

Meta-analysis and discussion on challenges to translate Leishmania drug resistance phenotyping into the clinic

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1 Review Meta-analysis and discussion on challenges to translate 2 Leishmania drug resistance phenotyping into the clinic 3 4 5 6 7 8 9 Denis Sereno^{1,2*}, Zoubir Harrat³, Naouel Eddaikra³ 10 ¹ IRD, Univ Montpellier, MIVEGEC, Montpellier, France; 11 ² IRD, Univ Montpellier, InterTryp, Montpellier, France; denis.sereno@ird.fr. 12 ² Laboratory of Eco-epidemiology and Parasitic Population Genetics, Pasteur Institute of Algier, Algier, 13 Algeria; zharrat@gmail.com, neddaikra@yahoo.fr. 14 15 * Correspondence: denis.sereno@ird.fr; Tel.: +33-046-741-6328 16 17 18

Abstract

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Antimicrobial resistance (AMR) threatens the prevention and treatment of infections caused by a large range of microorganisms. Leishmania is not an exception and treatment failure due to drug-resistant organisms is increasingly reported. Currently, no molecular methods and marker are validated to track drug-resistant organism and antimicrobial susceptibility tests are roughly not amenable to a clinical setting. Taking these facts into account, it is essential to reflect on ways to translate basic knowledge into methodologies aimed to diagnose leishmania drug resistance. As a matter of fact, a meta-analysis of the literature discloses the reliability of the promastigotes antimicrobial susceptibility tests (AST) to predict intracellular amastigotes susceptibility status. Promastigote cultures that are easy to perform, typically inexpensive and amenable to standardization should represent a candidate to diagnose resistance. Using AST performed on promastigote, we propose a way to improve leishmania drug resistance diagnosis in the framework of guidance and guideline of the bacterial drug resistance diagnosis. In this review, we highlight challenges that remained and discuss the definition of clinical breakpoints, including the epidemiological cutoff (ECOFF), to track drug-resistant isolates. Our analysis paves the ways to standardize and analyze anti-leishmania susceptibility tests output in order to guide the characterization of drug-resistant isolates, the clinical decision during treatment and the search for new molecular markers.

Leishmaniases are caused by obligate unicellular eukaryote parasites belonging to the genus Leishmania (Trypanosomatida: Trypanosomatidae). There are twenty-one Leishmania species with documented pathogenicity in humans (Akhoundi et al., 2016). These digenetic or heteroxenous parasites have a life cycle that involves two hosts, a vertebrate and an invertebrate (the sandfly). Infection is initiated when metacyclic promastigotes are regurgitated by sandflies having a blood meal on a vertebrate host. The clinical manifestations of leishmaniasis range from simple or diffuse cutaneous leishmaniasis (CL), mucocutaneous (MCL), mucosal (ML), post-Kala-azar dermal (PKDL) and visceral (VL) leishmaniasis (Akhoundi et al., 2017). These diseases rank after malaria in term of annual incidence and affect 98 countries and territories worldwide. Visceral leishmaniasis kill between 20 000 to 30 000 persons annually, 1 millions cutaneous leishmaniasis cases reported during the past 5 years and, over 1 billion peoples living in endemic area at risk of infection (Alvar et al., 2012; http://www.who.int/leishmaniasis/en/). Heterogeneity in clinical presentation, disease progression, complications and the response to treatment with various etiological agents of patients with leishmaniasis, makes the choice of therapy sometimes problematic. Guidelines for the treatment of the different clinical forms are published and include only a few a drugs: meglumine antimoniate, sodium stibogluconate, amphotericin B, miltefosine, pentamidine and paromomycin (Aronson et al., 2016; Gradoni et al., 2017; Uliana et al., 2017; Alves et al., 2018). The broad antimicrobial activity of Sb-containing compounds was investigated at the same time as the discovery of their antileishmanial and antitrypanosomal activities (Camac 1911); these compounds are currently the first-line drugs in most parts of the world. In 1997, the first indication of therapeutic failure related to leishmania drug-resistant isolates was reported in the northern Bihar province of India are now problematic (Lira et al., 1999). Amphotericin B (AmB), initially described as an alternative to Sb for the treatment of MCL, has also been successfully used to treat severe VL and HIV/Leishmania coinfection (Uliana et al., 2017). Therapeutic failure or relapse after treatment is reported but currently rare (Purkait et al., 2012; Pandey et al., 2012). Currently, AmB (especially in its liposomal form) is now recommended by the World Health Organization and by the

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main scientific societies as the first line drug to treat any form of VL worldwide, not only severe or HIV-associated conditions but also in children and immunocompetent adults. Miltefosine is the sole registered oral drug effective against leishmaniasis. Since its registration in India in 2002, a clinical decrease in its efficacy has been reported (Dorlo et al., 2012). Pentamidine is a second-line drug for the management of Sb-resistant VL cases, but its cure rate is inferior to that of amphotericin B (Mishra et al., 1992). Additionally, the toxicities associated with pentamidine (cardiac toxicity, diabetes mellitus, hypotension, and gastrointestinal side effects) limit its use. Paromomycin, an aminoglycoside antibiotic, was rediscovered as an antileishmanial agent for the treatment of VL in the 1980s (Jha et al., 1998), but its clinical use remains limited.

In recent decades, the rise of antibiotic-resistant bacteria and the extensive use of antibiotics have led to a global public health crisis that has prompted considerable efforts to standardize guidance related to antibiotic-resistant bacteria (http://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance). Unfortunately, neglected tropical infectious diseases, such as leishmaniasis, have not yet been included in these efforts, even if leishmania resistance are reported with increasing frequency and will certainly pose future challenges (Ponte-Sucre et al., 2017). Here, we performed a meta-analysis of information related to the susceptibility of leishmania parasites to the main molecules used to treat leishmaniasis and propose ways to translate drug resistance phenotyping into the clinical setting, within the framework of the well-defined guidelines of the bacterial antibiotic resistance.

2. Leishmania drug resistance diagnosis: Where are we?

Drug resistance and therapeutic failure are not synonymous. Therapeutic failure encompasses an ensemble of factors linked to the host (i.e Genetic, Immunologic...) to the infective agent (i.e Drug resistance...), to the drugs (i.e pharmacodynamics/pharmacokinetic...) and, to the chemotherapeutic protocol. Nevertheless, the first indication that informs a clinician on the therapeutic choice is the drug

resistance status of the isolate. A schematic representation of the protocols that can be used is given in figure 1.

To carry AST, isolates from needle aspirates, punch biopsies, or blood samples are usually subjected to initial cultivation in a diphasic agar medium, such as NNN medium (reviewed in Evans DA, 1987) (Figure 1). Once established in this medium, parasites must be transferred into a semi-defined culture medium (reviewed in Schuster and Sullivan, 2002). Considering the workflow described in Figure 1, 4 to 30 days after biopsy are required to isolate promastigotes in culture. If the *in vitro* test is performed on the promastigote stage of the parasite, then another 3 days is required. For tests performed on intracellular amastigotes, after the initial proliferation phase in biphasic medium, parasites are transferred into a semi-defined medium, to obtain homogeneous populations of metacyclic promastigotes that are used to infect host macrophages, at a determined host cell/parasite ratio (Inocêncio da Luz et al., 2009). Infected macrophages are then incubated for 5 days (Maes et al., 2013).

The use of molecular markers of resistance has the advantages of being faster and not requiring parasite isolation and cultivation (Figure 1). As a matter of fact, currently no molecular markers are available to diagnose drug resistance in clinical settings.

3.1. Molecular marker

An exhaustive review of molecular mechanisms and markers of resistance was recently published (Ponte-Sucre et al., 2017). Here, we will highlight some key points for translating basic research on mechanisms of leishmania drug-resistance into clinical applications. Most Indian Sbresistant *L. donovani* isolates present molecular adaptations that were initially characterized in experimentally selected Sb-resistant strains. First, they present an intrachromosomal amplification of the 'H-Locus', which encodes MRPA, an ABC transporter that sequesters Sb within a vacuole after its conjugation with trypanothione (Leprohon et al., 2009). A second mechanism involves limiting the entry of Sb. In Leishmania, this metalloid enters via an AQP1 transporter. Modulation of AQP1 levels

prompted the emergence of resistant leishmania strains (Marquis et al., 2005). The level of AQP1 activity as an Sb transporter is abolished in isolates with a homozygous two-base pair insertion in the AQP1 sequence; this insertion is linked to some highly Sb-resistant field isolates (Marquis et al., 2010). Hybrid strains with intermediate Sb susceptibility are heterozygous for the AQP1 insertion (Imamura et al., 2016). Experimental selection for miltefosine resistance identified inactivating mutations or deletions in the MIL translocation machinery (LMT and/or LROs3) (Perez-Victoria et al., 2006). Mutations in LMT (2 sense mutations) are documented in *L. donovani* (Mittal et al., 2007; Cojean et al., 2012) and *L. infantum* (Mondelaers et al., 2016). Amphotericin B-resistant field isolates are scarce, mainly because of the high efficacy of this molecule in treating leishmania infection (Cojean et al., 2012). Experimental selection for amphotericin B resistance highlighted a change in the sterol composition of the membrane of drug-resistant organisms (Mbongo et al., 1998).

3.2. Antimicrobial susceptibility test (AST)

To perform AST (Box 1), living parasites must be isolated from biopsies to measure susceptibility of the isolates, then the diagnosis is empirical and relies on direct isolate-to-isolate comparisons (Mittal et al., 2007; Srivastava et al., 2017). A tentative plan for the standardization of antileishmanial testing processes was proposed (Maes et al., 2013; Hendrickx et al., 2016).

Intracellular amastigotes mimic the conditions encountered by the parasite in a human infection, they are considered as the ideal form to assay. The determination of drug activity model involves staining the slide and counting the mean number of intracellular amastigotes. The method is labor intensive and requires skilled individuals. The use of reporter gene technologies enable an easy and quick quantification of parasites within host cells, reduce the time to measure the intracellular burden of leishmania, and eliminate bias due to manual counting (Sereno et al., 2007; Dube et al., 2009; Lang et al., 2009; Singh et al., 2009; De La Llave et al., 2011; Michel et al., 2011; Pulido et al., 2012; Jaiswal et al., 2016). The ability of these technologies to ascertain the drug susceptibility of field isolates was probed (Hadighi et al., 2006; Lachaud et al., 2009). Indeed, the time required for the

selection of recombinant parasites limits its interest in the clinic. Progress in microscopy imaging techniques and methodologies for image analysis has allowed high spatial resolution allowing to simultaneously assesses a variety of host cell features in correlation with compound potency/toxicity. Such imaging methods make use of fluorescent dyes, allowing the visualization of DNA and/or cytoplasm to quantify drug-mediated effects on intracellular parasites (Forestier et al., 2015). The prohibitive cost and the technical skill required, render them impractical for an everyday use. Finally, the output of test on intramacrophagic amastigotes depends on factors related to the nature of the host cell (Berman et al., 1984; Gebre-Hiwot et al., 1992; Seifert et al., 2010) or to the inherent infective capacity of leishmania isolates (Inocêncio da Luz et al., 2009).

Leishmania can be grown in vitro as amastigotes under axenic conditions, i.e., without the requirement for a host cell (Sereno et al., 1997; Monte-Alegre et al., 2001; Guptan et al., 2001). These in vitro-cultured amastigotes have biochemical, morphological and immunological similarities to intracellularly cultured ones (Saar et al., 1998; Li et al., 2008; Pescher et al., 2011; Brotherton et al., 2012). Nevertheless, not all Leishmania species are amenable to culture as amastigotes in axenic condition, therefore no extensive studies have been performed on field isolates.

The usefulness of promastigotes in measuring the drug susceptibility of field isolates is debatable, but promastigote cultures of most of the 21 identified human pathogenic species can be achieved in large panels of culture media (Evans DA, 1987; Schuster and Sullivan, 2002) and drug susceptibility determinations can be achieved with various tests (Sereno et al., 2007; Kulshrestha et al., 2013). With this system, the determination of drug susceptibility is simple, rapid, cheap, and does not require host cells that simplify the standardization process.

3. What do we need to translate AST into the clinical setting?

Notably, the methodology used to ascertain the drug susceptibility of isolate must be 1) amenable to standardization, 2) inexpensive, 3) easy to handle, and 4) easy to interpret and normalize. In addition, to have direct patient benefit in terms of appropriate chemotherapy, the lag between

parasite isolation and drug susceptibility testing should be limited. All these requirements should be potentially fulfilled by AST carried out on promastigotes, therefore the first question to be studied is: does promastigotes AST reflect the susceptibility of intracellular amastigotes?

3.1. How to set AST for clinical setting: do promastigotes (AST) reflects amastigote susceptibility?

Taking the framework of recommendation of the PRISMA group (Moher et al., 2009), we collected data from seven databases: Scopus, PubMed, Science Direct, Web of Science, MEDLINE, EMBASE and Google Scholar, using the following keywords: Leishmania drug susceptibility, Leishmania antimony, Leishmania amphotericin, Leishmania pentamidine, Leishmania paromomycin, Leishmania miltefosine. Papers with a description of tests performed on promastigotes and/or intramacrophagic amastigotes were selected. Paper where checked for: information on the culture media for leishmania and of the host cell, the Host-cell nature, temperature of incubation, protocol to ascertain promastigote viability and amastigote burden. In addition, we selected only papers whom AST are performed at both parasitic stages on at least 5 isolates, belonging to the same species or not. Only 11 publications where selected. The data were extracted and statistical analyses performed using the linear regression function of GraphPad Prism 6.0 (GraphPad Software, La Jolla, CA, USA). Statistical significance at P<0.05 were calculated using Spearman's t-test.

It is thought that the susceptibility of leishmania promastigotes to trivalent-Sb (SbIII) does not accurately reflect the sensitivity of intramacrophagic amastigotes to SbV formulations (Sundar 2001; Yardley et al., 2006; Vermeersh et al., 2009). Our analysis revealed that promastigote susceptibility reflects of the susceptibility of intracellular amastigote (Table 1). We recorded a highly significant relationship (P<0.05 in 3 of the 6 data series extracted from the literature) between susceptibility at the two parasite stages (Table 1). Examples of correlation are given in figure 2A. For miltefosine, promastigote susceptibility was previously shown to reflect susceptibility of intracellular amastigotes (Kulshrestha et al., 2011; Kulshrestha et al., 2013). Our meta-analysis confirms this assertion with an additional set of data extracted from the literature (Table 1 and figure 2B). For amphotericin B, on 3 of

the 6 currently published studies selected, a highly significant relationship at P<0.05 is recorded, for the 3 other (Table 1 and figure 2C). No publications that satisfy our inclusion criteria were found for pentamidine. Only one publication was collected for paromomycin with no significant correlation recorded (Table 1). Altogather, with only one study performed on American Leishmania species, our meta analysis highlight the need of further studies to address such correlation in leshmania species responsible for cutaneous and mucocutaneous leishmaniasis in south and central America. Indeed, this meta analysis pinpoint that promastigote is of interest to perform AST in order to track Miltefosine, Amphotericin B as well as Antimony drug susceptibility status of new isolates. Further experiments are required to test this system on American Leishmania species and for pentamidine and paromomycin.

3.2. How to delineate drug resistant isolates

As the first set of breakpoints, the definition of ECOFF values is of major importance (Box 1). In contrast to clinical breakpoints, ECOFF does not define resistance based on the likelihood of treatment failure. The ecological concept of resistance that underlies the definition of the ECOFF states "a microorganism is defined as wild type for a species by the absence of acquired and mutational mechanisms of resistance to the agent" (Khalmeter 2014). The definition of the wild-type phenotype is obtained by the study of the susceptibility of several unrelated isolates, allowing for the establishment of the ECOFF, which is the upper limit of the normal susceptibility distribution for a given antimicrobial drug and a given species. Any isolate presenting susceptibility above this value is considered resistant, irrespective of whether the achieved level of resistance compromises therapy.

To compute the ECOFF, the susceptibility of at least 20 isolates must be ascertained. We therefore screened the literature previously gathered (Chapter 3.1) for papers in which the susceptibility toward antileishmanial drugs was performed on at least 20 isolates. Only 15 publications satisfy our criteria. Data were extracted and the ECOFF ascertained, using an online application, Cutoff Finder that use R

version 2.15.0 (2012-03-30) (http://molpath.charite.de/cutoff/) (Budczies et al., 2012). Strikingly, the

multiplicity of AST protocols described in the literature reveal that guidance and SOPSs previously published are not followed (Table 2). We further investigated if the amastigote ECOFF value can be deduced from AST performed on promastigote. Using the linear equation of the regression line (Figure 2), we calculated the IC50 of amastigote and then ascertained ECOFF (see Figure 2 and Table 3). The computed ECOFF reflects well those obtained on intramacrophagic amastigotes for Miltefosine and to a lesser extent for Antimony (Table 3). In conclusion AST performed on promastigotes reflect well the susceptibility status of intracellular amastigotes, giving the opportunity to compute the basal susceptibility level of the 21 human pathogenic leishmania species, but also to search for geographic variation in leishmania drug susceptibility and finally to be used as a parasite drug resistance diagnostic tool.

3.3. How to translate drug-resistance diagnosis into clinical setting

ECOFFs, pharmacokinetic (PK) and pharmacodynamic (PD) cutoffs and clinical cutoffs defined together clinical breakpoints (Box 1) that defines the clinical phenotypes: S (high likelihood of clinical success), I (uncertain clinical success) or R (high likelihood of therapeutic failure). Leishmania susceptibility is often defined by the IC₅₀ and less frequently by the IC₅₀ (concentrations of drug required to inhibit 50% or 90% of growth). Unfortunately, to compute these values, it is necessary to gather drug response information for at least 5 concentrations. This is time-consuming and do not provide information on the minimal critical concentration that kills or completely inhibits the growth of the parasite population, an important parameter for the clinician. From, the experience gained from medical bacteriology, methods that use agar or liquid dilution for the determination of the MIC (minimal inhibitory concentration) would be a faster and easier alternative to IC₅₀ or IC₅₀ calculation. In addition, the effort undertaken to standardize interpretation of AST results for the disc diffusion test (Kronvall and Smith, 2016) will be beneficial for leishmania drug resistance diagnosis, if amenable with this micro-organism.

243 4. Conclusions

To prevent and minimize the risk of the emergence of Leishmania drug resistance, there is an urgent need to reflect on the definitions and guidelines of drug resistance diagnosis. This will also be help to track the underlying factors triggering the emergence of drug-resistant isolates and to characterize new molecular markers of resistance. In addition, This will assist practitioners in the future definition of species-specific treatment schemes and help to define the most effective treatment protocols and molecules. Altogether, determining Leishmania drug resistance in the light of Clinical Breakpoints (CBPs) offer a unique opportunity to include neglected tropical diseases in the well-defined framework of antimicrobial therapy.

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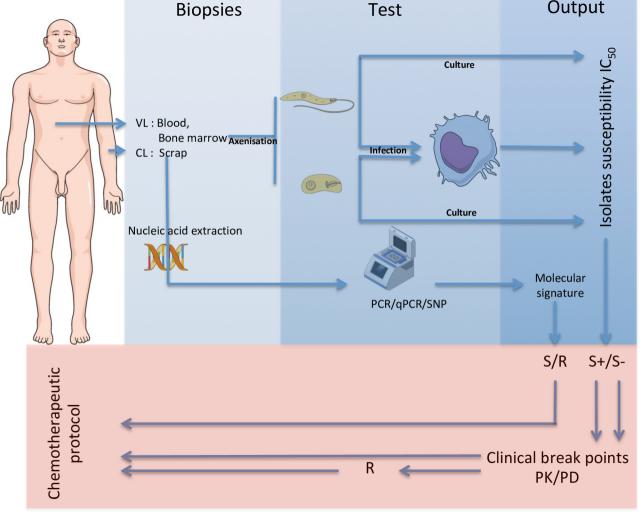
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Legends to the figures

Figure 1: The identification of drug-resistant *Leishmania* isolates. Two experimental protocols can be used to achieve this aim. The first method is based on *in vitro* isolate phenotyping. Living parasites must be collected from biopsies in order to measure their susceptibility to the molecules. For this purpose, various tests are available; easier ones rely on promastigote culture, and more complex ones require intracellular amastigote culture. In addition, other protocols, such as the axenic amastigote test protocol, can be considered. Once isolate susceptibility is measured, the main conceptual limitation is classifying the isolates as susceptible (S+) or non-susceptible (S-) and in conjunction with other clinical breakpoints to infer a success of therapy (S) or (R). An alternative is to characterize a molecular marker of drug-resistant parasites, these marker gives information on the presence of a known marker of resistance.

Figure 2: Exemple of linear correlation between promastigote and intracellular amastigote drug susceptibility. The identification of isolates included in the analysis of Miltefosine and Amphotericin b is provided in the figure. The regression line equations are given in the figure after being computed by forcing the regression to pass through the origin, dashed lines represent the 90% confidence interval values. Data were extracted from Kumar and collaborators (2009) and Eddaikra and collaborators (2018).



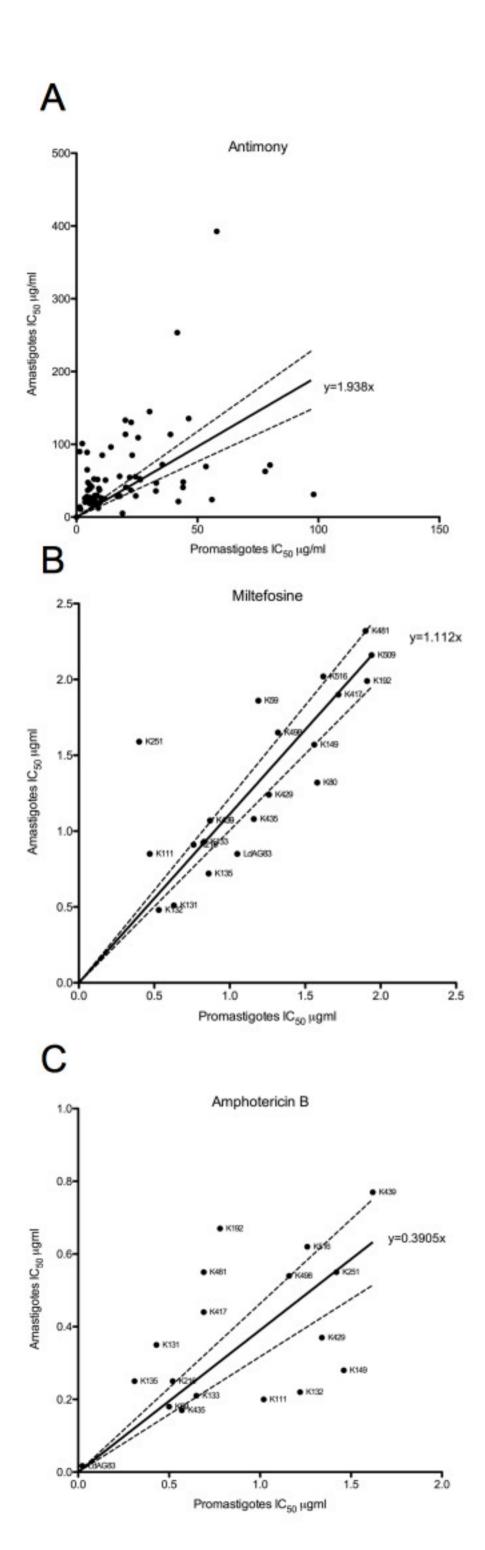


Table 1: Linear correlation between promastigotes and intracellular amastigotes susceptibility, as computed from the data extracted from the litterature.

Leishmania sp.	N	AmphoB/Fungizone	Miltefosine	Pentamidine	Paromomycin	Antimony SbIII/SbV	References
L. braziliensis, L. lainsoni, L.							
mexicana, L. infantum, L.							
guyanensis	9	NS-0.0549	NS-0.111	NA	NA	NA	Bilbao-Ramos et al., 2017
L. donovani	20	P<0.0018-0.4249	P<0.0001 -0.615	NA	NA	NA	Kumar et al., 2009
L. donovani	18	NA	P<0.0001 -0.9598	NA	NA	NA	Deep et al., 2017
L. donovani	20	NA	NA	NA	NS -0.01782	NA	Kulshrestha et al., 2011
L. donovani	17	NA	P<0.0001 -0.81	NA	NA	NA	Kulshrestha et al., 2013
L. donovani	21	NA	P<0.005 -0.72	NA	NA	NA	Kulshrestha et al., 2013
L. infantum	5	P<0.0008 -0.9845	NA	NA	NA	NA	Piñero et al., 2002
L. infantum	4	NS -0.4608	NA	NA	NA	NA	Lachaud et al., 2009
L. infantum	6	NS -0.1076	NS -0.4828	NA	NA	NA	Maia et al., 2013
L. infantum	28	P<0.0001 -0.9766	NA	NA	NA	P<0.0001 -0.9032	Aït-Oudhia et al., 2012
L. infantum	50	NA	NA	NA	NA	P=0.0071 -0.1390	Eddaikra et al. 2018a
L. major	12	NA	NA	NA	NA	NS-0.2085	Eddaikra et al. 2018b
L. major	7	NA	NA	NA	NA	P=0.0747 -0.5020	[Eddaikra et al. 2018a
L. tropica (L. killicki)	8	NA	NA	NA	NA	NS-0.00935	Eddaikra et al. 2018a
L. infantum, L. major,							
L. tropica (L. killicki)	73	NA	NA	NA	NA	P<0.0001 -0.1353	Eddaikra et al. 2018a

N: number of isolates/strains analyzed. **P** (Probability, computed using the Pearson correlation coefficient) and R^2 are given. NS not significant, NA not available, not tested in the study.

Table 2: Computed ECOFF values of various leishmania species for Miltefosine, Amphotericine B, Antimony, Stimaquine and Paromomycin.

			Promastigote	Amastigote			
Drugs	Leishmania sp	N	Medium/Time(d)/Meth	Host-cell/Time(d)/Meth	Promastigote	Amastigote	References
Miltefosine (μM)	L. donovani	22	M199/3d/Reazurin	NA	5.55	NA	Rai et al., 2013
	L. donovani	30	NA	J774/2d/Counting	NA	3.93	Bhandari et al., 2012
	L. donovani	54	M199/3d/Reazurin	NA	4.32	NA	Prajapati et al., 2013
	L. donovani	45	M199/3d/Reazurin	J774/2d/Counting	8.71	NA	Rijal et al., 2013
	L. donovani	19	M199/NA/Rh123Cytometry	J774/2d/Counting	1.442	1.513	Kumar et al. 2009
	L. aethiopica	23	NA	CD1M□/5d/Counting	NA	3.285	Utaile et al., 2013
Amphotericin B (μg/ml)	L. infantum	25	SDM79/3d/OD	U937/3d/LUC	0.408	ND	Lachaud et al., 2009
	L. infantum	25	SDM79/3d/ PropidiumCytometry	THP-1/5d/Counting	0.40	0.24	Aït-Oudhia et al., 2012
	L. donovani	19	M199/NA/Rh123Cytometry	J774/2d/Counting	0.97	0.42	Kumar et al. 2009
	L. aethiopica	23		CD1M□/5d/Counting	NA	0.23	Utaile et al., 2013
Antimony (µg/ml)	L. donovani	37	NA	J774/2d/Counting	NA	6.62(SbV)	Singh et al., 2006
(SbIII/SbV)	L. donovani	20	NA	J774A1/2d/Couning	NA	7.13(SbV)	Kulshrestha et al., 2011
	L. donovani	19	NA	J774/2d/Counting	NA	7.08(SbV)	Kumar et al. 2009
	L. donovani	24	M199-C/1d/H ³ Thymidin	BALBcM \(\textstyle /3d/Counting \)	87.97 (SbV)	3.71(SbV)	Lira et al., 1999
	L. donovani	30	NA	J774/2d/Counting	NA	7.42(SbV)	Bhandari et al., 2012
	L. aethiopica	23	NA	CD1M□/5d/Counting	NA	18.45(SbV)	Utaile et al., 2013
	L . tropica	25	NA	THP-1/5d/Counting	NA	42.09(SbV)	Hadighi et al., 2006
	L. infantum	26	SDM79/3d/PropidiumCytometry	THP-1/5d/Counting	10.48 (SbIII)	56.65(SbV)	Aït-Oudhia et al., 2012
	L. infantum	50	SDM79/3d/PropidiumCytometry	THP-1/5d/Counting	23.83 (SbIII)	59.09(SbV)	Eddaikra et al., 2018b
	L. infantum	37	NA	BALBcM \(\textstyle /7 d/\text{Counting} \)	NA	84.04(SbV)	Singh et al., 2006
	L. major	26	SDM79/3d /PropidiumCytometry	THP-1/5d/Counting	5.86(SbIII)	ND	Eddaikra et al., 2018a
	VL*	24	SDM79/3d /PropidiumCytometry	NA	23.83 (SbIII)	NA	Eddaikra et al., 2018a
	CL*	43	SDM79/3d /PropidiumCytometry	NA	15.91 (SbIII)	NA	Eddaikra et al., 2018a
Stimaquine (µM)	L. donovani	20	M199/3d/Counting	J774A1/2d/Couning	1.36	ND	Kulshrestha et al., 2011
Paromomycin (μM)	L. donovani	20	M199/3d/Counting	J774A1/2d/Couning	3.88	47.72	Kulshrestha et al., 2011
	L. aethiopica	23	NA	CD1M□/5d/Counting	NA	12.43	Utaile et al., 2013

^{*} Leishmania isolates collected from patients suffering of visceral (VL) or cutaneous (CL) leishmaniasis. NA: Not available, not tested in the study. (d) days of incubation

Table 3. Computed ECOFF value from promastigotes, amastigotes and from susceptibility of amastigotes deduced from promastigotes using the linear equation.

	Miltefosine	Amphotericin B	Antimony	
	*ECOFF-(S+ /S-) – N	*ECOFF-(S+/S-) – N	*ECOFF-(S+ /S-) - N	
Promastigote	1.442 μM-(70 /30)-20	NA	11.48 µg/ml-(54.4 /42.6)-68	
Amastigote	1.513 μM-(60 /40)-20	0.427 µg/ml-(60 /40)-20	59.09 µg/ml-(58.8 /41.2)-50	
Amastigote-cPro**	1.591 μM-(70 /30)-20	NA	17.03 µg/ml-(57.4 /42.6)-68	

^{*} ECOFF and percentage of susceptible (S+) and unsusceptible (S-) isolates. (N) number of sample. NA not available not tested in the study.

^{**} Values were deduced from promastigote AST using the equation of the regression analysis.