.00	0.00	0.00%	18.6	<		
		101.21)						0.0001		

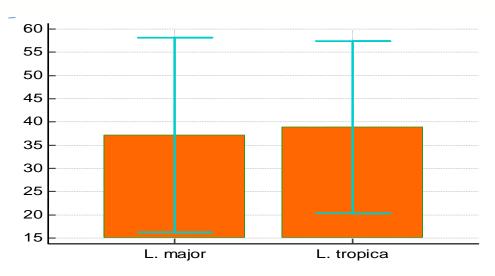


Fig.2. diagram of cutaneous leishmania species prevalence.



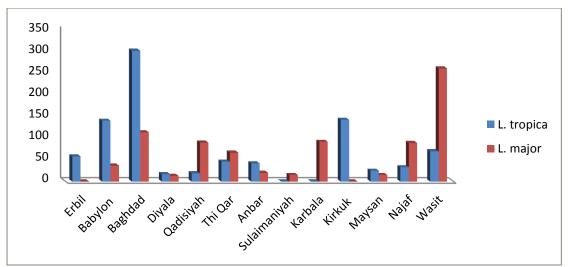


Fig. 3 Distribution of Leishmania species in different provinces.

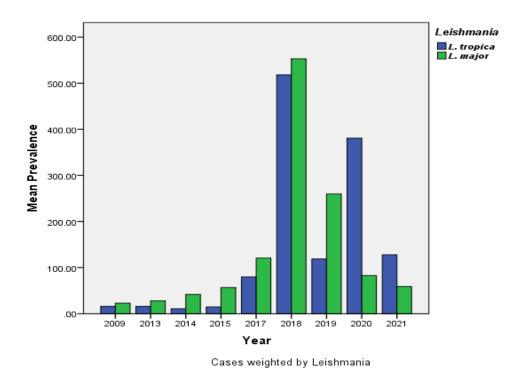


Fig. 4. Prevalence of Leishmania species among study years.