Life-histories as determinants of infection prevalence for trypanosomatids: A meta-analysis

Hawra, Al-Ghafli[1], Seth, M. Barribeau[1*]

[1] Department of Evolution, Ecology and Behaviour, Institute of Infection, Veterinary, and Ecological Sciences, University of Liverpool.

*sethb@liverpool.ac.uk

Abstract

Trypanosomatids are a diverse family of protozoan parasites, some of which cause devastating human and livestock diseases. There are two distinct infection life-cycles in trypanosomatids; some species complete their entire life-cycle in a single host (monoxenous) while others infect two hosts (dixenous). Dixenous trypanosomatids are mostly vectored by insects, and the human trypanosomatid diseases are transmitted mainly by vectored parasites. While infection prevalence has been described for subsets of hosts and trypanosomatids, little is known about whether monoxenous and dixenous trypanosomatids differ in infection prevalence. Here, we use meta-analyses to synthesise all published evidence of trypanosomatid infection prevalence for the last two decades. We employed a semi-automated screening protocol, using machine learning algorithms and natural language processing, resulting in the qualitative inclusion of 569 citations and quantitative inclusion of 261 citations. We find striking difference in infection prevalence with monoxenous species having twice the infection prevalence (19.8%) than dixenous species (8.68%) in both insect and non-insect hosts and are more than three-fold more prevalent in insects (20.9%) compared to their dixenous kins (6.61%). We also find that dixenous trypanosomatids have lower infection prevalence among insects compared to their definitive hosts, which is consistent across dixenous genera. Within the monoxenous trypanosomatids, genera infecting bees are characterised with the highest prevalence, which does not vary between wild and managed bees. To our knowledge, these results reveal for the first time, a fundamental difference in infection prevalence according to host specificity where vectored species suffer from lower infection prevalence as a result of a 'jack of all trades, master of none' style trade-off between the vector and definitive host.

Introduction

Trypanosomatids are Kinetoplastid protozoan parasites that infect a diverse range of hosts including vertebrates, invertebrates and plants. Among trypanosomatids, there are two distinct life-histories with some infecting only a single host for their whole life-cycle (monoxenous), and others that require two hosts to complete their development (dixenous). The dixenous lifestyle is thought to be evolutionarily derived and has evolved independently multiple times among the Kinetoplastids.[1] Dixenous trypanosomatids invariably include an insect vector that then transmits infection to a vertebrate or plant definitive host. Dixenous trypanosomatids consist of four main genera: *Leishmania, Trypanosoma, Endotrypanum and Phytomonas*. The vast majority of epidemiological and empirical evidence for all trypanosomatids comes from the former two genera (*Leishmania and Trypansoma*) as they are the most medically relevant. At least 20 species of *Leishmania*, cause cutaneous, mucocutaneous and visceral leishmaniasis; *Trypanosoma cruzi* causes Chagas disease and *Trypanosoma brucei* is the etiological agent of African sleeping sickness. These diseases cause more than 830,000 infections every year[2], causing significant disease burden, and their control is challenging. Estimates of incidence and mortality vary but some studies predict that more than 1 million people contract leishmaniasis annually, including up to 700,000 visceral cases (which is fatal in 95% of cases), and a further 1 billion people are at risk of infection.[3–5]

Monoxenous trypanosomatids not only have a simpler life-cycle and narrower host specificity, usually in a single invertebrate host, but they are also more common, more ancient (but see),[6] and more diverse than dixenous trypanosomatids.[7] There are 17 currently described monoxenous trypanosomatids genera: *Angomonas, Blastocrithidia, Blechomonas, Crithidia, Herpetomonas, Jaenimonas, Kentomonas, Lafontella, Leptomonas, Lotmaria, Novymonas, Paratrypanosoma, Rhynchoidomonas, Sergeia, Strigomonas, Wallacemonas,* and *Zelonia* in contrast to the four dixenous genera. Despite the overwhelming diversity of monoxenous trypanosomatids we know comparatively little about their natural history and prevalence, due to their perceived lack of medical relevance - although this has been called into question recently by opportunistic vertebrate infections by some monoxenous trypanosomatids.[8–10]

Monoxenous and dixenous trypanosomatids also appear to differ in their infection prevalence. Despite the substantive health burden of vectored trypanosomatids, they have surprisingly low infection prevalence in the vector insects. For instance, fewer than 3% of *Phlebotomus* sand flies carry *Leishmania*[11] and as few as 0.1% of adult tsetse flies have transmissible *Trypanosoma* cells in their saliva.[12] In contrast, trypanosomatids with only a single insect host can reach extremely high prevalence. In the bumblebee *Bombus terrestris* up to 35% of workers can be infected by its trypanosomatid parasite, *Crithidia bombi*.[13] These data hint at something crucial: that perhaps the major limiting factor for trypanosomatid infection transmission is the vector, not the vertebrate host. Therefore, a detailed understanding of insect-parasite interactions, and how they can be manipulated, will be vital to the control and potential eradication of these diseases.

Here, we set out to systematically test whether monoxenous and dixenous trypanosomatids indeed have different infection prevalences, and whether this is

consistent among hosts. While some systematic reviews have attempted to examine trypanosomatid pooled prevalence they have only done so in the context of either individual trypanosomatid or host taxa,[14,15] or summarised evidence across hosts but were restricted to one geographic region.[16–18] This is the first review of its type at this scale aimed to describe how fundamental aspects of parasite life-history influence disease prevalence in an important group of human, livestock, and wildlife parasites. We hope that our findings will help clarify the link between parasite life-history and infection in turn, potentially shed light onto better control strategies to combat the spread of trypanosomatid infections.

Methodology

Literature search

We searched Scopus and all available databases in Web of science, to identify all published studies that describe trypanosomatid prevalence in non-human hosts. Full search terms can be found in Supplementary Table 1. During the literature search, we did not apply any year or publication type restrictions (search stopped Jan 2020). To exhaustively find studies of neglected trypanosomatids, we further checked the references in relevant papers and added candidate citations to screening list of studies. All duplicate references were identified and removed.

Relevant screening stages and design

References were initially screened based on titles and abstracts manually by a single reviewer (HA) using Rayyan website as outlined in (Supplementary appendix). We further employed an automated second review protocol using Machine Learning Algorithm (MLA) and Natural Language Processing (NLP) during the initial screening phase, as has previously been suggested for large datasets[19] (and detailed in (Supplementary appendix). All studies that received a manual or an automated "include" decision were subsequently subjected to further eligibility assessment by full-text review by two different reviewers (Figure.1). Inclusion and exclusion criteria, as well as detailed protocol of study selection and data extraction can be found in (Supplementary appendix).

Selection of studies for meta-analysis

After filtering, 569 studies, with 1031 prevalences, were included in subsequent analyses. As expected, fewer (16%) of these were on non-human parasites. We included all of these studies in our meta-analysis. The remaining studies (84%) were on vector-borne human parasites such as *Leishmania* and *Trypanosoma* species. To capture all of the information about the less commonly studied trypanosomatids but without processing all of the over-represented parasites, we opted to qualitatively include only studies with > 400 sampled individuals. To confirm that this did not introduce any bias, we randomly selected 20 citations with fewer than 400 individuals. We made this selection approach based on the following considerations: (I) studies with larger sample size would be closer to the true population prevalence, (II) have stronger impact on the meta-analysis and (III) when

broken down to host and parasite taxa level they will remain statistically informative. As an additional confirmatory step, we compared the outcome and the fit of models with 261 studies (as per our selection strategy) or all of the studies (n= 569). To our assurance, while both models showed similar outcome, models with 265 studies had a better fit than the alternatives (i.e. lower AIC value:Δ153).

Meta-analysis

Estimates of proportion of infections were calculated using "metaphor" package[20] with the variance stabilised by Freeman-Tukey double arcsine transformation. Pooled estimates were back-transformed for each analysis and multiplied by 100 to get the pooled prevalence. Publication bias was assessed using a funnel plot with trim and fill method and Egger's test. We employed a random effect multilevel model (rma.mv) with a nested random design to account for the heterogeneity of evidence either due to different study protocols and/or different host/parasite taxa within and between studies. We assigned "study ID" as an outer random factor, and both "host type: 19 levels" and "parasite taxa: 47 levels" were considered inner-random factors. This was done for the general model with no moderator applied as well as meta-regression models with the following moderators: diagnostic method (3 levels [molecular, microscopic, serological]), life-history traits of the parasite (3 levels[dixenous, monoxenous, mixed trypansomatids), host groups (insects and non-insects), parasite taxa (47 levels), host taxa (19 levels). We also ran similar meta-regression models to assess pooled prevalence but in a subgroup of interest excluding some levels of the moderator as necessary . For instance, when comparing diagnostic methods among hosts we excluded serological approaches as they only apply to vertebrates. Between-study variation was assessed using the Higgins I^2 statistic, which usually indicates substantial heterogeneity if exceeding 50%. Q_M statistic, an omnibus test of all model coefficients except for the intercept, was conducted to conclude if a moderator significantly influences the mean effect size. All meta-regression models were run with and without the model intercept to statistically compare effect size of factors and generate pooled estimate for each factor respectively. Forest plots were presented using "orchaRd" package with "tanh" transformation as traditional forest plot will fail to present the large number of included citations.[21]

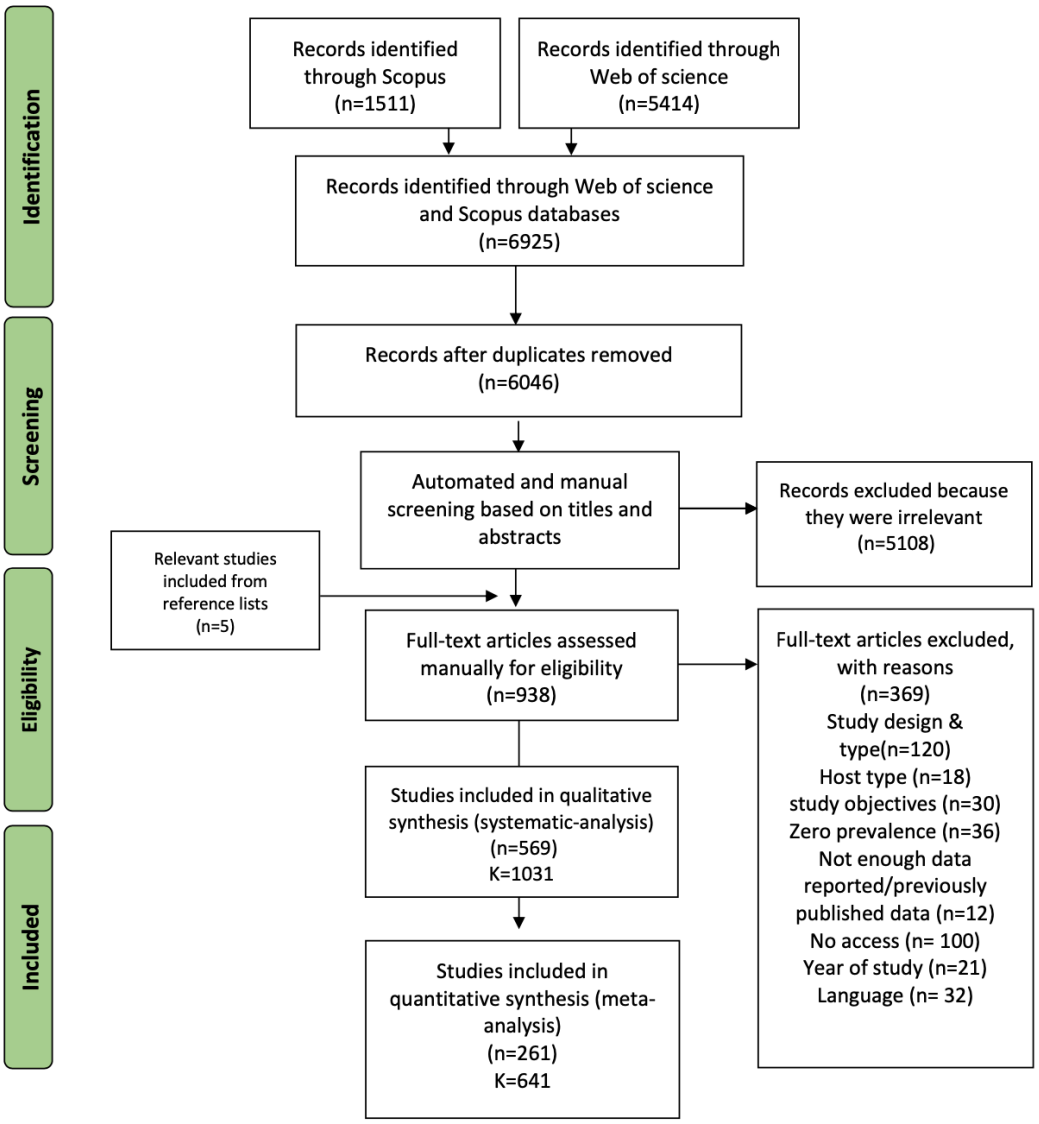

Figure1: ***Selection and screening stages***

A) The overall protocol utilised for literature search and screening, wherein (n) represents the number of studies included/excluded at each stage and (K) represents the number of data extracted from qualitatively or quantitatively included studies. All steps of the systematic review were in concordance with PRISMA guidelines.[22]

Results

Exploring the impact of host-parasite traits on prevalence patterns

Out of 6046 unique citations, we have qualitatively included 569 studies[23–591] and quantitatively included 261 studies.[23–283] Overall, these results demonstrate a growing number of trypanosomatids studies over the last two decades (Supplementary Fig.2). Additional information about the geographic distribution of trypanosomatids can also be found in (Supplementary appendix).

A summary of the pooled prevalence and the main features of included citations, stratified by parasite species, can be found in Table 1. We found that monoxenous parasites that usually infect the same host-order, show similar infection prevalence across hosts. This is the case both for monoxenous species with high prevalence (e.g. bees) and parasites with low pooled prevalence (e.g. monoxenous and dixenous species infecting flies)(Fig.2C). Subsequent analysis of various host-groupings show similar trends in infection prevalence in bees and flies to that presented in Table 1, though the latter remains influenced by both monoxenous and dixenous species (Supplementary Fig.6). In addition, fish, raccoons and buffaloes have high pooled prevalence although they are comparatively rarely studied (Supplementary Fig.3). In spite of the low number of studies, their total sample size indicates comparable robustness of analysis to that of other host groups, which supports our estimates of prevalence (Supplementary Fig.3B).

Infection prevalence is further stratified into within host prevalence in (Fig.2A). As expected, dogs and cats appear to be the main vertebrate-reservoirs for *Leishmania* and *Trypanosoma cruzi*. Additionally, the *Trypanosoma congolense* group seem to heavily infect certain domesticated animals such as pigs, sheep, and goats. Buffaloes, camels, and cattle appear to be the main reservoirs for Surra (*Trypanosoma evansi*). Some hosts have similar infection prevalence to various parasites of Trypanosomatidae (i.e. flies and rodents) while other parasite-groups show similar prevalence among various hosts (e.g. *Trypanosoma simia*).

Multiple analysis of monoxenous versus dixenous infections

We set out to test whether pooled prevalence of monoxenous infections differ from dixenous infections (both among insect and non-insect hosts). We find a strongly significant difference between pooled prevalence of monoxenous (19.8%) and dixenous infections (8.68%) (Fig.3A). Introducing “host-traits" as a sole moderator (i.e. insects and non-insects) reveals no significant difference between pooled prevalence of the two groups, 11.5% and 9.45% respectively (Fig.3B). Limiting the analysis to insects alone revealed an even stronger effect with monoxenous infections- three-fold more prevalent (20.9%) than dixenous infections (6.61%) (Fig.4, Table 2). We then compared prevalence in the groups of insects that had both dixenous and monoxenous parasites (true bugs and

flies). Here however, we find non-significantly higher pooled prevalence for dixenous infections in flies and similar pooled prevalence in true bugs (Table 2).

Notably, dixenous parasites consistently infect 4.54-8.00% of their insect hosts with no significant difference among parasite genera (Fig.4B). Common dixenous parasites, with prevalence data from both insects and non-insects, were significantly more prevalent in their non-insect hosts (9.38%) than their insect hosts (5.51%) (Table 2).

Monoxenous genera exhibit two alternative trends: high pooled prevalence for *Lotmaria*, *jaculum* and *Crithidia* species, but low pooled prevalence for *Herpetomonas*, *Leptomonas*, *Agomonas*, and *Blastocrithidia* groups (Fig.4 B). Taking into consideration that a considerable amount of monoxenous data (80%) were on bee infections, we performed an in depth sub-group analysis to further understand the main drivers of bee infection prevalence. While the majority of included data represent natural infection among wild bees, the remaining evidence describes spillover of infections e.g. by sampling non-native/commercial bees. We do not find any difference in trypanosomatid infection prevalence between wild-bees and commercial/managed bees for bumblebees or honeybees (Table 2).

Honeybee infections seem to predominantly occur in Western/European honeybees (e.g. *Apis mellifera Linnaeus*) compared to Asian honeybees (e.g. *Apis dorsata Fabricius* and *Apis cerana Fabricius*). We also noted a significant reduction in heterogeneity of evidence across all honeybee-infections due to spatial variations only (46% heterogeneity). However, a much higher diversity of infection prevalence was found in bumblebee taxa. Accounting for spatial and temporal factors failed to significantly reduce the heterogeneity in evidence for bumblebee infections, suggesting a unique impact of various bumblebee-trypanosomtids systems on different patterns of prevalence (Fig.2.B) and likely the greater diversity of bumblebees.

Diagnostic approach also affected infection prevalence but differ according to host. Microscopic diagnostics revealed higher infection prevalence in insects whereas molecular assays report higher infection prevalence in non-insects (Table 2).

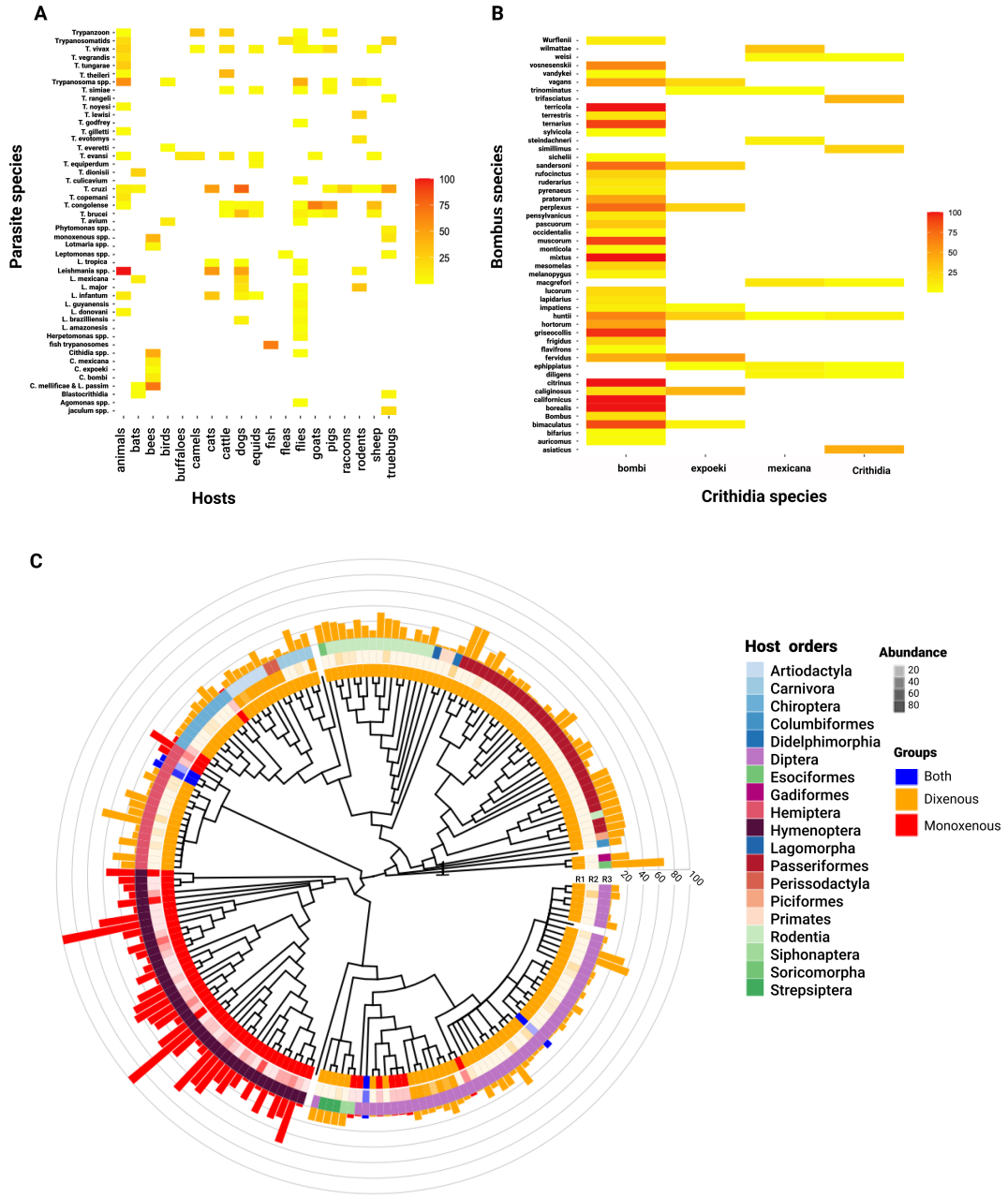

Figure 2: ***Infection prevalence among host-trypanosomatid systems***

A heat-map of prevalence of all host-parasite systems (A), of bumblebee-trypanosomatids (B). A phylogenetic representation of all host taxa examined here. The first (inner) ring (R1) illustrates the parasite taxon's life-history (dixenous, monoxenous or both), the second ring (R2) highlights the abundance of prevalence data for each taxon, and the third ring (R3) is host order. Prevalence of infection (%) is shown in the outer scaled ring, which is coloured according to parasite life-history.

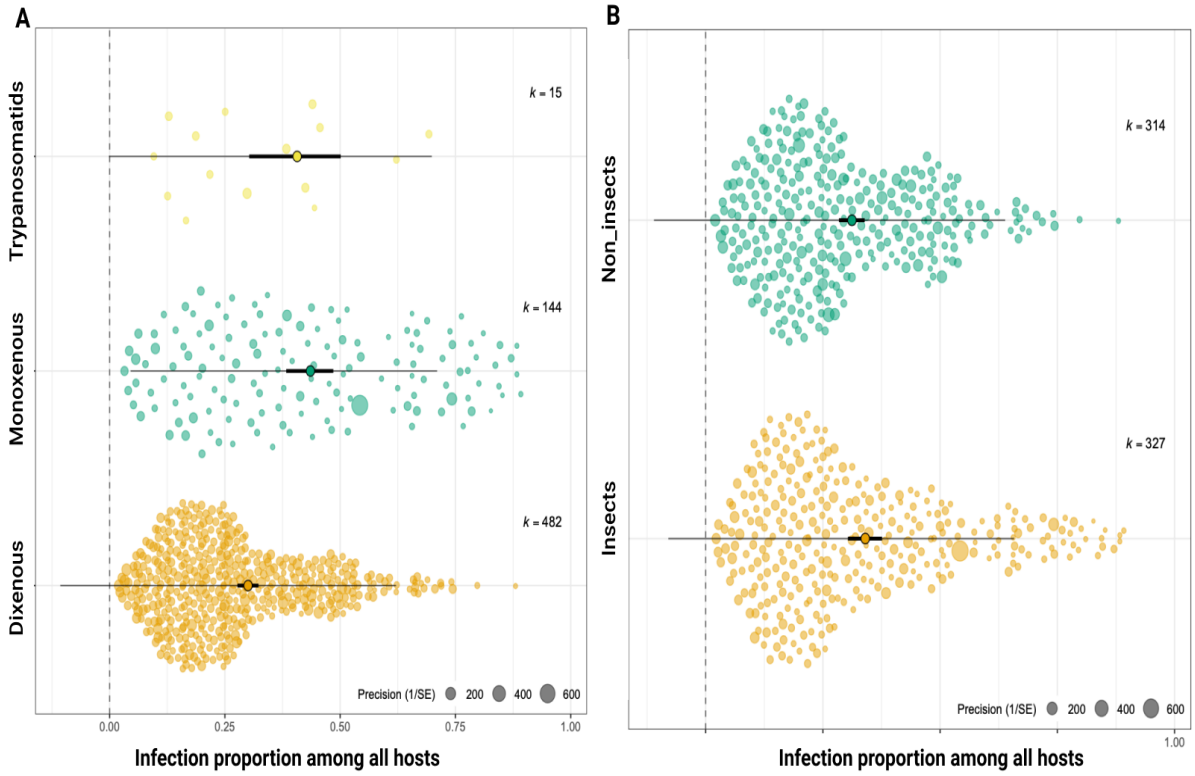

Figure 3: ***Forest plots of main meta-regression models***

A) Pooled estimate of infection prevalence of dixenous (0.310, 95% CI:0.285, 0.335), monoxenous (0.467, 95% CI:0.404, 0.530), and mixed trypanosomatids (0.427, 95% CI:0.313, 0.551) with significant difference between them ($P<0.05$). These pooled estimates back-transform to 8.68%, 19.8%, and 17.0%, respectively. B) There is no overall significant difference between the pooled estimate of infection prevalence of insect (0.354, 95% CI: 0.313, 0.396) and non-insect (0.320, 95% CI:0.292, 0.353) hosts ($P>0.05$). These pooled estimates correspond to 11.5% and 9.45%.

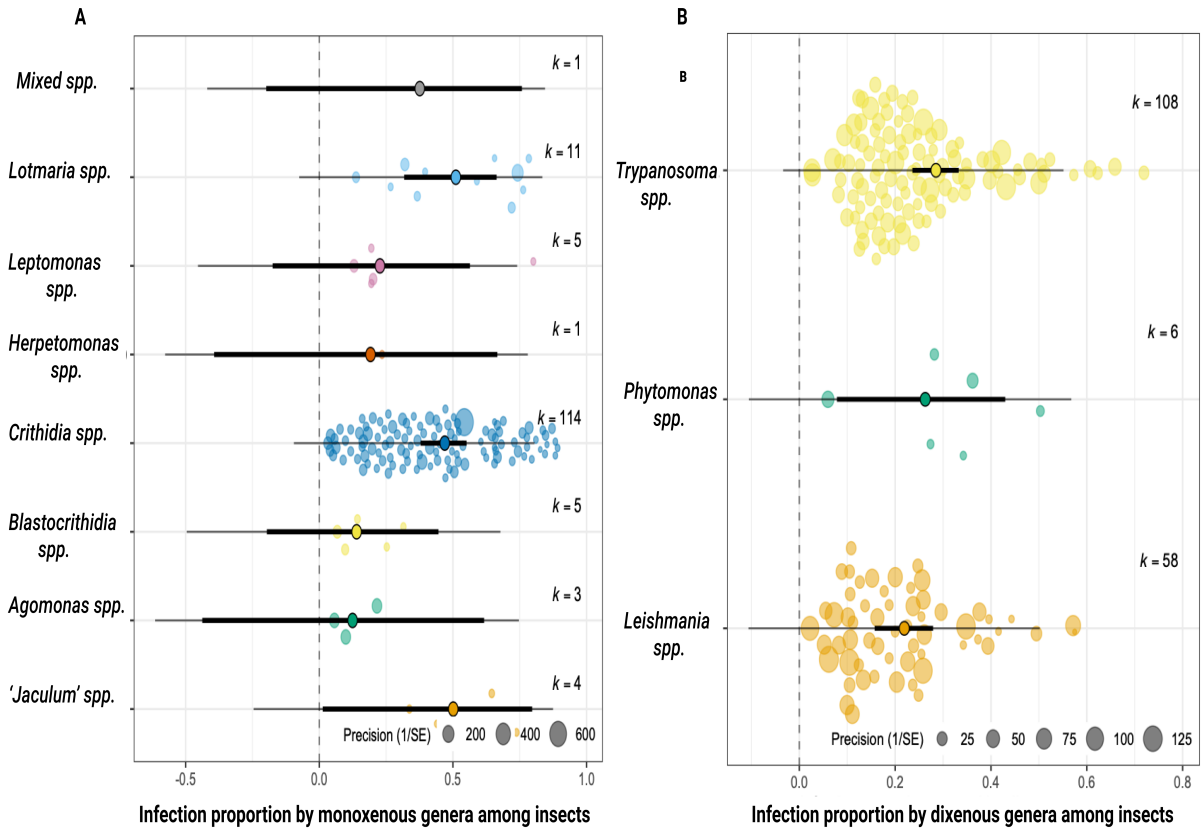

Figure 4*: Forest plots of meta-regression models based on parasites-grouping among insects*

A) Pooled estimate of infection prevalence of monoxenous genera, representing a pooled estimate of 0.395 (95% CI:-0.201, 0.992), 0.566 (95% CI:0.332, 0.801), 0.235 (95% CI:-0.1764, 0.6468), 0.197 (95% CI:-0.415, 0.8085), 0.524 (95% CI:0.4118, 0.6371), 0.158 (95% CI:-0.2545, 0.5707), 0.125 (95% CI: -0.469, 0.720) and 0.557 (95% CI:0.012, 1.10) for *monoxenous, Lotmaria, Leptomonas, Herpetomonas, Crithidia, Blastocrithidia, Angomonas and 'jaculum'* species respectively with no significant difference between them (P>0.05). These pooled estimates were back-transformed to a prevalence of 13.4%, 27.9%, 3.70%, 2.13%, 24.0%, 0.882%, 0.185% and 27.0%. B) Pooled estimates of infection prevalence in dixenous genera, of 0.293 (95% CI:0.2407, 0.3458), 0.269 (95% CI:0.0786, 0.4597) and 0.223 (95% CI:0.1586, 0.2868) for *Trypanosoma, Phytomonas* and *Leishmania* respectively with no significant difference between subgroups (P>0.05) corresponding to prevalence of 8.00%, 6.76% and 4.543%.

Discussion

Trypanosomatid parasites have two distinct life-histories that vary in the number of host species and the complexity of their life-cycle. This difference is profound and will have commensurately profound effects on the evolution of parasite traits, including their ability

to establish infection. How these alternative life-history strategies influence infection prevalence, however, is poorly understood. To our knowledge, this is the first comprehensive study designed to test for differences in infection prevalence. Our semi-automated screening protocol, resulted in the qualitative inclusion of 569 citations and quantitative inclusion of 261 citations.

We find that monoxenous trypanosomatids are far more prevalent in their hosts than are dixenous species. Across all hosts, we find at least two-fold higher prevalence in monoxenous species (Fig.3A) and more than three-fold higher when we examine infection prevalence in insects alone (Table 2). Taken together, one cannot escape the impression that complex parasite life-cycles have a cost to infection prevalence. In line with such speculation, high prevalence for monoxenous species was mainly notable among genera that infects bees such as *Crithidia* and *Lotmaria* with pooled prevalence of 24.0% and 27.9% respectively; ranking bees with the highest pooled prevalence among all insects (26.3%). It is striking to realise that greater than a quarter of surveyed bees are infected by trypanosomatid pathogens. This is of a particular concern considering the crucial role of bees as pollinators, which, with other insect pollinators, account for the fertilisation of 83% of flowering plants[592] including nutritionally and economically important crop species[593,594]. Bees and other pollinators have been declining. Among the presumed causes of pollinator declines are infectious diseases.[595] Despite the attention that bee-trypanosomatid infection has attracted, the distribution of interest remains uneven. Infection prevalence of trypanosomatids is largely unexplored outside of Europe and North America (Supplementary Fig.4)

The relationship between wild and managed bees, and the risk of spillover in either direction, has received particular attention and concern in the literature. While managed bees have been blamed for parasite transmission to wild bees,[74,596] we find no significant difference between managed and wild honeybees and bumblebees (either independently or combined) in trypanosomatid infection prevalence. Whether this reflects shared susceptibility to infection or ongoing spillover to and from wild pollinators remains unknown.

To our knowledge this is the first study to provide such concise statistical summary of prevalence data among all host-trypanosomatids systems. Encouragingly, our findings recapitulate those of several other, taxon- or geographically-restricted, systematic reviews. For instance, A similar range of prevalence (2.4-9.2%) for trypanosomatids was reported in sand-flies (*Phlebotomus* spp.) in Iran,[597] which largely agrees with our finding of 2.02%. Another meta-analysis on trypanosomatids in tsetse flies revealed a prevalence of 10%, which is somewhat higher than we find in flies (5.51%).[15] The variation between these prevalence data could be due to different study design, year of publications of included studies and data analysis. Unlike our study, all prevalence data from[15] were uncovered using microscopic examination and the analysis was done using STAT. Thus, although biting flies are responsible for most human trypanosomatids, our results seem to comport with previous studies revealing low infection prevalence in flies as a group, with no significant difference between monoxenous and dixenous parasites within flies (Table 2). Meanwhile, pooled prevalence for trypanosomosis in cattle, sheep and goats was reported

as ranging between 1-9%, which is comparable to what we find (Table 2. and Supplementary Fig.6).[17,18,598]

We also reveal significantly higher prevalence in the definitive vertebrate hosts than vector flies which is consistent among dixenous genera. This brings to the fore a possibility that dixenous trypanosomatids infect more of their vertebrate hosts than their insects vectors. Evolutionary theories predict a life history trade-off between investment in survival (within-host persistence and growth) and reproduction (between-host transmission). For dixenous trypanosomatids, such relationship is amplified by the number of host species needed to complete the life-cycle.[599] This trend warrants further investigations as understanding how these species are maintained in the metapopulation holds great potential in managing the spread of vector-borne diseases. For instance, if the prevalence of infection in vectors is low, further reduction in insect hosts may better control infection in the metapopulation than suppression in vertebrate hosts.

In this study, we find that microscopic diagnostics revealed higher infection prevalence in insects but greater infection prevalence was revealed from molecular assays in non-insects (Table 2). This result does not necessarily indicate greater accuracy for either assay, but may rather indicate the preferred methodology of researchers working with insect versus vertebrate hosts. In line with this explanation, Abdi and researchers[15] concluded that microscopic diagnostics were more common in surveys of tsetse flies than molecular assays and Aregawi *et al.*[14] reported a higher range of prevalence (6–28%) by molecular tests in vertebrates compared to microscopic tests (2–9%) for the detection of *Trypanosoma evansi*. Standardising the diagnostic method applied for the detection of trypanosomatids within insects and non-insects is crucial consideration for future research to enable accurate comparisons of prevalence that is unlikely due variations in diagnostic protocols. We took this factor into consideration while doing all sub-group analysis (meta-regression models) presented in this study to ensure that the difference in prevalence is real and not due to variable diagnostics. To our assurance, in all of the main subgroup analysis, there was no significant difference in pooled prevalence due different diagnostic tools. This is true for monoxenous or dixenous trypanosomatids in insects and dixenous trypanosomatids among vertebrate hosts (e.g. cats, dogs, rodents, goats, pigs, bats and buffaloes).

The key takeaway from this study is the unique pattern of infection prevalence in association with different life-history traits of trypanosomatids: revealing both (I) higher pooled prevalence for monoxenous species in insects and across all hosts, and (II) significantly lower prevalence among vectors compared to definitive hosts for dixenous species. We present three non-mutually exclusive arguments that could explain this finding:

- First, monoxenous species are subject to selection pressure from only one host, thereby affording these species more opportunity to adapt to this host than parasites that must co-evolve with both a vector and definitive host. We would thus expect to see greater parasite fitness in specialized monoxenous parasites than in dixenous parasites as the monoxenous parasites would arrive closer to their

evolutionary optima. Dixenous parasites, in contrast, may be forced to trade-off infection relevant traits in one host for traits in the second host.

- Second, our finding may be the result of an equal force of infection shared among differing numbers of host species. Here, we offer a numerical explanation, where the same hypothetical number of infectious units are simply shared among more host species in dixenous parasites, thus diluting the infection prevalence in any one host species - to approximately half. This explanation is more than passingly similar to the “dilution effect" which is often, and sometimes controversially, used to describe infection risk in human populations when the natural host is not usually the human - eg. Lyme disease,[600–602] although to our knowledge it has not been invoked to explain variation in infection prevalence among vectored and non-vectored parasites.

- Finally, host characteristics such as lifespan, recruitment rate, sociality, and physiology may explain some of the variation in infection prevalence. For instance, social bees, which have higher infection prevalence, differ from the rest of insect hosts not only in their sociality but also in their lifespan. The biological unit for social bees is the colony, which can extend the lifespan of an infection to at least a year (bumblebees) and to several years in honeybees. The other insect hosts live for up to a few months, and have high birth and death rates which, along with rarer direct interactions can reduce the overall prevalence of infection regardless of the parasite life-cycle strategy. Consistent with this view, we found low pooled prevalence among flies with no significant difference between monoxenous and dixenous species. Furthermore, flies might be physiologically harder to infect by trypanosomatids than bees as genomic studies have described a reduced immune repertoire in bees relative to dipterans.[603,604]

While this study was ambitious in scope and exhaustive in design, there are limitations. Foremost is the small number of studies describing prevalence in monoxenous species. But, as our analyses demonstrate earlier, this is more likely due to scarcity of publications for neglected trypanosomatids rather than study selection/handling approaches employed here. Finally, although this study is far-reaching and inclusive to all reported trypanosomatids systems contributing to slyvatic transmission cycles, it does not include humans as vertebrate hosts. Despite the exclusion of human infections, their impact and contribution to the transmission cycles either directly (to insects) or indirectly (to non-insects) have been accounted for by including studies surveying animals living nearby to humans. This includes pets (dogs, cats), domesticated animals, and the vectors, such as true bugs (tritomines), which are particularly found in houses. Thus, although the direct interaction in humans-trypanosomatids systems fall beyond the scope of this study, what we show here (i.e. how trypanosomatids differ in their infection prevalence among various non-human hosts) is particularly important to enable effective prevention plans for neglected tropical diseases of humans and livestock. Understanding the fundamental processes that determine infection prevalence will help us better understand trypanosomatids in general and identifying “weak-links" in the infection chain of vectored parasites - here in the vectored species, will enable better tailored control strategies for

trypanosomatid diseases relevant to human, livestock, and wildlife health as well as food-security.

References

1 Lukeš J, Skalický T, Týč J, Votýpka J, Yurchenko V. Evolution of parasitism in kinetoplastid flagellates. *Molecular and Biochemical Parasitology* 2014; **195**: 115–22.

2 Global burden of disease (GBD). 2017; published online March.

3 Georgiadou SP, Makaritsis KP, Dalekos GN. Leishmaniasis revisited: Current aspects on epidemiology,diagnosis and treatment. *J Transl Int Med* 2015; **3**: 43–50.

4 TDR. WHO | disease watch focus: leishmaniasis. *Nat Rev Microbiol* 2004.

5 Alvar IDAB Jorge AND Vélez. Leishmaniasis worldwide and global estimates of its incidence. *PLOS ONE* 2012; **7**: 1–2.

6 Frolov AO, Malysheva MN, Yurchenko V, Kostygov AYu. Back to monoxeny: Phytomonas nordicus descended from dixenous plant parasites. *European Journal of Protistology* 2016; **52**: 1–0.

7 Podlipaev S. The more insect trypanosomatids under study-the more diverse trypanosomatidae appears. *International Journal for Parasitology* 2001; **31**: 648–52.

8 Ghosh S, Banerjee P, Sarkar A, Datta S, Chatterjee M. Coinfection of leptomonas seymouri and leishmania donovani in indian leishmaniasis. *Journal of Clinical Microbiology* 2012; **50**: 2774–8.

9 Chicharro C, Alvar J. Lower trypanosomatids in HIV/AIDS patients. *Annals of Tropical Medicine & Parasitology* 2003; **97**: 75–8.

10 Ghobakhloo N, Motazedian MH, Naderi S, Ebrahimi S. Isolation of crithidia spp. From lesions of immunocompetent patients with suspected cutaneous leishmaniasis in iran. *Tropical Medicine & International Health* 2019; **24**: 116–26.

11 Tiwary P, Kumar D, Mishra M, Singh RP, Rai M, Sundar S. Seasonal variation in the prevalence of sand flies infected with leishmania donovani. *PLoS One* 2013; **8**: e61370.

12 Stuart K, Brun R, Croft S, *et al.* Kinetoplastids: Related protozoan pathogens, different diseases. *The Journal of clinical investigation* 2008; **118**: 1301–10.

13 Schmid-Hempel P, Wilfert L, Schmid-Hempel R. Pollinator diseases: The bombus–crithidia system. In: Wilson K, Fenton A, Tompkins D, eds. Wildlife disease ecology: Linking theory to data and application. Cambridge University Press, 2019: 3–1.

14 Aregawi A W. G., Abdi RD. Systematic review and meta-analysis on the global distribution, host range, and prevalence of trypanosoma evansi. *Parasites Vectors* 2019; **12**. DOI:https://doi.org/10.1186/s13071-019-3311-4.

15 Abdi A R. D., Duchateau L. A systematic review and meta-analysis of trypanosome prevalence in tsetse flies. *BMC Vet Res* 2017; **13**: 100.

16 Correa JP, Bacigalupo A, Yefi-Quinteros E, *et al.* Trypanosomatid infections among vertebrates of chile: A systematic review. *Pathogens* 2020; **9**. DOI:10.3390/pathogens9080661.

17 Leta S, Alemayehu G, Tarekegn Z, Tessema MB. Prevalence of bovine trypanosomosis in ethiopia: A meta-analysis. *Parasites & Vectors* 2016; **9**. DOI:10.1186/s13071-016-1404-x.

18 Ebhodaghe F, Ohiolei JA, Isaac C. A systematic review and meta-analysis of small ruminant and porcine trypanosomiasis prevalence in sub-saharan africa (1986 to 2018). *Acta Tropica* 2018; **188**: 118–31.

19 Marshall I, Wallace B. Toward systematic review automation: A practical guide to using machine learning tools in research synthesis. *Systematic Reviews* 2019; **8**. DOI:10.1186/s13643-019-1074-9.

20 Viechtbauer W. Conducting meta-analyses in r with the metafor package. *Journal of Statistical Software, Articles* 2010; **36**: 1–48.

21 Nakagawa S, Lagisz M, O'Dea RE, *et al.* The orchard plot: Cultivating a forest plot for use in ecology, evolution, and beyond. *Research Synthesis Methods* 2021; **12**: 4–12.

22 Moher AAT David AND Liberati. Preferred reporting items for systematic reviews and meta-analyses: The PRISMA statement. *PLOS Medicine* 2009; **6**: 1–6.

23 Abebe G R., Simon I. Bovine trypanosomosis and vector density in omo-ghibe tsetse belt, south ethiopia. *Acta Trop* 2017; **167**: 79–85.

24 Adam M Y., Van den Bossche P. Bovine trypanosomosis in the upper west region of ghana: Entomological, parasitological and serological cross-sectional surveys. *Res Vet Sci* 2012; **92**: 462–8.

25 Adams H E. R., Gibson WC. The identification, diversity and prevalence of trypanosomes in field caught tsetse in tanzania using ITS-1 primers and fluorescent fragment length barcoding. *Infect Genet Evol* 2008; **8**: 439–44.

26 Ajaoud E-S M., Lemrani M. Phlebotomus sergenti in a cutaneous leishmaniasis focus in azilal province (high atlas, morocco): Molecular detection and genotyping of leishmania tropica, and feeding behavior. *PLoS Negl Trop Dis* 2015; **9**: e0003687.

27 Akhoundi B M., Parvizi P. Molecular characterization of leishmania infection from naturally infected sand flies caught in a focus of cutaneous leishmaniasis (eastern iran). *J Arthropod Borne Dis* 2013; **7**: 122–31.

28 Akhoundi M M., Mirzaei A. Molecular characterization of leishmania spp. In reservoir hosts in endemic foci of zoonotic cutaneous leishmaniasis in iran. *Folia Parasitol (Praha)* 2013; **60**: 218–24.

29 Alanazi P A. D., Al-Shehri HR. Molecular detection of equine trypanosomiasis in the riyadh province of saudi arabia. *J Vet Diagn Invest* 2018; **30**: 942–5.

30 Alanazi P A. D., Alraey YA. Molecular detection of leishmania spp. In skin and blood of stray dogs from endemic areas of cutaneous leishmaniasis in saudi arabia. *Iran J Parasitol* 2019; **14**: 231–9.

31 Elsiddig M, Mohamed Y, Elshafie E, Alharbi Y, Al-Mekhlafi H. Molecular detection of trypanosoma evansi in camels (camelus dromedarius) in southwestern saudi arabia. *The Thai veterinary medicine* 2019; **49**: 93–100.

32 Aleman G A., Hahn D. The prevalence of trypanosoma cruzi, the causal agent of chagas disease, in texas rodent populations. *Ecohealth* 2017; **14**: 130–43.

33 Alias S S. N., Mohd-Zain SN. Epidemiology of blood parasitic infections in the urban rat population in peninsular malaysia. *Trop Biomed* 2014; **31**: 230–40.

34 Amusategui AA I.Sainz. Annals of the new york academy of sciences. 2004: 154–7.

35 Anderson S J. M., Kamhawi S. Seasonality and prevalence of leishmania major infection in phlebotomus duboscqi neveu-lemaire from two neighboring villages in central mali. *PLoS Negl Trop Dis* 2011; **5**: e1139.

36 Anez AV-D N.Rojas. Epidemiological study on visceral leishmaniasis in the semiarid region of western venezuela with special reference to inapparent infections. *Boletin De Malariologia Y Salud Ambiental* 2012; **52**: 245–56.

37 Angwech N H., Skilton RA. Heterogeneity in the prevalence and intensity of bovine trypanosomiasis in the districts of amuru and nwoya, northern uganda. *BMC Vet Res* 2015; **11**: 255.

38 Arismendi B N., Vargas M. PCR-specific detection of recently described lotmaria passim (trypanosomatidae) in chilean apiaries. *J Invertebr Pathol* 2016; **134**: 1–5.

39 Astudillo H V. G., Yabsley MJ. Spatial, temporal, molecular, and intraspecific differences of haemoparasite infection and relevant selected physiological parameters of wild birds in georgia, USA. *Int J Parasitol Parasites Wildl* 2013; **2**: 178–89.

40 Atarhouch R T., Dakkak A. Camel trypanosomosis in morocco 1: Results of a first epidemiological survey. *Vet Parasitol* 2003; **111**: 277–86.

41 Athanasiou K L. V., Diakou A. A cross-sectional sero-epidemiological study of canine leishmaniasis in greek mainland. *Acta Trop* 2012; **122**: 291–5.

42 Babuadze A G., Imnadze P. Epidemiology of visceral leishmaniasis in georgia. *PLoS Negl Trop Dis* 2014; **8**: e2725.

43 Bacigalupo T-P A., Cattan PE. Sylvatic foci of the chagas disease vector triatoma infestans in chile: Description of a new focus and challenges for control programs. *Mem Inst Oswaldo Cruz* 2010; **105**: 633–41.

44 Bajer P A., Sinski E. Factors affecting the component community structure of haemoparasites in bank voles (clethrionomys glareolus) from the mazury lake district region of poland. *Parasitology* 2001; **122 Pt 1**: 43–54.

45 Bamorovat S M., Keyhani A. Leishmania tropica in stray dogs in southeast iran. *Iran J Public Health* 2015; **44**: 1359–66.

46 Batistoti C M., Jankevicius SI. Genetic variability of trypanosomatids isolated from phytophagous hemiptera defined by morphological, biochemical, and molecular taxonomic markers. *J Parasitol* 2001; **87**: 1335–41.

47 Belo G V. S., Silva ES da. Reliability of techniques used in the diagnosis of canine visceral leishmaniasis by the national control program in brazil: A survey in an area of recent transmission. *Prev Vet Med* 2017; **146**: 10–5.

48 Bento G-H E. C., Ramirez LE. Identification of bat trypanosomes from minas gerais state, brazil, based on 18S rDNA and cathepsin-l-like targets. *Parasitol Res* 2018; **117**: 737–46.

49 Berlin N D., Baneth G. Prevalence of trypanosoma evansi in horses in israel evaluated by serology and reverse dot blot. *Res Vet Sci* 2012; **93**: 1225–30.

50 Bernal XE, Pinto CM. Sexual differences in prevalence of a new species of trypanosome infecting tungara frogs. *Int J Parasitol Parasites Wildl* 2016; **5**: 40–7.

51 Berzunza-Cruz R-M M., Becker I. Leishmania (l.) Mexicana infected bats in mexico: Novel potential reservoirs. *PLoS Negl Trop Dis* 2015; **9**: e0003438.

52 Bezerra C C. M., Diotaiut L. Domestic, peridomestic and wild hosts in the transmission of trypanosoma cruzi in the caatinga area colonised by triatoma brasiliensis. *Mem Inst Oswaldo Cruz* 2014; **109**: 887–98.

53 Bhattarai D N. R., Dujardin JC. Natural infection of phlebotomus argentipes with leishmania and other trypanosomatids in a visceral leishmaniasis endemic region of nepal. *Trans R Soc Trop Med Hyg* 2009; **103**: 1087–92.

54 Birhanu F H., Buscher P. Epidemiology of trypanosoma evansi and trypanosoma vivax in domestic animals from selected districts of tigray and afar regions, northern ethiopia. *Parasit Vectors* 2015; **8**: 212.

55 Biryomumaisho R S., Lubega GW. Livestock trypanosomosis in uganda: Parasite heterogeneity and anaemia status of naturally infected cattle, goats and pigs. *Parasitol Res* 2013; **112**: 1443–50.

56 Borghesan C T. C., Camargo EP. Genetic diversity and phylogenetic relationships of coevolving symbiont-harboring insect trypanosomatids, and their neotropical dispersal by invader african blowflies (calliphoridae). *Front Microbiol* 2018; **9**: 131.

57 Botero T A., Thompson RC. Trypanosomes genetic diversity, polyparasitism and the population decline of the critically endangered australian marsupial, the brush tailed bettong or woylie (bettongia penicillata). *Int J Parasitol Parasites Wildl* 2013; **2**: 77–89.

58 Boushaki A D., Kechemir Issad N. Epidemiological investigations on trypanosoma evansi infection in dromedary camels in the south of algeria. *Heliyon* 2019; **5**: e02086.

59 Buendía M-H Maria, Higes M. Epidemiological study of honeybee pathogens in europe: The results of castilla-la mancha (spain). *Spanish Journal of Agricultural Research* 2018; **16**. DOI:10.5424/sjar/2018162-11474.

60 Can D H., Guruz Y. Seroprevalence of leishmania infection and molecular detection of leishmania tropica and leishmania infantum in stray cats of izmir, turkey. *Exp Parasitol* 2016; **167**: 109–14.

61 Cardia C D. F., Bresciani KD. Prevalence of toxoplasma gondii and leishmania spp. Infection in cats from brazil. *Vet Parasitol* 2013; **197**: 634–7.

62 Cardinal O M. V., Gurtler RE. Heterogeneities in the ecoepidemiology of trypanosoma cruzi infection in rural communities of the argentinean chaco. *Am J Trop Med Hyg* 2014; **90**: 1063–73.

63 Cardoso R L., Schallig HD. Sero-epidemiological study of canine leishmania spp. Infection in the municipality of alijo (alto douro, portugal). *Vet Parasitol* 2004; **121**: 21–32.

64 Carvalho W F. S., Rezende RP. Leishmania (viannia) braziliensis in dogs in brazil: Epidemiology, co-infection, and clinical aspects. *Genet Mol Res* 2015; **14**: 12062–73.

65 Cassini S R., Pietrobelli M. Preliminary study of the effects of preventive measures on the prevalence of canine leishmaniosis in a recently established focus in northern italy. *Vet Ital* 2013; **49**: 157–61.

66 Castillo-Neyra CC R., Levy MZ. The potential of canine sentinels for reemerging trypanosoma cruzi transmission. *Prev Vet Med* 2015; **120**: 349–56.

67 Cavigli D I., Flenniken ML. Pathogen prevalence and abundance in honey bee colonies involved in almond pollination. *Apidologie* 2016; **47**: 251–66.

68 Ceballos C L. A., Gurtler RE. Long-term reduction of trypanosoma cruzi infection in sylvatic mammals following deforestation and sustained vector surveillance in northwestern argentina. *Acta Trop* 2006; **98**: 286–96.

69 Chagas S Ecds, Guerra M. Composition of sand fly fauna (diptera: Psychodidae) and detection of leishmania DNA (kinetoplastida: Trypanosomatidae) in different ecotopes from a rural settlement in the central amazon, brazil. *Parasit Vectors* 2018; **11**: 180.

70 Chargui H N., Babba H. Use of PCR, IFAT and in vitro culture in the detection of leishmania infantum infection in dogs and evaluation of the prevalence of canine leishmaniasis in a low endemic area in tunisia. *Parasite* 2009; **16**: 65–9.

71 Chemkhi S J., Guerbouj S. Natural infection of algerian hedgehog, atelerix algirus (lereboullet 1842) with leishmania parasites in tunisia. *Acta Trop* 2015; **150**: 42–51.

72 Cherenet S T., Bossche P van den. Seasonal prevalence of bovine trypanosomosis in a tsetse-infested zone and a tsetse-free zone of the amhara region, north-west ethiopia. *Onderstepoort J Vet Res* 2004; **71**: 307–12.

73 Clausen C P. H., Schein E. A field study to estimate the prevalence of trypanosoma equiperdum in mongolian horses. *Vet Parasitol* 2003; **115**: 9–18.

74 Colla O Sheila R., Thomson JD. Plight of the bumble bee: Pathogen spillover from commercial to wild populations. *Biological Conservation* 2006; **129**: 461–7.

75 Comeaux C-R J. M., Hamer SA. Survey of feral swine (sus scrofa) infection with the agent of chagas disease (trypanosoma cruzi) in texas, 2013-14. *J Wildl Dis* 2016; **52**: 627–30.

76 Cordes H N., Solter LF. Interspecific geographic distribution and variation of the pathogens nosema bombi and crithidia species in united states bumble bee populations. *J Invertebr Pathol* 2012; **109**: 209–16.

77 Coura-Vital M W., Carneiro M. Prevalence and factors associated with leishmania infantum infection of dogs from an urban area of brazil as identified by molecular methods. *PLoS Negl Trop Dis* 2011; **5**: e1291.

78 Cringoli R G., Capelli G. Serological survey of neospora caninum and leishmania infantum co-infection in dogs. *Vet Parasitol* 2002; **106**: 307–13.

79 Crisante R G., Anez N. Infected dogs as a risk factor in the transmission of human trypanosoma cruzi infection in western venezuela. *Acta Trop* 2006; **98**: 247–54.

80 D'Alvise S P., Hasselmann M. Seasonal dynamics and co-occurrence patterns of honey bee pathogens revealed by high-throughput RT-qPCR analysis. *Ecol Evol* 2019; **9**: 10241–52.

81 D'Andrea FE L. A., Tolezano JE. The shadows of a ghost: A survey of canine leishmaniasis in presidente prudente and its spatial dispersion in the western region of sao paulo state, an emerging focus of visceral leishmaniasis in brazil. *BMC Vet Res* 2015; **11**: 273.

82 Costa C da A. P., Marcili A. Trypanosoma cruzi and leishmania infantum chagasi infection in wild mammals from maranhao state, brazil. *Vector Borne Zoonotic Dis* 2015; **15**: 656–66.

83 Davison T H. C., Luckins AG. The occurrence of trypanosoma evansi in buffaloes in indonesia, estimated using various diagnostic tests. *Epidemiol Infect* 2000; **124**: 163–72.

84 Almeida Ado S de B., Madeira Mde F. Canine visceral leishmaniasis: Seroprevalence and risk factors in cuiaba, mato grosso, brazil. *Rev Bras Parasitol Vet* 2012; **21**: 359–65.

85 Avelar B de D. M., Linardi PM. Endosymbionts of ctenocephalides felis felis (siphonaptera: Pulicidae) obtained from dogs captured in belo horizonte, minas gerais, brazil. *J Invertebr Pathol* 2007; **94**: 149–52.

86 Carvalho L A. G., Fontes CJF. High seroprevalence and peripheral spatial distribution of visceral leishmaniasis among domestic dogs in an emerging urban focus in central brazil: A cross-sectional study. *Pathog Glob Health* 2018; **112**: 29–36.

87 Matos C Amrn, Navarro IT. Antibodies anti-trypanosomatides in domestic cats in parana: Who is at highest risk of infection? *Rev Bras Parasitol Vet* 2018; **27**: 232–6.

88 Paula C M. B., Costa-Cruz JM. Occurrence of positivity for trypanosoma cruzi in triatomine from municipalities in southeastern brazil, from 2002 to 2004. *Rev Soc Bras Med Trop* 2010; **43**: 9–14.

89 Thoisy M de B., Vie JC. A survey of hemoparasite infections in free-ranging mammals and reptiles in french guiana. *J Parasitol* 2000; **86**: 1035–40.

90 Delafosse A, Doutoum AA. Prevalence of trypanosoma evansi infection and associated risk factors in camels in eastern chad. *Vet Parasitol* 2004; **119**: 155–64.

91 Delafosse T A., Michaux Y. Epidemiology of trypanosoma vivax infection in cattle in the tse-tse free area of lake chad. *Prev Vet Med* 2006; **74**: 108–19.

92 Dennis D J. W., MacLeod ET. Sodalis glossinidius prevalence and trypanosome presence in tsetse from luambe national park, zambia. *Parasit Vectors* 2014; **7**: 378.

93 Desquesnes K M., Jittapalapong S. Antibody-ELISA for trypanosoma evansi: Application in a serological survey of dairy cattle, thailand, and validation of a locally produced antigen. *Prev Vet Med* 2009; **90**: 233–41.

94 Dias R-S E. S., Fortes-Dias CL. Eco-epidemiology of visceral leishmaniasis in the urban area of paracatu, state of minas gerais, brazil. *Vet Parasitol* 2011; **176**: 101–11.

95 Dias T-S R. C. F., Navarro IT. Variables associated with the prevalence of anti-leishmania spp. Antibodies in dogs on the tri-border of foz do iguacu, parana, brazil. *Rev Bras Parasitol Vet* 2018; **27**: 338–47.

96 Dorn D P. L., Phillippi-Falkenstein KM. Low prevalence of chagas parasite infection in a nonhuman primate colony in louisiana. *J Am Assoc Lab Anim Sci* 2012; **51**: 443–7.

97 Elmayan T A., Dumonteil E. High prevalence of trypanosoma cruzi infection in shelter dogs from southern louisiana, USA. *Parasit Vectors* 2019; **12**: 322.

98 Elshafie RAH E. I.Sani. Active infection and morphometric study of trypanosoma evansi among horses in peninsula malaysia. *Tropical Biomedicine* 2013; **30**: 444–50.

99 Felipe A I. M., Caldas Ade J. Leishmania infection in humans, dogs and sandflies in a visceral leishmaniasis endemic area in maranhao, brazil. *Mem Inst Oswaldo Cruz* 2011; **106**: 207–11.

100 Fernandez-Bellon S-G H., Ramis A. Little evidence of seasonal variation of natural infection by leishmania infantum in dogs in spain. *Vet Parasitol* 2008; **155**: 32–6.

101 Ferroglio B E., Biglino A. Epidemiological evaluation of leishmania infantum zoonotic transmission risk in the recently established endemic area of northwestern italy. *Zoonoses Public Health* 2018; **65**: 675–82.

102 Figueiredo M F. B., Schubach TM. Canine visceral leishmaniasis: Study of methods for the detection of IgG in serum and eluate samples. *Rev Inst Med Trop Sao Paulo* 2010; **52**: 193–6.

103 Fikru G R., Buscher P. Widespread occurrence of trypanosoma vivax in bovines of tsetse- as well as non-tsetse-infested regions of ethiopia: A reason for concern? *Vet Parasitol* 2012; **190**: 355–61.

104 Franca-Silva da C J. C., Nascimento E. Epidemiology of canine visceral leishmaniosis in the endemic area of montes claros municipality, minas gerais state, brazil. *Vet Parasitol* 2003; **111**: 161–73.

105 Freitas N R. A., Barrett TV. Species diversity and flagellate infections in the sand fly fauna near porto grande, state of amapa, brazil (diptera: Psychodidae. Kinetoplastida: trypanosomatidae). *Mem Inst Oswaldo Cruz* 2002; **97**: 53–9.

106 Fujimori A M.de Almeida. Prevalence and associated factors of canine visceral leishmaniasis in an endemic area of mato grosso, brazil. *Acta Scientiae Veterinariae* 2016; **44**. <Go to ISI>://WOS:000392090700003.

107 Gallot-Lavallee S-H M., Schmid-Hempel P. Large scale patterns of abundance and distribution of parasites in mexican bumblebees. *J Invertebr Pathol* 2016; **133**: 73–82.

108 Galvez M R., Molina R. Emerging trends in the seroprevalence of canine leishmaniasis in the madrid region (central spain). *Vet Parasitol* 2010; **169**: 327–34.

109 Galvis-Ovallos C F., Galati EAB. Ecological parameters of the (s)-9-methylgermacrene-b population of the lutzomyia longipalpis complex in a visceral leishmaniasis area in sao paulo state, brazil. *Parasit Vectors* 2017; **10**: 269.

110 Garcia R H. A., Teixeira MMG. Remarkable richness of trypanosomes in tsetse flies (glossina morsitans morsitans and glossina pallidipes) from the gorongosa national park and niassa national reserve of mozambique revealed by fluorescent fragment length barcoding (FFLB). *Infect Genet Evol* 2018; **63**: 370–9.

111 Garcia G H., Mendoza-Leon A. Trypanosomiasis in venezuelan water buffaloes: Association of packed-cell volumes with seroprevalence and current trypanosome infection. *Ann Trop Med Parasitol* 2006; **100**: 297–305.

112 Garvin S M. C., Moore FR. Blood parasites of nearctic-neotropical migrant passerine birds during spring trans-gulf migration: Impact on host body condition. *J Parasitol* 2006; **92**: 990–6.

113 Gebre-Michael B T., Gramiccia M. The isolation of leishmania tropica and l. Aethiopica from phlebotomus (paraphlebotomus) species (diptera: Psychodidae) in the awash valley, northeastern ethiopia. *Trans R Soc Trop Med Hyg* 2004; **98**: 64–70.

114 Ghawar T W., Ben-Salah A. Leishmania major infection among psammomys obesus and meriones shawi: Reservoirs of zoonotic cutaneous leishmaniasis in sidi bouzid(central tunisia). *Vector Borne Zoonotic Dis* 2011; **11**: 1561–8.

115 Gillespie S. Factors affecting parasite prevalence among wild bumblebees. *Ecological Entomology* 2010; **35**: 737–47.

116 Gillingwater M K., Majiwa PA. Prevalence of mixed trypanosoma congolense infections in livestock and tsetse in KwaZulu-natal, south africa. *J S Afr Vet Assoc* 2010; **81**: 219–23.

117 Giorgobiani C E., Sacks D. Epidemiologic aspects of an emerging focus of visceral leishmaniasis in tbilisi, georgia. *PLoS Negl Trop Dis* 2011; **5**: e1415.

118 Gizzarelli FM M., Maurelli MP. Simultaneous detection of parasitic vector borne diseases: A robust cross-sectional survey in hunting, stray and sheep dogs in a mediterranean area. *Front Vet Sci* 2019; **6**: 288.

119 Godoi S M. M., Camargo EP. A PCR-based survey on phytomonas (euglenozoa: Trypanosomatidae) in phytophagous hemipterans of the amazon region. *J Eukaryot Microbiol* 2002; **49**: 275–9.

120 Goossens M B., Vreysen M. Trypanosomosis prevalence in cattle on mafia island (tanzania). *Vet Parasitol* 2006; **139**: 74–83.

121 Goulson O Dave, Park KJ. The impacts of predators and parasites on wild bumblebee colonies. *Ecological Entomology* 2018; **43**: 168–81.

122 Goulson W Dave, Fowley M. Influence of urbanisation on the prevalence of protozoan parasites of bumblebees. *Ecological Entomology* 2012; **37**: 83–9.

123 Greenaway C, Castelli F. Migration medicine. *Infect Dis Clin North Am* 2019; **33**: 265–87.

124 Grijalva V M. J., Baus EG. Comprehensive survey of domiciliary triatomine species capable of transmitting chagas disease in southern ecuador. *PLoS Negl Trop Dis* 2015; **9**: e0004142.

125 Grybchuk-Ieremenko L A., Yurchenko V. High prevalence of trypanosome co-infections in freshwater fishes. *Folia Parasitol (Praha)* 2014; **61**: 495–504.

126 Gutierrez J C., Montoya JA. Camel trypanosomosis in the canary islands: Assessment of seroprevalence and infection rates using the card agglutination test (CATT/t. Evansi) and parasite detection tests. *Veterinary Parasitology* 2000; **90**: 155–9.

127 Hagos A A., Claes F. Serological and parasitological survey of dourine in the arsi-bale highlands of ethiopia. *Trop Anim Health Prod* 2010; **42**: 769–76.

128 Hagos D A., Goddeeris BM. Seroepidemiological survey of trypanozoon infection in horses in the suspected dourine-infected bale highlands of the oromia region, ethiopia. *Rev Sci Tech* 2010; **29**: 649–54.

129 Hamel S D., Rehbein S. Parasites and vector-borne pathogens in client-owned dogs in albania. Blood pathogens and seroprevalences of parasitic and other infectious agents. *Parasitol Res* 2016; **115**: 489–99.

130 Hauptmanova VL K.Benedikt. Blood parasites in passerine birds in slovakian east carpathians. *Acta Protozoologica* 2006; **45**: 105–9.

131 Herrera D H. M., Jansen AM. Enzootiology of trypanosoma evansi in pantanal, brazil. *Vet Parasitol* 2004; **125**: 263–75.

132 Hodo G C. L., Hamer SA. Trypanosome species, including trypanosoma cruzi, in sylvatic and peridomestic bats of texas, USA. *Acta Trop* 2016; **164**: 259–66.

133 Hosseininejad MH M.Mohebali. Seroprevalence of canine visceral leishmaniasis in asymptomatic dogs in iran. *Iranian Journal of Veterinary Research* 2012; **13**: 54–7.

134 Isaac C C., Turner CM. Molecular identification of different trypanosome species and subspecies in tsetse flies of northern nigeria. *Parasit Vectors* 2016; **9**: 301.

135 Jabal-Uriel M-H Clara, De la Rua P. Short communication: First data on the prevalence and distribution of pathogens in bumblebees (bombus terrestris and bombus pascuorum) from spain. *Spanish Journal of Agricultural Research* 2017; **15**. DOI:10.5424/sjar/2017151-9998.

136 Jaimes-Duenez Z-Z J., Mejia-Jaramillo AM. Evaluation of an alternative indirect-ELISA test using in vitro-propagated trypanosoma brucei brucei whole cell lysate as antigen for the detection of anti-trypanosoma evansi IgG in colombian livestock. *Prev Vet Med* 2019; **169**: 104712.

137 Jaimes-Duenez T-C J., Mejia-Jaramillo AM. Parasitological and molecular surveys reveal high rates of infection with vector-borne pathogens and clinical anemia signs associated with infection in cattle from two important livestock areas in colombia. *Ticks Tick Borne Dis* 2017; **8**: 290–9.

138 Jiang W W., Wang Q. Seroepidemiological study of canine leishmania infantum and toxoplasma gondii infections in shanghai, china, and analysis of risk factors. *Ann Agric Environ Med* 2016; **23**: 420–4.

139 Karakus T M., Ozbel Y. Evaluation of conjunctival swab sampling in the diagnosis of canine leishmaniasis: A two-year follow-up study in cukurova plain, turkey. *Vet Parasitol* 2015; **214**: 295–302.

140 Karlsbakk E. Prevalence of trypanosome infections in marine fishes from western norway. *Sarsia* 2010; **89**: 459–66.

141 Karshima A S. N., Mohammed G. Eco-epidemiology of porcine trypanosomosis in karim lamido, nigeria: Prevalence, seasonal distribution, tsetse density and infection rates. *Parasit Vectors* 2016; **9**: 448.

142 Kassahun S A., Votypka J. Detection of leishmania donovani and l. Tropica in ethiopian wild rodents. *Acta Trop* 2015; **145**: 39–44.

143 Katakweba M Abdul A. S., Belmain SR. Prevalence of haemoparasites, leptospires and coccobacilli with potential for human infection in the blood of rodents and shrews from selected localities in tanzania, namibia and swaziland†. *African Zoology* 2012; **47**: 119–27.

144 Kato G Hirotomo, Cáceres AG. Molecular mass screening to incriminate sand fly vectors of andean-type cutaneous leishmaniasis in ecuador and peru. *The American Journal of Tropical Medicine and Hygiene* 2008; **79**: 719–21.

145 Kato C H., Hashiguchi Y. First evidence of a hybrid of leishmania (viannia) braziliensis/l. (V.) Peruviana DNA detected from the phlebotomine sand fly lutzomyia tejadai in peru. *PLoS Negl Trop Dis* 2016; **10**: e0004336.

146 Khan ASH A. U.Qureshi. Molecular identification of trypanosomes and their effects on hematological and biochemical parameters in donkeys in punjab, pakistan. *International Journal of Agriculture and Biology* 2018; **20**: 1607–12.

147 Kidanemariam H A., Sahle M. Parasitological prevalence of bovine trypanosomosis in kindo koisha district, wollaita zone, south ethiopia. *Onderstepoort J Vet Res* 2002; **69**: 107–13.

148 Kissinger C C. N., Solter LF. Survey of bumble bee (bombus) pathogens and parasites in illinois and selected areas of northern california and southern oregon. *J Invertebr Pathol* 2011; **107**: 220–4.

149 Kocher D A., Jittapalapong S. Evaluation of an indirect-ELISA test for trypanosoma evansi infection (surra) in buffaloes and its application to a serological survey in thailand. *Biomed Res Int* 2015; **2015**: 361037.

150 Korner P, Schmid-Hempel P. Correlates of parasite load in bumblebees in an alpine habitat. *Entomological Science* 2005; **8**: 151–60.

151 Kouam D M. K., Theodoropoulos G. A seroepidemiological study of exposure to toxoplasma, leishmania, echinococcus and trichinella in equids in greece and analysis of risk factors. *Vet Parasitol* 2010; **170**: 170–5.

152 Kozminsky K E., Maslov DA. Host-specificity of monoxenous trypanosomatids: Statistical analysis of the distribution and transmission patterns of the parasites from neotropical heteroptera. *Protist* 2015; **166**: 551–68.

153 Lana M R. S., Dias ES. Ecoepidemiological aspects of visceral leishmaniasis in an endemic area in the steel valley in brazil: An ecological approach with spatial analysis. *PLoS One* 2018; **13**: e0206452.

154 Laohasinnarong G D., Namangala B. Studies of trypanosomiasis in the luangwa valley, north-eastern zambia. *Parasit Vectors* 2015; **8**: 497.

155 Lardeux A F., Depickere S. Bias due to methods of parasite detection when estimating prevalence of infection of triatoma infestans by trypanosoma cruzi. *J Vector Ecol* 2016; **41**: 285–91.

156 Lauricella S M. A., Gurtler RE. Distribution and pathogenicity of trypanosoma cruzi isolated from peridomestic populations of triatoma infestans and triatoma guasayana from rural western argentina. *Mem Inst Oswaldo Cruz* 2005; **100**: 123–9.

157 Leal C G. G. A., Coura-Vital W. Risk profile for leishmania infection in dogs coming from an area of visceral leishmaniasis reemergence. *Prev Vet Med* 2018; **150**: 1–7.

158 Lledo G-P L., Serrano JL. Wild red foxes (vulpes vulpes) as sentinels of parasitic diseases in the province of soria, northern spain. *Vector Borne Zoonotic Dis* 2015; **15**: 743–9.

159 Lopez-Cespedes L A., Marin C. Leishmania spp. Epidemiology of canine leishmaniasis in the yucatan peninsula. *ScientificWorldJournal* 2012; **2012**: 945871.

160 Lopez-Cespedes L A., Marin C. Seroprevalence of antibodies against the excreted antigen superoxide dismutase by trypanosoma cruzi in dogs from the yucatan peninsula (mexico). *Zoonoses Public Health* 2013; **60**: 277–83.

161 Machila S N., Eisler MC. Antibody-ELISA seroprevalence of bovine trypanosomosis in the eastern province of zambia. *Prev Vet Med* 2001; **49**: 249–57.

162 Magallon-Gastelum L-K E., Breniere SF. Epidemiological risk for trypanosoma cruzi transmission by species of phyllosoma complex in the occidental part of mexico. *Acta Trop* 2006; **97**: 331–8.

163 Maia R C., Campino L. Bacterial and protozoal agents of feline vector-borne diseases in domestic and stray cats from southern portugal. *Parasit Vectors* 2014; **7**: 115.

164 Majekodunmi F A. O., Welburn SC. A longitudinal survey of african animal trypanosomiasis in domestic cattle on the jos plateau, nigeria: Prevalence, distribution and risk factors. *Parasit Vectors* 2013; **6**: 239.

165 Malele C Imna, Gibson W. The use of specific and generic primers to identify trypanosome infections of wild tsetse flies in tanzania by PCR. *Infection, Genetics and Evolution* 2003; **3**: 271–9.

166 Malfi RL, Roulston TH. Patterns of parasite infection in bumble bees (bombusspp.) Of northern virginia. *Ecological Entomology* 2014; **39**: 17–29.

167 Maloney N J., Moncayo AC. Seroprevalence of trypanosoma cruzi in raccoons from tennessee. *J Parasitol* 2010; **96**: 353–8.

168 Mamoudou N A., Achukwi MD. Animal trypanosomosis in clinically healthy cattle of north cameroon: Epidemiological implications. *Parasit Vectors* 2016; **9**: 206.

169 Marti E G. A., Garcia JJ. Prevalence and distribution of parasites and pathogens of triatominae from argentina, with emphasis on triatoma infestans and triatoma virus TrV. *J Invertebr Pathol* 2009; **102**: 233–7.

170 Martin-Sanchez G J., Morillas-Marquez F. Pool screen PCR for estimating the prevalence of leishmania infantum infection in sandflies (diptera: Nematocera, phlebotomidae). *Trans R Soc Trop Med Hyg* 2006; **100**: 527–32.

171 Martinez-Hernandez R-F F., Villalobos G. Follow up of natural infection with trypanosoma cruzi in two mammals species, nasua narica and procyon lotor (carnivora: Procyonidae): Evidence of infection control? *Parasit Vectors* 2014; **7**: 405.

172 Mascolli S Roberta, Vasconcellos SA. Prevalence and risk factors for leishmaniasis and chagas disease in the canine population of the tourist city of ibiúna, são paulo, brazil. *Semina: Ciências Agrárias* 2016; **37**: 1971–80.

173 Maslov W D. A., Sturm NR. Discovery and barcoding by analysis of spliced leader RNA gene sequences of new isolates of trypanosomatidae from heteroptera in costa rica and ecuador. *J Eukaryot Microbiol* 2007; **54**: 57–65.

174 Mejia-Jaramillo A-U A. M., Triana-Chavez O. Genotyping of trypanosoma cruzi in a hyper-endemic area of colombia reveals an overlap among domestic and sylvatic cycles of chagas disease. *Parasit Vectors* 2014; **7**: 108.

175 Mekata K H., Ohashi K. Prevalence and source of trypanosome infections in field-captured vector flies (glossina pallidipes) in southeastern zambia. *J Vet Med Sci* 2008; **70**: 923–8.

176 Mekata K H., Ohashi K. Molecular detection of trypanosomes in cattle in south america and genetic diversity of trypanosoma evansi based on expression-site-associated gene 6. *Infect Genet Evol* 2009; **9**: 1301–5.

177 Mekibib MT B.Manegerew. Prevalence of haemoparasites and associated risk factors in working donkeys in adigudem and kwiha districts of tigray region, northern ethiopia. *Journal of Animal and Veterinary Advances* 2010; **9**: 2249–55.

178 Mekonnen VK B.Regassa. Epidemiology of trypanosomosis in goats in abelti, bede and ghibe valley, south west ethiopia. *International Journal of Tropical Medicine* 2014; **9**: 10–4.

179 Araujo Melo B de S., Abreu-Silva AL. Bovine trypanosomiasis an emerging disease in maranhao state-brazil. *Vector Borne Zoonotic Dis* 2011; **11**: 853–6.

180 Menezes FE J. A., Margonari C. An integrated approach using spatial analysis to study the risk factors for leishmaniasis in area of recent transmission. *Biomed Res Int* 2015; **2015**: 621854.

181 Meyers M A. C., Hamer SA. Widespread trypanosoma cruzi infection in government working dogs along the texas-mexico border: Discordant serology, parasite genotyping and associated vectors. *PLoS Negl Trop Dis* 2017; **11**: e0005819.

182 Mihret A, Mamo G. Bovine trypanosomosis in three districts of east gojjam zone bordering the blue nile river in ethiopia. *J Infect Dev Ctries* 2007; **1**: 321–5.

183 Miro C G., Galvez R. Current situation of leishmania infantum infection in shelter dogs in northern spain. *Parasit Vectors* 2012; **5**: 60.

184 Miro M G., Molina R. A leishmaniosis surveillance system among stray dogs in the region of madrid: Ten years of serodiagnosis (1996-2006). *Parasitol Res* 2007; **101**: 253–7.

185 Mohebali H M., Fakhar M. Epidemiological aspects of canine visceral leishmaniosis in the islamic republic of iran. *Vet Parasitol* 2005; **129**: 243–51.

186 Molina R J. M., Gutiérrez C. Seroprevalence of trypanosoma evansi in dromedaries (camelus dromedarius) from the canary islands (spain) using an antibody ab-ELISA. *Preventive Veterinary Medicine* 2000; **47**: 53–9.

187 Monroy R C., Tabaru Y. Epidemiology of chagas disease in guatemala: Infection rate of triatoma dimidiata, triatoma nitida and rhodnius prolixus (hemiptera, reduviidae) with trypanosoma cruzi and trypanosoma rangeli (kinetoplastida, trypanosomatidae). *Mem Inst Oswaldo Cruz* 2003; **98**: 305–10.

188 Morimoto K T., Kadowaki T. Molecular detection of protozoan parasites infecting apis mellifera colonies in japan. *Environ Microbiol Rep* 2013; **5**: 74–7.

189 Muhanguzi M D., Tweyongyere R. African animal trypanosomiasis as a constraint to livestock health and production in karamoja region: A detailed qualitative and quantitative assessment. *BMC Vet Res* 2017; **13**: 355.

190 Muhanguzi P D., Welburn SC. The burden and spatial distribution of bovine african trypanosomes in small holder crop-livestock production systems in tororo district, south-eastern uganda. *Parasit Vectors* 2014; **7**: 603.

191 N'Djetchi I M. K., Jamonneau V. The study of trypanosome species circulating in domestic animals in two human african trypanosomiasis foci of cote d'ivoire identifies pigs and cattle as potential reservoirs of trypanosoma brucei gambiense. *PLoS Negl Trop Dis* 2017; **11**: e0005993.

192 Nakayima N J., Sugimoto C. Molecular epidemiological studies on animal trypanosomiases in ghana. *Parasit Vectors* 2012; **5**: 217.

193 Sachman-Ruiz N-P Bernardo, Reynaud E. Commercial bombus impatiens as reservoirs of emerging infectious diseases in central méxico. *Biological Invasions* 2015; **17**: 2043–53.

194 Ngaira B J. M., Karanja SM. Animal-level risk factors for trypanosoma evansi infection in camels in eastern and central parts of kenya. *Onderstepoort J Vet Res* 2002; **69**: 263–71.

195 Ngonyoka G A., Cattadori IM. Patterns of tsetse abundance and trypanosome infection rates among habitats of surveyed villages in maasai steppe of northern tanzania. *Infect Dis Poverty* 2017; **6**: 126.

196 Mbang Nguema BA O., Mawili Mboumba DP. Variations of glossina sp. And trypanosome species frequency within different habitats in a sleeping sickness focus, gabon. *J Infect Dev Ctries* 2019; **13**: 67–72.

197 Njiokou N F., Herder S. Domestic animals as potential reservoir hosts of trypanosoma brucei gambiense in sleeping sickness foci in cameroon. *Parasite* 2010; **17**: 61–6.

198 Njiru C Z. K., Reid SA. Detection of trypanosoma evansi in camels using PCR and CATT/t. Evansi tests in kenya. *Vet Parasitol* 2004; **124**: 187–99.

199 Northover G A. S., Thompson RCA. Increased trypanosoma spp. Richness and prevalence of haemoparasite co-infection following translocation. *Parasit Vectors* 2019; **12**: 126.

200 Oakgrove H K. S., Sehgal RN. Distribution, diversity and drivers of blood-borne parasite co-infections in alaskan bird populations. *Int J Parasitol* 2014; **44**: 717–27.

201 Odeniran M P. O., Welburn SC. Molecular identification of bovine trypanosomes in relation to cattle sources in southwest nigeria. *Parasitol Int* 2019; **68**: 1–8.

202 Oliveira P G. C., Langoni H. Antibodies to leishmania spp. In domestic felines. *Rev Bras Parasitol Vet* 2015; **24**: 464–70.

203 Onyekwelu FEE K. C.Ejezie. Molecular identification of trypanosomes in tsetse flies trapped from onicha ugbo in delta state of nigeria. *Biomedical Research-India* 2017; **28**: 5463–7.

204 Opara BO M. N.Fagbemi. Animal biodiversity and emerging diseases: Prediction and prevention. 2008; **1149**: 394–7.

205 Oshaghi R M. A., Rassi Y. Vector incrimination of sand flies in the most important visceral leishmaniasis focus in iran. *Am J Trop Med Hyg* 2009; **81**: 572–7.

206 Otranto N D., Brianti E. Feline and canine leishmaniosis and other vector-borne diseases in the aeolian islands: Pathogen and vector circulation in a confined environment. *Vet Parasitol* 2017; **236**: 144–51.

207 Otranto T D., Breitschwerdt EB. Diagnosis of canine vector-borne diseases in young dogs: A longitudinal study. *J Clin Microbiol* 2010; **48**: 3316–24.

208 Ouedraogo D-U G. M. S., Abd-Alla AMM. Prevalence of trypanosomes, salivary gland hypertrophy virus and wolbachia in wild populations of tsetse flies from west africa. *BMC Microbiol* 2018; **18**: 153.

209 Ozbel O Y., Ozcel MA. A survey on canine leishmaniasis in western turkey by parasite, DNA and antibody detection assays. *Acta Trop* 2000; **74**: 1–6.

210 Paiz F L. M., Langoni H. Serological evidence of infection by leishmania (leishmania) infantum (synonym: Leishmania (leishmania) chagasi) in free-ranging wild mammals in a nonendemic region of the state of sao paulo, brazil. *Vector Borne Zoonotic Dis* 2015; **15**: 667–73.

211 Parashar S R., Bal MS. Unraveling cryptic epizootiology of equid trypanosomosis in punjab state of india by parasitological and sero-molecular techniques. *Acta Trop* 2018; **185**: 18–26.

212 Paz R G. F., Dias ES. Association between the prevalence of infestation by rhipicephalus sanguineus and ctenocephalides felis felis and the presence of anti-leishmania antibodies: A case-control study in dogs from a brazilian endemic area. *Prev Vet Med* 2010; **97**: 131–3.

213 Plischuk A S., Lange CE. Long-term prevalence of the protists crithidia bombi and apicystis bombi and detection of the microsporidium nosema bombi in invasive bumble bees. *Environ Microbiol Rep* 2017; **9**: 169–73.

214 Popp E M., Lattorff HM. Seasonal variability of prevalence and occurrence of multiple infections shape the population structure of crithidia bombi, an intestinal parasite of bumblebees (bombus spp.). *Microbiologyopen* 2012; **1**: 362–72.

215 Rangel L D. A., Roque ALR. Isolation and characterization of trypanosomatids, including crithidia mellificae, in bats from the atlantic forest of rio de janeiro, brazil. *PLoS Negl Trop Dis* 2019; **13**: e0007527.

216 Ravel M S., Davoust B. A study on african animal trypanosomosis in four areas of senegal. *Folia Parasitol (Praha)* 2015; **62**. DOI:10.14411/fp.2015.044.

217 Ravoet M J., Graaf DC de. Comprehensive bee pathogen screening in belgium reveals crithidia mellificae as a new contributory factor to winter mortality. *PLoS One* 2013; **8**: e72443.

218 Reid SA, Copeman DB. Surveys in papua new guinea to detect the presence of trypanosoma evansi infection. *Aust Vet J* 2000; **78**: 843–5.

219 Reithinger E R., Davies CR. Evaluation of PCR as a diagnostic mass-screening tool to detect leishmania (viannia) spp. In domestic dogs (canis familiaris). *J Clin Microbiol* 2003; **41**: 1486–93.

220 Reithinger BEB R.Lambson. Use of PCR to detect leishmania (viannia) spp. In dog blood and bone marrow. *Journal of Clinical Microbiology* 2000; **38**: 748–51.

221 Resadore J F., Medeiros JF. Composition and vertical stratification of phlebotomine sand fly fauna and the molecular detection of leishmania in forested areas in rondonia state municipalities, western amazon, brazil. *Vector Borne Zoonotic Dis* 2019; **19**: 347–57.

222 Ribeiro M A. R., Rosa JA da. Trypanosoma cruzi strains from triatomine collected in bahia and rio grande do sul, brazil. *Rev Saude Publica* 2014; **48**: 295–302.

223 Rocha M Avvo, Costa APD. Diagnosis and epidemiology of leishmania infantum in domestic cats in an endemic area of the amazon region, brazil. *Vet Parasitol* 2019; **273**: 80–5.

224 Rodrigues S A. C., Bevilaqua CM. Epidemiological survey of lutzomyia longipalpis infected by leishmania infantum in an endemic area of brazil. *Rev Bras Parasitol Vet* 2014; **23**: 55–62.

225 Rodriguez T-J N. F., Gutierrez C. Cross-sectional study on prevalence of trypanosoma evansi infection in domestic ruminants in an endemic area of the canary islands (spain). *Prev Vet Med* 2012; **105**: 144–8.

226 Rohousova T-F I., Baneth G. Exposure to leishmania spp. And sand flies in domestic animals in northwestern ethiopia. *Parasit Vectors* 2015; **8**: 360.

227 Rondon B F. C., Diniz AT. Cross-sectional serological study of canine leishmania infection in fortaleza, ceara state, brazil. *Vet Parasitol* 2008; **155**: 24–31.

228 Rowland M M. E., Moncayo AC. Factors associated with trypanosoma cruzi exposure among domestic canines in tennessee. *J Parasitol* 2010; **96**: 547–51.

229 Saghafipour V A., Hanafi-Bojd AA. Epidemiological study on cutaneous leishmaniasis in an endemic area, of qom province, central iran. *J Arthropod Borne Dis* 2017; **11**: 403–13.

230 Salim B B., Sugimoto C. Molecular epidemiology of camel trypanosomiasis based on ITS1 rDNA and RoTat 1.2 VSG gene in the sudan. *Parasit Vectors* 2011; **4**: 31.

231 Salim B B., Sugimoto C. Molecular detection of equine trypanosomes in the sudan. *Vet Parasitol* 2014; **200**: 246–50.

232 Santos G Helcileia Dias, Minharro S. High frequency of visceral leishmaniasis in dogs under veterinary clinical care in an intense transmission area in the state of tocantins, brazil. *Ciência Rural* 2017; **47**. DOI:10.1590/0103-8478cr20160260.

233 Saraiva L L., Andrade JDF. Seasonality of sand flies (diptera: Psychodidae) and leishmania DNA detection in vector species in an area with endemic visceral leishmaniasis. *Mem Inst Oswaldo Cruz* 2017; **112**: 309–18.

234 Sarquis B-P O., Lima MM. Epidemiology of chagas disease in jaguaruana, ceara, brazil. I. Presence of triatomines and index of trypanosoma cruzi infection in four localities of a rural area. *Mem Inst Oswaldo Cruz* 2004; **99**: 263–70.

235 Sauda M F., Perrucci S. Leishmania infantum, dirofilaria spp. And other endoparasite infections in kennel dogs in central italy. *Parasite* 2018; **25**: 2.

236 Savage R A. F., Greiner EC. Blood parasites in birds from madagascar. *J Wildl Dis* 2009; **45**: 907–20.

237 Schoener U E., Fuehrer HP. Trypanosomatid parasites in austrian mosquitoes. *PLoS One* 2018; **13**: e0196052.

238 Schultz U Albert, Underhill G. Infection prevalence and absence of positive correlation between avian haemosporidian parasites, mass and body condition in the cape weaver ploceus capensis. *Ostrich* 2010; **81**: 69–76.

239 Sebaio B Fabiane, Marini MÂn. Blood parasites in brazilian atlantic forest birds: Effects of fragment size and habitat dependency. *Bird Conservation International* 2010; **20**: 432–9.

240 Sebaio B F., Marini MA. Blood parasites in passerine birds from the brazilian atlantic forest. *Rev Bras Parasitol Vet* 2012; **21**: 7–15.

241 Seck B M. T., Vreysen MJ. The prevalence of african animal trypanosomoses and tsetse presence in western senegal. *Parasite* 2010; **17**: 257–65.

242 Sehgal J R. N., Smith TB. Host specificity and incidence of trypanosoma in some african rainforest birds: A molecular approach. *Mol Ecol* 2001; **10**: 2319–27.

243 Shahzad M W., Iqbal M. Prevalence and molecular diagnosis of trypanosoma evansi in nili-ravi buffalo (bubalus bubalis) in different districts of punjab (pakistan). *Trop Anim Health Prod* 2010; **42**: 1597–9.

244 Sharma DS A., Juyal PD. Molecular prevalence of babesia bigemina and trypanosoma evansi in dairy animals from punjab, india, by duplex PCR: A step forward to the detection and management of concurrent latent infections. *Biomed Res Int* 2013; **2013**: 893862.

245 Sharma J P., Pawar H. Comparative evaluation of real time PCR assay with conventional parasitological techniques for diagnosis of trypanosoma evansi in cattle and buffaloes. *Vet Parasitol* 2012; **190**: 375–82.

246 Sheferaw B D., Woldesenbet Z. Bovine trypanosomosis and glossina distribution in selected areas of southern part of rift valley, ethiopia. *Acta Trop* 2016; **154**: 145–8.

247 Shereni A W., Cecchi G. Spatial distribution and trypanosome infection of tsetse flies in the sleeping sickness focus of zimbabwe in hurungwe district. *Parasit Vectors* 2016; **9**: 605.

248 Silva P R. B. S., Melo MA. Seroprevalence and risk factors associated with canine visceral leishmaniasis in the state of paraiba, brazil. *Rev Soc Bras Med Trop* 2018; **51**: 683–8.

249 Simo S G., Asonganyi T. Identification and genetic characterization of trypanosoma congolense in domestic animals of fontem in the south-west region of cameroon. *Infect Genet Evol* 2013; **18**: 66–73.

250 Simukoko M H., Van den Bossche P. The comparative role of cattle, goats and pigs in the epidemiology of livestock trypanosomiasis on the plateau of eastern zambia. *Vet Parasitol* 2007; **147**: 231–8.

251 Simwango N M., Gwakisa PS. Molecular prevalence of trypanosome infections in cattle and tsetse flies in the maasai steppe, northern tanzania. *Parasit Vectors* 2017; **10**: 507.

252 Singh AKS A. P.Tripathi. Seroprevalence of trypanosoma evansi in buffaloes in south western semiarid plane zone of uttarpradesh. *Buffalo Bulletin* 2017; **36**: 483–8.

253 Sinshaw A A., Yoni W. Biting flies and trypanosoma vivax infection in three highland districts bordering lake tana, ethiopia. *Vet Parasitol* 2006; **142**: 35–46.

254 Sousa L S., Cordeiro da Silva A. Seroepidemiological survey of leishmania infantum infection in dogs from northeastern portugal. *Acta Trop* 2011; **120**: 82–7.

255 Specht EJ. Prevalence of bovine trypanosomosis in central mozambique from 2002 to 2005. *Onderstepoort J Vet Res* 2008; **75**: 73–81.

256 Suh N P. F., Garabed R. Bovine trypanosomiasis in tsetse-free pastoral zone of the far-north region, cameroon. *J Vector Borne Dis* 2017; **54**: 263–9.

257 Svobodova V M., Votypka J. Trypanosomatids in ornithophilic bloodsucking diptera. *Med Vet Entomol* 2015; **29**: 444–7.

258 Takeet F M. I., Imumorin IG. Molecular survey of pathogenic trypanosomes in naturally infected nigerian cattle. *Res Vet Sci* 2013; **94**: 555–61.

259 Tasew R S.Duguma. Cattle anaemia and trypanosomiasis in western oromia state, ethiopia. *Revue De Medecine Veterinaire* 2012; **163**: 581–8.

260 Tatard G C., Dobigny G. Rodent-borne trypanosoma from cities and villages of niger and nigeria: A special role for the invasive genus rattus? *Acta Trop* 2017; **171**: 151–8.

261 Tehseen J S., Buscher P. Parasitological, serological and molecular survey of trypanosoma evansi infection in dromedary camels from cholistan desert, pakistan. *Parasit Vectors* 2015; **8**: 415.

262 Teles S C. B., Camargo LM. Phlebotomine sandfly (diptera: Psychodidae) diversity and their leishmania DNA in a hot spot of american cutaneous leishmaniasis human cases along the brazilian border with peru and bolivia. *Mem Inst Oswaldo Cruz* 2016; **0**: 0.

263 Terefe H E., Mwai O. Phenotypic characteristics and trypanosome prevalence of mursi cattle breed in the bodi and mursi districts of south omo zone, southwest ethiopia. *Trop Anim Health Prod* 2015; **47**: 485–93.

264 Thies R S. F., Dias ES. Phlebotomine sandfly fauna and natural leishmania infection rates in a rural area of cerrado (tropical savannah) in nova mutum, state of mato grosso in brazil. *Rev Soc Bras Med Trop* 2013; **46**: 293–8.

265 Tiwary K P., Sundar S. Prevalence of sand flies and leishmania donovani infection in a natural population of female phlebotomus argentipes in bihar state, india. *Vector Borne Zoonotic Dis* 2012; **12**: 467–72.

266 Tognazzo S-H M., Schmid-Hempel P. Probing mixed-genotype infections II: High multiplicity in natural infections of the trypanosomatid, crithidia bombi, in its host, bombus spp. *PLoS One* 2012; **7**: e49137.

267 Tripodi C-S Amber D., Szalanski AL. Nosema bombi(microsporidia: Nosematidae) and trypanosomatid prevalence in spring bumble bee queens (hymenoptera: Apidae:bombus) in kansas. *Journal of the Kansas Entomological Society* 2014; **87**: 225–33.

268 Tripodi S A. D., Strange JP. Novel multiplex PCR reveals multiple trypanosomatid species infecting north american bumble bees (hymenoptera: Apidae: bombus). *J Invertebr Pathol* 2018; **153**: 147–55.

269 Vanderplanck R Maryse, Michez D. Bumble bee parasite prevalence but not genetic diversity impacted by the invasive plant impatiens glandulifera. *Ecosphere* 2019; **10**. DOI:10.1002/ecs2.2804.

270 Vavilova K V. Y., Blinov AG. Parasites of the genus nosema, crithidia and lotmaria in the honeybee and bumblebee populations: A case study in india. *Vavilov Journal of Genetics and Breeding* 2017; **21**: 943–51.

271 Villagran M M. E., Diego JA de. Natural infection and distribution of triatomines (hemiptera: Reduviidae) in the state of queretaro, mexico. *Trans R Soc Trop Med Hyg* 2008; **102**: 833–8.

272 Votypka K J., Lukes J. High prevalence and endemism of trypanosomatids on a small caribbean island. *J Eukaryot Microbiol* 2019; **66**: 600–7.

273 Votypka M J., Lukes J. Probing into the diversity of trypanosomatid flagellates parasitizing insect hosts in south-west china reveals both endemism and global dispersal. *Mol Phylogenet Evol* 2010; **54**: 243–53.

274 Votypka S J., Yurchenko V. Diversity of trypanosomatids (kinetoplastea: Trypanosomatidae) parasitizing fleas (insecta: Siphonaptera) and description of a new genus blechomonas gen. n. *Protist* 2013; **164**: 763–81.

275 Waiswa O-M C., Katunguka-Rwakishaya E. Domestic animals as reservoirs for sleeping sickness in three endemic foci in south-eastern uganda. *Ann Trop Med Parasitol* 2003; **97**: 149–55.

276 Weber N J. S., Kelm S. Genetic diversity of trypanosome species in tsetse flies (glossina spp.) In nigeria. *Parasit Vectors* 2019; **12**: 481.

277 Wei S F., Liu Q. Molecular detection and genetic diversity of leishmania donovani in naturally infected phlebotomus chinensi from southwestern china. *Vector Borne Zoonotic Dis* 2011; **11**: 849–52.

278 Whitehorn T P. R., Goulson D. Genetic diversity, parasite prevalence and immunity in wild bumblebees. *Proc Biol Sci* 2011; **278**: 1195–202.

279 Whitehorn T Penelope R., Goulson D. Investigating the impact of deploying commercial bombus terrestris for crop pollination on pathogen dynamics in wild bumble bees. *Journal of Apicultural Research* 2015; **52**: 149–57.

280 Wilfert L L., Jiggins FM. Trypanosomatids are common and diverse parasites of drosophila. *Parasitology* 2011; **138**: 858–65.

281 Xu P-Y G., Rich S. Triplex real-time PCR for detection of crithidia mellificae and lotmaria passim in honey bees. *Parasitol Res* 2018; **117**: 623–8.

282 Yadav K S. C., Kumar R. Seroprevalence of trypanosoma evansi infection in equines of north and north western states of india. *J Equine Vet Sci* 2019; **79**: 63–7.

283 Zorrilla DLS V., Valdivia HO. Distribution and identification of sand flies naturally infected with leishmania from the southeastern peruvian amazon. *PLoS Negl Trop Dis* 2017; **11**: e0006029.

284 Abbaszadeh Afshar S M. J., Naderi A. Canine visceral leishmaniasis; a seroepidemiological survey in jiroft district, southern kerman province, southeastern iran in 2015. *Iran J Parasitol* 2018; **13**: 67–71.

285 Abdeen S Z. A., Baneth G. Epidemiology of visceral leishmaniasis in the jenin district, west bank: 1989-1998. *Am J Trop Med Hyg* 2002; **66**: 329–33.

286 Abebe R, Wolde A. A cross-sectional study of trypanosomosis and its vectors in donkeys and mules in northwest ethiopia. *Parasitol Res* 2010; **106**: 911–6.

287 Abrantes MM T. R., Figueiredo FB. Identification of canine visceral leishmaniasis in a previously unaffected area by conventional diagnostic techniques and cell-block fixation. *Rev Inst Med Trop Sao Paulo* 2016; **58**: 3.

288 Abrantes W T. R., Figueiredo FB. Environmental factors associated with canine visceral leishmaniasis in an area with recent introduction of the disease in the state of rio de janeiro, brazil. *Cad Saude Publica* 2018; **34**: e00021117.

289 Akhavan Y-E A., Khamesipour A. Molecular epizootiology of rodent leishmaniasis in a hyperendemic area of iran. *Iran J Public Health* 2010; **39**: 1–7.

290 Akhtardanesh S B., Pourafshar NG. Feline visceral leishmaniasis in kerman, southeast of iran: Serological and molecular study. *J Vector Borne Dis* 2017; **54**: 96–102.

291 Akinpelu AI. Prevalence and intensity of blood parasites in wild pigeons and doves (family: Columbidae) from shasha forest reserve, ile-ife, nigeria. *Asian Journal of Animal and Veterinary Advances* 2008; **3**: 109–14.

292 Akter A S., Katakura K. Molecular and serological evidence of leishmania infection in stray dogs from visceral leishmaniasis-endemic areas of bangladesh. *Am J Trop Med Hyg* 2016; **95**: 795–9.

293 Albuquerque C A., Cortes S. Evaluation of four molecular methods to detect leishmania infection in dogs. *Parasit Vectors* 2017; **10**: 57.

294 Alho P A. M., Carvalho LM de. Seroprevalence of vector-borne pathogens and molecular detection of borrelia afzelii in military dogs from portugal. *Parasit Vectors* 2016; **9**: 225.

295 Almeida F C. E., Harry M. Molecular individual-based approach on triatoma brasiliensis: Inferences on triatomine foci, trypanosoma cruzi natural infection prevalence, parasite diversity and feeding sources. *PLoS Negl Trop Dis* 2016; **10**: e0004447.

296 Alroy H K. A., Working Group on Chagas Disease in P. Prevalence and transmission of trypanosoma cruzi in people of rural communities of the high jungle of northern peru. *PLoS Negl Trop Dis* 2015; **9**: e0003779.

297 Alvasen J K., Emanuelson U. A field survey on parasites and antibodies against selected pathogens in owned dogs in lilongwe, malawi. *J S Afr Vet Assoc* 2016; **87**: e1–6.

298 Leite Rabelo T Elida Mara, Bhering LL. Comparison of three methods for diagnosis of trypanosoma (duttonella) vivax in cattle. *Genetics and Molecular Research* 2017; **16**. DOI:10.4238/gmr16039811.

299 Amer R S., Nakai Y. Molecular identification and phylogenetic analysis of trypanosoma evansi from dromedary camels (camelus dromedarius) in egypt, a pilot study. *Acta Trop* 2011; **117**: 39–46.

300 Amiri Ghannat Saman D I., Pirestani M. Biodiversity, leishmania genetic typing and host identification of phlebotomine species in endemic foci of southeastern iran. *Heliyon* 2019; **5**: e02369.

301 Antonio M E. G., Machado-Coelho GL. Canine visceral leishmaniasis in the krenak indigenous community, resplendor, minas gerais state, brazil, 2007. *Cad Saude Publica* 2011; **27**: 603–7.

302 Aragort A W., Sanmartin ML. Blood protozoans in elasmobranchs of the family rajidae from galicia (NW spain). *Dis Aquat Organ* 2005; **65**: 63–8.

303 Arce-Fonseca C-S M., Rodriguez-Morales O. Seropositivity for trypanosoma cruzi in domestic dogs from sonora, mexico. *Infect Dis Poverty* 2017; **6**: 120.

304 Cruz B SM Luis, Arjona J G. Anticuerpos de trypanosoma cruzi, leishmania mexicana y leishmania braziliensis en perros domiciliados de tabasco, méxico. *Revista MVZ Córdoba* 2017; **22**: 5829–36.

305 Aslantas O O., Babur C. Seroepidemiology of leptospirosis, toxoplasmosis, and leishmaniosis among dogs in ankara, turkey. *Vet Parasitol* 2005; **129**: 187–91.

306 Attipa P C., Tasker S. Prevalence study and risk factor analysis of selected bacterial, protozoal and viral, including vector-borne, pathogens in cats from cyprus. *Parasit Vectors* 2017; **10**: 130.

307 Austen O J. M., Ryan U. High prevalence of trypanosoma vegrandis in bats from western australia. *Vet Parasitol* 2015; **214**: 342–7.

308 Azeem T Tamoor, Umar S. Hematobiochemical disorder in camels suffering from different hemoparasites. *Pakistan Journal of Zoology* 2019; **51**: 591–6.

309 Azpurua DLC J., Windsor D. Lutzomyia sand fly diversity and rates of infection by wolbachia and an exotic leishmania species on barro colorado island, panama. *PLoS Negl Trop Dis* 2010; **4**: e627.

310 Bakirci B Serkan, KaragenÇ T. Molecular and seroprevalence of canine visceral leishmaniasis in west anatolia, turkey. *Turkish Journal of Veterinary and Animal Sciences* 2016; **40**: 637–44.

311 Bamorovat S M., Aflatoonian MR. Canine visceral leishmaniasis in kerman, southeast of iran: A seroepidemiological, histopathological and molecular study. *Iran J Parasitol* 2014; **9**: 342–9.

312 Bar ME, Wisnivesky-Colli C. Triatoma sordida stal 1859 (hemiptera, reduviidae: Triatominae) in palms of northeastern argentina. *Mem Inst Oswaldo Cruz* 2001; **96**: 895–9.

313 Barbosa A A., Ryan U. First report of trypanosoma vegrandis in koalas (phascolarctos cinereus). *Parasitol Int* 2016; **65**: 316–8.

314 Barbosa G A. D., Ryan U. Increased genetic diversity and prevalence of co-infection with trypanosoma spp. In koalas (phascolarctos cinereus) and their ticks identified using next-generation sequencing (NGS). *PLoS One* 2017; **12**: e0181279.

315 Barbosa R A., Ryan U. Prevalence, genetic diversity and potential clinical impact of blood-borne and enteric protozoan parasites in native mammals from northern australia. *Vet Parasitol* 2017; **238**: 94–105.

316 Barnard M-H William H., Matsuoka SM. Prevalence of hematozoa infections among breeding and wintering rusty blackbirds. *The Condor* 2010; **112**: 849–53.

317 Barros X J. H. S., Jansen AM. Identification of novel mammalian hosts and brazilian biome geographic distribution of trypanosoma cruzi TcIII and TcIV. *Acta Trop* 2017; **172**: 173–9.

318 Ben Othman G S., Ben Abderrazak S. First detection of leishmania DNA in psammomys obesus and psammomys vexillaris: Their potential involvement in the epidemiology of leishmaniasis in tunisia. *Infect Genet Evol* 2018; **59**: 7–15.

319 Benassi B J. C., Oliveira T. Detection of leishmania infantum DNA in conjunctival swabs of cats by quantitative real-time PCR. *Exp Parasitol* 2017; **177**: 93–7.

320 Berger W R., Kotler BP. Zoonotic disease in a peripheral population: Persistence and transmission of leishmania major in a putative sink-source system in the negev highlands, israel. *Vector Borne Zoonotic Dis* 2014; **14**: 592–600.

321 Bhattarai D N. R., Van der Auwera G. Development and evaluation of different PCR-based typing methods for discrimination of leishmania donovani isolates from nepal. *Parasitology* 2010; **137**: 947–57.

322 Bhutto JAS B.Gadahi. Field investigation on the prevalence of trypanosomiasis in camels in relation to sex, age, breed and herd size. *Pakistan Veterinary Journal* 2010; **30**: 175–7.

323 Bigeli O J. G., Teles NM. Diagnosis of leishmania (leishmania) chagasi infection in dogs and the relationship with environmental and sanitary aspects in the municipality of palmas, state of tocantins, brazil. *Rev Soc Bras Med Trop* 2012; **45**: 18–23.

324 Bilgin NY Z.Turan. Prevalence of leishmaniosis in dogs in istanbul, turkey determined by using PCR. *Journal of the Hellenic Veterinary Medical Society* 2015; **66**: 106–12.

325 Bitew YA M.Amedie. Prevalence of bovine trypanosomosis in selected areas of jabi tehenan district, west gojam of amhara regional state, northwestern ethiopia. *African Journal of Agricultural Research* 2011; **6**: 140–4.

326 Bolukbas GZG C. S.Pekmezci. Evidence of leishmania spp. Antibodies and DNA in dogs in the middle black sea region of turkey. *Ankara Universitesi Veteriner Fakultesi Dergisi* 2016; **63**: 111–4.

327 Borji GP H.Razmi. Epidemiological study on haemoparasites of dromedary (camelus dromedarius) in iran. *Journal of Camel Practice and Research* 2009; **16**: 217–9.

328 Botto-Mahan B C., Solari A. Field assessment of trypanosoma cruzi infection and host survival in the native rodent octodon degus. *Acta Trop* 2012; **122**: 164–7.

329 Brasil M Arthur Willian de Lima, Azevedo SS de. Prevalence and risk factors associated with leishmania spp. And trypanosoma cruzi infections in dogs presented at veterinary clinics in joão pessoa, paraíba state, northeastern brazil. *Semina: Ciências Agrárias* 2018; **39**: 2293–300.

330 Bray B D. P., Birtles RJ. Haemoparasites of common shrews (sorex araneus) in northwest england. *Parasitology* 2007; **134**: 819–26.

331 Breniere A S. F., Noireau F. Genetic characterization of trypanosoma cruzi DTUs in wild triatoma infestans from bolivia: Predominance of TcI. *PLoS Negl Trop Dis* 2012; **6**: e1650.

332 Brigada D A. M., Basso B. American tripanosomiasis: A study on the prevalence of trypanosoma cruzi and trypanosoma cruzi-like organisms in wild rodents in san luis province, argentina. *Rev Soc Bras Med Trop* 2010; **43**: 249–53.

333 Brito L F. G., Paz GS. Canine visceral leishmaniasis in the northeast region of brazil. *J Venom Anim Toxins Incl Trop Dis* 2016; **22**: 15.

334 Brown R E. L., Yabsley MJ. Seroprevalence of trypanosoma cruzi among eleven potential reservoir species from six states across the southern united states. *Vector Borne Zoonotic Dis* 2010; **10**: 757–63.

335 Buhaya G M. H., Maldonado RA. Incidence of trypanosoma cruzi infection in triatomines collected at indio mountains research station. *Acta Trop* 2015; **150**: 97–9.

336 Bustamante DU-S D. M., Pennington PM. Ecological, social and biological risk factors for continued trypanosoma cruzi transmission by triatoma dimidiata in guatemala. *PLoS One* 2014; **9**: e104599.

337 Cai W Y., Zhang X. First report of the prevalence and genotype of trypanosoma spp. In bats in yunnan province, southwestern china. *Acta Trop* 2019; **198**: 105105.

338 Caldart C Eloiza Teles, Freire RL. Zoonosis in dogs and cats attended by the birth control project: Toxoplasma gondii, leishmania spp. And leptospira spp., Serodiagnosis and epidemiology. *Semina: Ciências Agrárias* 2015; **36**: 253–65.

339 Caldart F E. T., Navarro IT. Leishmania in synanthropic rodents (rattus rattus): New evidence for the urbanization of leishmania (leishmania) amazonensis. *Rev Bras Parasitol Vet* 2017; **26**: 17–27.

340 Calzada S J. E., Chaves LF. Cutaneous leishmaniasis in dogs: Is high seroprevalence indicative of a reservoir role? *Parasitology* 2015; **142**: 1202–14.

341 Camejo PMG M. I.Aso. Relationship between asymptomatic infections with anaplasma marginale, babesia spp. And trypanosoma vivax in bulls and testosterone levels. *Revista Cientifica-Facultad De Ciencias Veterinarias* 2016; **26**: 13–9.

342 Cardoso G L., Baneth G. First report of anaplasma platys infection in red foxes (vulpes vulpes) and molecular detection of ehrlichia canis and leishmania infantum in foxes from portugal. *Parasit Vectors* 2015; **8**: 144.

343 Cardoso L L., Solano-Gallego L. Low seroprevalence of leishmania infantum infection in cats from northern portugal based on DAT and ELISA. *Vet Parasitol* 2010; **174**: 37–42.

344 Castro B J. C., Barcante JMP. Molecular detection of leishmania spp in lutzomyia longipalpis in the city of lavras, minas gerais, brazil. *Braz J Med Biol Res* 2019; **52**: e8224.

345 Chargui S N., Babba H. Transmission cycle analysis in a leishmania infantum focus: Infection rates and blood meal origins in sand flies (diptera: psychodidae). *J Vector Ecol* 2018; **43**: 321–7.

346 Charles K R. A., Yabsley MJ. Southern plains woodrats (neotoma micropus) from southern texas are important reservoirs of two genotypes of trypanosoma cruzi and host of a putative novel trypanosoma species. *Vector Borne Zoonotic Dis* 2013; **13**: 22–30.

347 Chatzis A M. K., Saridomichelakis MN. Cytological and molecular detection of leishmania infantum in different tissues of clinically normal and sick cats. *Vet Parasitol* 2014; **202**: 217–25.

348 Chaudhary ZI, Iqbal J. Incidence, biochemical and haematological alterations induced by natural trypanosomosis in racing dromedary camels. *Acta Trop* 2000; **77**: 209–13.

349 Chaudhry AA Z. I.JahanzaibAslam. Prevalence of trypanosoma evansi in camels through polymerase chain reaction and haematocrit centrifugation technique in punjab (pakistan). *Journal of Camel Practice and Research* 2008; **15**: 183–5.

350 Chen L H., Chen J. Multi-locus characterization and phylogenetic inference of leishmania spp. In snakes from northwest china. *PLoS One* 2019; **14**: e0210681.

351 Cherenet S T., Van den Bossche P. A comparative longitudinal study of bovine trypanosomiasis in tsetse-free and tsetse-infested zones of the amhara region, northwest ethiopia. *Vet Parasitol* 2006; **140**: 251–8.

352 Chitimia M-G L., Berriatua E. Cryptic leishmaniosis by leishmania infantum, a feature of canines only? A study of natural infection in wild rabbits, humans and dogs in southeastern spain. *Vet Parasitol* 2011; **181**: 12–6.

353 Concannon W-O R., Birtles RJ. Molecular characterization of haemoparasites infecting bats (microchiroptera) in cornwall, UK. *Parasitology* 2005; **131**: 489–96.

354 Constantino P Caroline, Navarro IT. Seroepidemiology of leishmania spp. In dogs residing in telêmaco borba, paraná, brazil. *Semina: Ciências Agrárias* 2014; **35**: 3181–90.

355 Coronado R X., Solari A. Molecular epidemiology of chagas disease in the wild transmission cycle: The evaluation in the sylvatic vector mepraia spinolai from an endemic area of chile. *Am J Trop Med Hyg* 2009; **81**: 656–9.

356 Cortada D V. M., Goncalves da Costa SC. Canine visceral leishmaniosis in anastacio, mato grosso do sul state, brazil. *Vet Res Commun* 2004; **28**: 365–74.

357 Cortez V A. P., Teixeira MM. The taxonomic and phylogenetic relationships of trypanosoma vivax from south america and africa. *Parasitology* 2006; **133**: 159–69.

358 Coulibaly T C. A., Doumbia S. Impact of insecticide-treated bednets and indoor residual spraying in controlling populations of phlebotomus duboscqi, the vector of leishmania major in central mali. *Parasit Vectors* 2018; **11**: 345.

359 Couto L C. G., Ruano R. Serological study of selected vector-borne diseases in shelter dogs in central spain using point-of-care assays. *Vector Borne Zoonotic Dis* 2010; **10**: 885–8.

360 Cuba A-F C. A., Miles MA. The triatomines of northern peru, with emphasis on the ecology and infection by trypanosomes of rhodnius ecuadoriensis (triatominae). *Mem Inst Oswaldo Cruz* 2002; **97**: 175–83.

361 Curi M N. H., Talamoni SA. Serologic evidence of leishmania infection in free-ranging wild and domestic canids around a brazilian national park. *Mem Inst Oswaldo Cruz* 2006; **101**: 99–101.

362 Curtis-Robles Z R., Hamer SA. Trypanosoma cruzi (agent of chagas disease) in sympatric human and dog populations in "colonias" of the lower rio grande valley of texas. *Am J Trop Med Hyg* 2017; **96**: 805–14.

363 Costa C Letícia Da, Freire RL. Leishmaniasis in dogs from recycling centers and from a neighborhood with adjacent forest in an urban area of londrina, paraná, brazil. *Semina: Ciências Agrárias* 2016; **37**: 1407–14.

364 Dantas-Torres de P-C F., Brandao-Filho SP. Cutaneous and visceral leishmaniasis in dogs from a rural community in northeastern brazil. *Vet Parasitol* 2010; **170**: 313–7.

365 Dario L M. A., Jansen AM. High trypanosoma spp. Diversity is maintained by bats and triatomines in espirito santo state, brazil. *PLoS One* 2017; **12**: e0188412.

366 Davami M M. H., Pourahmad M. Molecular survey on detection of leishmania infection in rodent reservoirs in jahrom district, southern iran. *J Arthropod Borne Dis* 2014; **8**: 139–46.

367 Dayo B G. K., Thevenon S. Prevalence and incidence of bovine trypanosomosis in an agro-pastoral area of southwestern burkina faso. *Res Vet Sci* 2010; **88**: 470–7.

368 Curi P N. H., Chiarello AG. Factors associated with the seroprevalence of leishmaniasis in dogs living around atlantic forest fragments. *PLoS One* 2014; **9**: e104003.

369 Carvalho V de M. R., Brandao Filho SP. Natural leishmania infantum infection in migonemyia migonei (franca, 1920) (diptera:psychodidae:phlebotominae) the putative vector of visceral leishmaniasis in pernambuco state, brazil. *Acta Trop* 2010; **116**: 108–10.

370 Lima G J. T., Soares RM. Serodiagnosis of visceral and cutaneous leishmaniasis in human and canine populations living in indigenous reserves in the brazilian amazon region. *Rev Soc Bras Med Trop* 2017; **50**: 61–6.

371 Mendonca B de I. L., Alves LC. Leishmania (infantum) chagasi in canine urinary sediment. *Rev Bras Parasitol Vet* 2015; **24**: 92–4.

372 Oliveira C E. F., Galati EA. Leishmania amazonensis DNA in wild females of lutzomyia cruzi (diptera: Psychodidae) in the state of mato grosso do sul, brazil. *Mem Inst Oswaldo Cruz* 2015; **110**: 1051–7.

373 Oliveira A L. C., Mendonca-Lima FW. Seroprevalence and risk factors for canine visceral leishmaniasis in the endemic area of dias d'avila, state of bahia, brazil. *Rev Soc Bras Med Trop* 2010; **43**: 400–4.

374 Oliveira G Patrícia Magalhães de, Saut JPE. Seroepidemiology ofLeishmaniaspp. In equids from uberlândia, minas gerais, brazil. *Ciência Rural* 2017; **47**. DOI:10.1590/0103-8478cr20160697.

375 Padua I de S. B., Pilarski F. First record of trypanosoma sp. (Protozoa: Kinetoplastida) in tuvira (gymnotus aff. Inaequilabiatus) in the pantanal wetland, mato grosso do sul state, brazil. *Rev Bras Parasitol Vet* 2011; **20**: 85–7.

376 Seabra P de N. M., Oliveira TM. Toxoplasma gondii, neospora caninum and leishmania spp. Serology and leishmania spp. PCR in dogs from pirassununga, SP. *Rev Bras Parasitol Vet* 2015; **24**: 454–8.

377 Sousa H K. C., Andre MR. Serological detection of toxoplasma gondii, leishmania infantum and neospora caninum in cats from an area endemic for leishmaniasis in brazil. *Rev Bras Parasitol Vet* 2014; **23**: 449–55.

378 Deiró M Ana Graziela De Jesus, Albuquerque GR. Antibody occurrence of anti-toxoplasma gondii, leishmania sp. And ehrlichia canis in dogs in bahia state. *Semina: Ciências Agrárias* 2018; **39**: 199–210.

379 Demir S, Karakus M. Natural leishmania infection of phlebotomus sergenti (diptera: Phlebotominae) in an endemic focus of cutaneous leishmaniasis in sanliurfa, turkey. *Acta Trop* 2015; **149**: 45–8.

380 Deviche G P., Manteca X. Interspecific variability of prevalence in blood parasites of adult passerine birds during the breeding season in alaska. *J Wildl Dis* 2001; **37**: 28–35.

381 Dia ML. Parasites of the camel in burkina faso. *Trop Anim Health Prod* 2006; **38**: 17–21.

382 Diakou P A., Lazarides K. Specific anti-leishmania spp. Antibodies in stray cats in greece. *J Feline Med Surg* 2009; **11**: 728–30.

383 Diaz-Saez M-E V., Martin-Sanchez J. High rates of leishmania infantum and trypanosoma nabiasi infection in wild rabbits (oryctolagus cuniculus) in sympatric and syntrophic conditions in an endemic canine leishmaniasis area: Epidemiological consequences. *Vet Parasitol* 2014; **202**: 119–27.

384 Dogan O N., Bor O. Sero-epidemological survey on canine visceral leishmaniasis and the distribution of sandfly vectors in northwestern turkey: Prevention strategies for childhood visceral leishmaniasis. *J Trop Pediatr* 2006; **52**: 212–7.

385 Dos Santos L F. C. B., Jansen AM. Trypanosoma sp. Diversity in amazonian bats (chiroptera; mammalia) from acre state, brazil. *Parasitology* 2018; **145**: 828–37.

386 Duarte C A., Vaz Y. Survey of infectious and parasitic diseases in stray cats at the lisbon metropolitan area, portugal. *J Feline Med Surg* 2010; **12**: 441–6.

387 Dumitrache N-B M. O., Baneth G. The quest for canine leishmaniasis in romania: The presence of an autochthonous focus with subclinical infections in an area where disease occurred. *Parasit Vectors* 2016; **9**: 297.

388 Durrani B A. Z., Azeem M. Use of physiological biomarkers in diagnosis along with field trials of different trypanisidal drugs in camels of cholistan desert. *Microb Pathog* 2017; **108**: 1–5.

389 Ebani P V. V., Mancianti F. Serological survey on some pathogens in wild brown hares (lepus europaeus) in central italy. *Asian Pac J Trop Med* 2016; **9**: 465–9.

390 Echchakery C M., Boumezzough A. Molecular detection of leishmania infantum and leishmania tropica in rodent species from endemic cutaneous leishmaniasis areas in morocco. *Parasit Vectors* 2017; **10**: 454.

391 Echeverria S J. T., Borges FA. Clinical and therapeutic aspects of an outbreak of canine trypanosomiasis. *Rev Bras Parasitol Vet* 2019; **28**: 320–4.

392 Elhaig MM, Sallam NH. Molecular survey and characterization of trypanosoma evansi in naturally infected camels with suspicion of a trypanozoon infection in horses by molecular detection in egypt. *Microb Pathog* 2018; **123**: 201–5.

393 Estrada-Franco B J. G., Garg N. Human trypanosoma cruzi infection and seropositivity in dogs, mexico. *Emerg Infect Dis* 2006; **12**: 624–30.

394 Fallah MR E.Khanmohammadi. Serological survey and comparison of two polymerase chain reaction (PCR) assays with enzyme-linked immunosorbent assay (ELISA)

for the diagnosis of canine visceral leishmaniasis in dogs. *African Journal of Biotechnology* 2011; **10**: 648–56.

395 Faye B B., Gaye O. Seroprevalence of leishmania infantum in a rural area of senegal: Analysis of risk factors involved in transmission to humans. *Trans R Soc Trop Med Hyg* 2011; **105**: 333–40.

396 Faye P de A D., Geerts S. Prevalence and incidence of trypanosomosis in horses and donkeys in the gambia. *Vet Parasitol* 2001; **101**: 101–14.

397 Fereig M R. M., Nishikawa Y. Seroprevalence of babesia bovis, b. Bigemina, trypanosoma evansi, and anaplasma marginale antibodies in cattle in southern egypt. *Ticks Tick Borne Dis* 2017; **8**: 125–31.

398 Fernandes C Annielle Regina da Fonseca, Azevedo SS. Occurrence and risk factors of zoonoses in dogs and owners in sertão, paraíba state, northeastern brazil. *Semina: Ciências Agrárias* 2018; **39**: 1057–65.

399 Ferreira Ede C C., Gontijo CM. Mixed infection of leishmania infantum and leishmania braziliensis in rodents from endemic urban area of the new world. *BMC Vet Res* 2015; **11**: 71.

400 Castro Ferreira P de E., Gontijo CMF. Leishmania (v.) Braziliensis infecting bats from pantanal wetland, brazil: First records for platyrrhinus lineatus and artibeus planirostris. *Acta Trop* 2017; **172**: 217–22.

401 Ferreira C R. T. B., Moreira OC. Detection and genotyping of trypanosoma cruzi from acai products commercialized in rio de janeiro and para, brazil. *Parasit Vectors* 2018; **11**: 233.

402 Figueiredo M F. B., Schubach TM. Efficacy of an indirect immunofluorescence test in the diagnosis of canine leishmaniosis. *Vet J* 2010; **186**: 123–4.

403 Figueiredo LD de V F. B.Nascimento. Serological diagnosis of feline tegumentary leishmaniasis by indirect immunofluorescence (IFI) and enzyme-linked immunosorbent assay (ELISA) in an endemic area in brazil. *Acta Scientiae Veterinariae* 2016; **44**. <Go to ISI>://WOS:000392090700001.

404 Fikru A R., Buscher P. Trypanosome infection in dromedary camels in eastern ethiopia: Prevalence, relative performance of diagnostic tools and host related risk factors. *Vet Parasitol* 2015; **211**: 175–81.

405 Silva Filho T Mauro de F., Navarro IT. Infection by toxoplasma gondii and leishmania spp. In humans and dogs from rural settlements in northern paraná state, brazil. *Semina: Ciências Agrárias* 2012; **33**: 3251–64.

406 Freitas S Y. B. N., Amora SSA. Natural infection by trypanosoma cruzi in triatomines and seropositivity for chagas disease of dogs in rural areas of rio grande do norte, brazil. *Rev Soc Bras Med Trop* 2018; **51**: 190–7.

407 Galaviz-Silva M-H L., Molina-Garza ZJ. Prevalence of trypanosoma cruzi infection in dogs and small mammals in nuevo leon, mexico. *Rev Argent Microbiol* 2017; **49**: 216–23.

408 Garcia M N., Dominguez M. Evidence of leishmania infantum infection in rabbits (oryctolagus cuniculus) in a natural area in madrid, spain. *Biomed Res Int* 2014; **2014**: 318254.

409 Gari A F. R., Claes F. Comparative diagnosis of parasitological, serological, and molecular tests in dourine-suspected horses. *Trop Anim Health Prod* 2010; **42**: 1649–54.

410 Garvin M M. C., Crain SK. Prevalence of hematozoa in overwintering american redstarts (setophaga ruticilla): No evidence for local transmission. *J Wildl Dis* 2004; **40**: 115–8.

411 Gavgani M A. S., Davies CR. Domestic dog ownership in iran is a risk factor for human infection with leishmania infantum. *Am J Trop Med Hyg* 2002; **67**: 511–5.

412 Ghaemi Z M., Jannati Pirouz H. Evaluation of trypanosama evansi prevalence and risk factors in the one-humped camels (camelus dromedarius) of the north-east of iran by a real-time PCR test. *Prev Vet Med* 2019; **168**: 60–5.

413 Giannakopoulos CNP A.Tsokana. Molecular investigation and geographical distribution of leishmania spp infection in stray and owned cats (felis catus) in thessaly, central greece. *Journal of the Hellenic Veterinary Medical Society* 2017; **68**: 27–34.

414 Gicheru J M. M., Suleman MA. Prevalence of antibodies and cell mediated immune response against leishmania major in feral nonhuman primates from kenya. *Acta Trop* 2009; **109**: 136–40.

415 Gontijo da S C. M., Melo MN. Epidemiological studies of an outbreak of cutaneous leishmaniasis in the rio jequitinhonha valley, minas gerais, brazil. *Acta Trop* 2002; **81**: 143–50.

416 Grisard C-P E. C., Steindel M. Trypanosoma cruzi infection in didelphis marsupialis in santa catarina and arvoredo islands, southern brazil. *Mem Inst Oswaldo Cruz* 2000; **95**: 795–800.

417 Guimaraes B K. S., Abreu-Silva AL. Canine visceral leishmaniasis in sao jose de ribamar, maranhao state, brazil. *Vet Parasitol* 2005; **131**: 305–9.

418 Gunasekara S E., Yokoyama N. Epidemiological survey of hemoprotozoan parasites in cattle from low-country wet zone in sri lanka. *Parasitol Int* 2019; **71**: 5–10.

419 Haas L M., Hrehova Z. Occurrence of blood parasites and intensity of infection in prunella modularis in the montane and subalpine zone in the slovak carpathians. *Acta Parasitol* 2012; **57**: 221–7.

420 Haenen L O. L. M., Breteler JK. The health status of european silver eels, anguilla anguilla, in the dutch river rhine watershed and lake IJsselmeer. *Aquaculture* 2010; **309**: 15–24.

421 Haji M I. J., Namangala B. Occurrence of haemoparasites in cattle in monduli district, northern tanzania. *Onderstepoort J Vet Res* 2014; **81**. DOI:10.4102/ojvr.v81i1.843.

422 Hamad F I., Bittar F. Wild gorillas as a potential reservoir of leishmania major. *J Infect Dis* 2015; **211**: 267–73.

423 Hamarsheh N O., Al-Jawabreh A. Serological and molecular survey of leishmania parasites in apparently healthy dogs in the west bank, palestine. *Parasit Vectors* 2012; **5**: 183.

424 Hamill K L. C., Picozzi K. Domestic pigs as potential reservoirs of human and animal trypanosomiasis in northern tanzania. *Parasit Vectors* 2013; **6**: 322.

425 Hanel D J., Votypka J. Blood parasites in northern goshawk (accipiter gentilis) with an emphasis to leucocytozoon toddi. *Parasitol Res* 2016; **115**: 263–70.

426 Hassan O M. M., Elnaiem DE. Role of the domestic dog as a reservoir host of leishmania donovani in eastern sudan. *Parasit Vectors* 2009; **2**: 26.

427 Hernandez S C., Ramirez JD. Untangling the transmission dynamics of primary and secondary vectors of trypanosoma cruzi in colombia: Parasite infection, feeding sources and discrete typing units. *Parasit Vectors* 2016; **9**: 620.

428 Herrera L C. P., Wesson DM. Genotype diversity of trypanosoma cruzi in small rodents and triatoma sanguisuga from a rural area in new orleans, louisiana. *Parasit Vectors* 2015; **8**: 123.

429 Hodo R C. L., Hamer SA. Repeated cross-sectional study of trypanosoma cruzi in shelter dogs in texas, in the context of dirofilaria immitis and tick-borne pathogen prevalence. *J Vet Intern Med* 2019; **33**: 158–66.

430 Hofmann H M., Joachim A. Vector-borne pathogens affecting shelter dogs in eastern crete, greece. *Parasitol Res* 2019; **118**: 1661–6.

431 Holland T W. G., Vercruysse J. Prevalence of trypanosoma evansi in water buffaloes in remote areas in northern vietnam using PCR and serological methods. *Trop Anim Health Prod* 2004; **36**: 45–8.

432 Holmstad A P. R., Skorping A. Standard sampling techniques underestimate prevalence of avian hematozoa in willow ptarmigan (lagopus lagopus). *J Wildl Dis* 2003; **39**: 354–8.

433 Hussain ZG M.Saeed. Molecular detection and seasonal prevalence of trypanosoma brucei and its effect on hematobiochemical parameters in donkeys from dera ghazi khan district in southern punjab, pakistan. *Pakistan Journal of Zoology* 2016; **48**: 1781–6.

434 Hussain K R., Mehmood K. Clinico-hematological and oxidative stress status in nili ravi buffaloes infected with trypanosoma evansi. *Microb Pathog* 2018; **123**: 126–31.

435 Jafari N R., Parvizi P. Molecular characterization of sandflies and leishmania detection in main vector of zoonotic cutaneous leishmaniasis in abarkouh district of yazd province, iran. *Asian Pac J Trop Med* 2013; **6**: 792–7.

436 Jakes O K. A., Adlard R. Hemoprotozoa of freshwater turtles in queensland. *J Wildl Dis* 2001; **37**: 12–9.

437 Jing M Z., Inoue N. A field study to estimate the prevalence of bovine african trypanosomosis in butaleja district, uganda. *J Vet Med Sci* 2009; **71**: 525–7.

438 Karakus A M., Ozbel Y. Vector and reservoir surveillance study in a canine and human leishmaniasis endemic area in most western part of turkey, karaburun. *Acta Trop* 2019; **190**: 177–82.

439 Karbowiak R Grzegorz, Wita I. Natural infections of small mammals with blood parasites on the borderland of boreal and temperate forest zones. *Acta Theriologica* 2005; **50**: 31–42.

440 Karimuribo M E. D., Ballingall KT. Analysis of host genetic factors influencing african trypanosome species infection in a cohort of tanzanian bos indicus cattle. *Vet Parasitol* 2011; **179**: 35–42.

441 Kassa TC T.Eguale. Prevalence of camel trypanosomosis and its vectors in fentale district, south east shoa zone, ethiopia. *Veterinarski Arhiv* 2011; **81**: 611–21.

442 Kato U H., Hashiguchi Y. Establishment of a mass screening method of sand fly vectors for leishmania infection by molecular biological methods. *Am J Trop Med Hyg* 2007; **77**: 324–9.

443 Keck J N.Dereuer. Epidemiology of canine leishmaniasis by cross-sectional study in the french focus of cevennes. *Revue De Medecine Veterinaire* 2003; **154**: 599–604.

444 Kelly B E., Lymbery AJ. Haematozoa of wild catfishes in northern australia. *Int J Parasitol Parasites Wildl* 2018; **7**: 12–7.

445 Kenubih D A., Lemma W. Preliminary survey of domestic animal visceral leishmaniasis and risk factors in north-west ethiopia. *Trop Med Int Health* 2015; **20**: 205–10.

446 Khanmohammadi ER M.Fallah. Study on seroprevalence of canine visceral leishmaniasis (CVL) in ownership dogs of sarab, east azerbaijan, province, northwest of iran with indirect immuno fluorescence antibody test (IFAT) and its health importance in 2008-2009. *Journal of Animal and Veterinary Advances* 2010; **9**: 139–43.

447 Kilic CO S.Babur. Investigation of anti-toxoplasma gondii and anti-leishmania infantum antibodies among sivas kangal dogs. *Turkish Journal of Veterinary & Animal Sciences* 2008; **32**: 299–304.

448 Kovalenko R D. A., Baneth G. Canine leishmaniosis and its relationship to human visceral leishmaniasis in eastern uzbekistan. *Parasit Vectors* 2011; **4**: 58.

449 Kubacka G J., Podmokla E. Correlates of blood parasitism in a threatened marshland passerine: Infection by kinetoplastids of the genus trypanosoma is related to landscape metrics of habitat edge. *Parasitology* 2019; **146**: 1036–46.

450 Laohasinnarong T D., Inoue N. Prevalence of trypanosoma sp. In cattle from tanzania estimated by conventional PCR and loop-mediated isothermal amplification (LAMP). *Parasitol Res* 2011; **109**: 1735–9.

451 Laranjeira M D. F., Laurenti MD. Serological and infection statuses of dogs from a visceral leishmaniasis-endemic area. *Rev Saude Publica* 2014; **48**: 563–71.

452 Leca Junior G N. F., Silva FL. Epidemiology of canine leishmaniasis in southern bahia, brazil. *Acta Trop* 2015; **148**: 115–9.

453 Lemma B W., Hailu A. Preliminary study on investigation of zoonotic visceral leishmaniasis in endemic foci of ethiopia by detecting leishmania infections in rodents. *Asian Pac J Trop Med* 2017; **10**: 418–22.

454 Leontides S L. S., Mylonakis ME. A cross-sectional study of leishmania spp. Infection in clinically healthy dogs with polymerase chain reaction and serology in greece. *Vet Parasitol* 2002; **109**: 19–27.

455 Leppert D L. L., Kaltenecker GS. Survey of blood parasites in two forest owls, northern saw-whet owls and flammulated owls, of western north america. *J Wildl Dis* 2008; **44**: 475–9.

456 Lima D-T B. S., Brandao-Filho SP. Small mammals as hosts of leishmania spp. In a highly endemic area for zoonotic leishmaniasis in north-eastern brazil. *Trans R Soc Trop Med Hyg* 2013; **107**: 592–7.

457 Lima-Oliveira F T. M., Almeida CE. Molecular eco-epidemiology on the sympatric chagas disease vectors triatoma brasiliensis and triatoma petrocchiae: Ecotopes, genetic variation, natural infection prevalence by trypanosomatids and parasite genotyping. *Acta Trop* 2020; **201**: 105188.

458 Lins S T. N. B., Ramos RAN. Seroprevalence and spatial distribution of canine leishmaniasis in an endemic region in brazil: How has the situation changed after 10 years? *Rev Soc Bras Med Trop* 2018; **51**: 680–2.

459 Lisi D O., Maroli M. Persistence of phlebotomine leishmania vectors in urban sites of catania (sicily, italy). *Parasit Vectors* 2014; **7**: 560.

460 Lisulo S M., Namangala B. Determination of the prevalence of african trypanosome species in indigenous dogs of mambwe district, eastern zambia, by loop-mediated isothermal amplification. *Parasit Vectors* 2014; **7**: 19.

461 Lopes S A. P., Cordeiro-da-Silva A. Prevalence of antibodies to leishmania infantum and toxoplasma gondii in horses from the north of portugal. *Parasit Vectors* 2013; **6**: 178.

462 Lopes SE P. M., Sousa VR. Seroprevalence and risk factors associated with visceral leishmaniasis in dogs in jaciara, state of mato grosso. *Rev Soc Bras Med Trop* 2014; **47**: 791–5.

463 Maganga M G. D., Ollomo B. Molecular identification of trypanosome species in trypanotolerant cattle from the south of gabon. *Parasite* 2017; **24**: 4.

464 Maharjan DR M.Mishra. Impact of emerging zoonotic diseases on animal health. 2006; **1081**: 320–1.

465 Maia A C., Roura X. Molecular detection of leishmania infantum, filariae and wolbachia spp. In dogs from southern portugal. *Parasit Vectors* 2016; **9**: 170.

466 Maia C C., Campino L. Serological investigation of leishmania infantum, dirofilaria immitis and angiostrongylus vasorum in dogs from southern portugal. *Parasit Vectors* 2015; **8**: 152.

467 Maia G C., Campino L. Feline leishmania infection in a canine leishmaniasis endemic region, portugal. *Vet Parasitol* 2010; **174**: 336–40.

468 Maia R C., Campino L. Prevalence of dirofilaria immitis antigen and antibodies to leishmania infantum in cats from southern portugal. *Parasitol Int* 2015; **64**: 154–6.

469 Malele M II, Kimbita EN. Multiple trypanosoma infections are common amongst glossina species in the new farming areas of rufiji district, tanzania. *Parasit Vectors* 2011; **4**: 217.

470 Foglia Manzillo G V., Oliva G. Serological and entomological survey of canine leishmaniasis in lampedusa island, italy. *BMC Vet Res* 2018; **14**: 286.

471 Marcelino F A. P., Gontijo CM. Molecular detection of leishmania braziliensis in rattus norvegicus in an area endemic for cutaneous leishmaniasis in brazil. *Vet Parasitol* 2011; **183**: 54–8.

472 Martinez-Sanchez C A., Alejandre-Aguilar R. Effect of ectoparasitic pimeliaphilus plumifer mites (acari: Pterygosomatidae) on meccus pallidipennis (hemiptera: Reduviidae) and several other chagas' disease vectors under laboratory conditions. *Exp Appl Acarol* 2007; **42**: 139–49.

473 Matete GO. Occurrence, clinical manifestation and the epidemiological implications of naturally occurring canine trypanosomosis in western kenya. *Onderstepoort J Vet Res* 2003; **70**: 317–23.

474 Mattioli F R. C., Jaitner J. Estimation of trypanosomal status by the buffy coat technique and an antibody ELISA for assessment of the impact of trypanosomosis on health and productivity of n'dama cattle in the gambia. *Vet Parasitol* 2001; **95**: 25–35.

475 Maziero T-S N., Nascimento AJ. Rural-urban focus of canine visceral leishmaniosis in the far western region of santa catarina state, brazil. *Vet Parasitol* 2014; **205**: 92–5.

476 Medkour D H., Mediannikov O. Potential animal reservoirs (dogs and bats) of human visceral leishmaniasis due to leishmania infantum in french guiana. *PLoS Negl Trop Dis* 2019; **13**: e0007456.

477 Mekuria AR S.Eyob. A cross-sectional study of equine trypanosomosis and its vectors in wolayta zone, southern ethiopia. *Journal of Animal and Veterinary Advances* 2010; **9**: 2061–6.

478 Melo T-N S. N., Belo VS. Prevalence of visceral leishmaniasis in a population of free-roaming dogs as determined by multiple sampling efforts: A longitudinal study analyzing the effectiveness of euthanasia. *Prev Vet Med* 2018; **161**: 19–24.

479 Millan J. Molecular investigation of vector-borne parasites in wild micromammals, barcelona (spain). *Parasitol Res* 2018; **117**: 3015–8.

480 Miranda R J. C., Barral A. Frequency of infection of lutzomyia phlebotomines with leishmania braziliensis in a brazilian endemic area as assessed by pinpoint capture and polymerase chain reaction. *Mem Inst Oswaldo Cruz* 2002; **97**: 185–8.

481 Miro H G., Pedraza-Diaz S. First description of naturally acquired tritrichomonas foetus infection in a persian cattery in spain. *Parasitol Res* 2011; **109**: 1151–4.

482 Mirzaei R A., Parvizi P. Isolation and detection of leishmania species among naturally infected rhombomis opimus, a reservoir host of zoonotic cutaneous leishmaniasis in turkemen sahara, north east of iran. *Exp Parasitol* 2011; **129**: 375–80.

483 Mohammad B K. N., Zainal-Abidin AH. Protozoan parasites of four species of wild anurans from a local zoo in malaysia. *Trop Biomed* 2013; **30**: 615–20.

484 Montenegro J V. M., Zeledon R. Chagas disease in dogs from endemic areas of costa rica. *Mem Inst Oswaldo Cruz* 2002; **97**: 491–4.

485 Montoya G A., Miro G. Implications of zoonotic and vector-borne parasites to free-roaming cats in central spain. *Vet Parasitol* 2018; **251**: 125–30.

486 Morales M E. A., Lescano AG. Prevalence of trypanosoma cruzi and other trypanosomatids in frequently-hunted wild mammals from the peruvian amazon. *Am J Trop Med Hyg* 2017; **97**: 1482–5.

487 Morelli C S., Traversa D. Exposure of client-owned cats to zoonotic vector-borne pathogens: Clinic-pathological alterations and infection risk analysis. *Comp Immunol Microbiol Infect Dis* 2019; **66**: 101344.

488 Morganti V G., Gramiccia M. Emerging feline vector-borne pathogens in italy. *Parasit Vectors* 2019; **12**: 193.

489 Moudy M R. M., Wesson DM. Factors associated with peridomestic triatoma sanguisuga (hemiptera: Reduviidae) presence in southeastern louisiana. *J Med Entomol* 2014; **51**: 1043–50.

490 Moya G S. L., Liotta DJ. Leishmania infantum DNA detected in phlebotomine species from puerto iguazu city, misiones province, argentina. *Acta Trop* 2017; **172**: 122–4.

491 Murphy M N., Miles MA. Lineage-specific rapid diagnostic tests can resolve trypanosoma cruzi TcII/v/VI ecological and epidemiological associations in the argentine chaco. *Parasit Vectors* 2019; **12**: 424.

492 Nadeem AC A.Aslam. Indirect fluorescent antibody technique based prevalence of surra in equines. *Pakistan Veterinary Journal* 2011; **31**: 169–70.

493 Nair R A. S., Ghosh S. Haemoprotozoa of cattle in northern kerala, india. *Trop Biomed* 2011; **28**: 68–75.

494 Nardoni A S., Mancianti F. Serological and molecular findings of leishmania infection in healthy donkeys (equus asinus) from a canine leishmaniosis endemic focus in tuscany, italy: A preliminary report. *Pathogens* 2019; **8**. DOI:10.3390/pathogens8030099.

495 Navea-Perez D-S H. M., Martin-Sanchez J. Leishmania infantum in wild rodents: Reservoirs or just irrelevant incidental hosts? *Parasitol Res* 2015; **114**: 2363–70.

496 Ngomtcho W S. C. H., Achukwi MD. Molecular screening of tsetse flies and cattle reveal different trypanosoma species including t. Grayi and t. Theileri in northern cameroon. *Parasit Vectors* 2017; **10**: 631.

497 Nguyen M T. T., Inoue N. Application of crude and recombinant ELISAs and immunochromatographic test for serodiagnosis of animal trypanosomosis in the umkhanyakude district of KwaZulu-natal province, south africa. *J Vet Med Sci* 2015; **77**: 217–20.

498 Nunes L J. B., Marques MJ. Leishmania infantum INFECTION IN DOGS FROM THE SOUTHERN REGION OF MINAS GERAIS STATE, BRAZIL. *Rev Inst Med Trop Sao Paulo* 2016; **58**: 75.

499 Nurcahyo Y W., Prastowo J. The prevalence of horse trypanosomiasis in sumba island, indonesia and its detection using card agglutination tests. *Vet World* 2019; **12**: 646–52.

500 Odeniran M P. O., Welburn SC. Molecular identification of bloodmeal sources and trypanosomes in glossina spp., Tabanus spp. And stomoxys spp. Trapped on cattle farm settlements in southwest nigeria. *Med Vet Entomol* 2019; **33**: 269–81.

501 Odongo D S., Magez S. Comparative evaluation of the nested ITS PCR against the 18S PCR-RFLP in a survey of bovine trypanosomiasis in kwale county, kenya. *J Vet Diagn Invest* 2016; **28**: 589–94.

502 Oleaga Z A., Ferroglio E. Leishmania in wolves in northern spain: A spreading zoonosis evidenced by wildlife sanitary surveillance. *Vet Parasitol* 2018; **255**: 26–31.

503 Oliveira P F. S., Pacheco RS. PCR-based diagnosis for detection of leishmania in skin and blood of rodents from an endemic area of cutaneous and visceral leishmaniasis in brazil. *Vet Parasitol* 2005; **129**: 219–27.

504 Oliveira G T. N., Silva FL. Diagnosis and epidemiology of canine leishmaniasis in southeastern bahia, brazil. *Genet Mol Res* 2016; **15**. DOI:10.4238/gmr.15038684.

505 Orozco E M. M., Gurtler RE. A comparative study of trypanosoma cruzi infection in sylvatic mammals from a protected and a disturbed area in the argentine chaco. *Acta Trop* 2016; **155**: 34–42.

506 Padilla M A. M., Basombrio MA. Canine infection and the possible role of dogs in the transmission of american tegumentary leishmaniosis in salta, argentina. *Vet Parasitol* 2002; **110**: 1–0.

507 Palangar HK M.Jamali. Molecular study of cutaneous leishmaniasis human reservoirs and infections in bastak. *Iioab Journal* 2017; **8**: 33–8.

508 Panti-May R J. A., Costa F. A survey of zoonotic pathogens carried by house mouse and black rat populations in yucatan, mexico. *Epidemiol Infect* 2017; **145**: 2287–95.

509 Paoletta LA M. S., Wilkowsky SE. Epidemiology of babesia, anaplasma and trypanosoma species using a new expanded reverse line blot hybridization assay. *Ticks Tick Borne Dis* 2018; **9**: 155–63.

510 Parrado R R., Garcia AL. Prevalence of leishmania spp. Infection in domestic dogs in chapare, bolivia. *Vet Parasitol* 2011; **177**: 171–4.

511 Parvizi A P., Baghban N. Occurrence of low density of leishmania infantum in sandflies from a new focus of visceral leishmaniasis in northwest of iran. *J Vector Borne Dis* 2013; **50**: 127–32.

512 Pasa TV S., Ozbel Y. Detection of leishmania major and leishmania tropica in domestic cats in the ege region of turkey. *Vet Parasitol* 2015; **212**: 389–92.

513 Pasos-Pinto LS-M S.Sanchez-Garcia. Genetic diversity and prevalence of leishmania mexicana in bichromomyia olmeca olmeca(1) in an endemic area of mexico. *Southwestern Entomologist* 2017; **42**: 983–94.

514 Perez F T. D., Coura JR. Prevalence of american trypanosomiasis and leishmaniases in domestic dogs in a rural area of the municipality of sao joao do piaui, piaui state, brazil. *Rev Inst Med Trop Sao Paulo* 2016; **58**: 79.

515 Piantedosi V D., Gramiccia M. Epidemiological survey on leishmania infection in red foxes (vulpes vulpes) and hunting dogs sharing the same rural area in southern italy. *Acta Parasitol* 2016; **61**: 769–75.

516 Pineda S V., Calzada JE. Prevalence of trypanosome infections in dogs from chagas disease endemic regions in panama, central america. *Vet Parasitol* 2011; **178**: 360–3.

517 Pinto O-M C. M., Grijalva MJ. Infection by trypanosomes in marsupials and rodents associated with human dwellings in ecuador. *J Parasitol* 2006; **92**: 1251–5.

518 Pinto O-M C. M., Perkins SL. Bats, trypanosomes, and triatomines in ecuador: New insights into the diversity, transmission, and origins of trypanosoma cruzi and chagas disease. *PLoS One* 2015; **10**: e0139999.

519 Qiu K Y., Sugimoto C. Molecular characterization and phylogenetic analysis of trypanosoma spp. Detected from striped leaf-nosed bats (hipposideros vittatus) in zambia. *Int J Parasitol Parasites Wildl* 2019; **9**: 234–8.

520 Quintal RE A. P., Nunes CM. Leishmania spp. In didelphis albiventris and micoureus paraguayanus (didelphimorphia: Didelphidae) of brazil. *Vet Parasitol* 2011; **176**: 112–9.

521 Ramsey G-C J. M., Ibarra-Cerdena CN. Ecological connectivity of trypanosoma cruzi reservoirs and triatoma pallidipennis hosts in an anthropogenic landscape with endemic chagas disease. *PLoS One* 2012; **7**: e46013.

522 Rassi KM Y.Azizi. The seminested PCR based detection of leishmania infantum infection in asymptomatic dogs in a new endemic focus of visceral leishmaniasis in iran. *Iranian Journal of Arthropod-Borne Diseases* 2007; **1**: 38–42.

523 Razzaghi Maensh SG M.Mahabadi. Prevalence of canine visceral leishmaniasis in dogs at adrestan district detected by PCR. *Veterinary Research* 2012; **5**: 22–5.

524 Rodrigues P F. T., Lopes AP. Seroprevalence of toxoplasma gondii and leishmania spp. In domestic donkeys from portugal. *Rev Bras Parasitol Vet* 2019; **28**: 172–6.

525 Rodriguez T-J N. F., Gutierrez C. The role of wild rodents in the transmission of trypanosoma evansi infection in an endemic area of the canary islands (spain). *Vet Parasitol* 2010; **174**: 323–7.

526 Rodriguez OA, Matta NE. Blood parasites in some birds from eastern plains of colombia. *Mem Inst Oswaldo Cruz* 2001; **96**: 1173–6.

527 Rossi B E., Maroli M. Seasonal phenology, host-blood feeding preferences and natural leishmania infection of phlebotomus perniciosus (diptera, psychodidae) in a high-endemic focus of canine leishmaniasis in rome province, italy. *Acta Trop* 2008; **105**: 158–65.

528 Rosypal C-V A. C., Lindsay DS. Serological survey of leishmania infantum and trypanosoma cruzi in dogs from urban areas of brazil and colombia. *Vet Parasitol* 2007; **149**: 172–7.

529 Ruiz N J. P., Malele I. The role of domestic animals in the epidemiology of human african trypanosomiasis in ngorongoro conservation area, tanzania. *Parasit Vectors* 2015; **8**: 510.

530 Ruiz-Pina HA, Cruz-Reyes A. The opossum didelphis virginiana as a synanthropic reservoir of trypanosoma cruzi in dzidzilche, yucatan, mexico. *Mem Inst Oswaldo Cruz* 2002; **97**: 613–20.

531 Saldana C A., Chaves LF. Risk factors associated with trypanosoma cruzi exposure in domestic dogs from a rural community in panama. *Mem Inst Oswaldo Cruz* 2015; **110**: 936–44.

532 Saldana S A., Calzada JE. A darker chromatic variation of rhodnius pallescens infected by specific genetic groups of trypanosoma rangeli and trypanosoma cruzi from panama. *Parasit Vectors* 2018; **11**: 423.

533 Sallemi R S., Gharbi M. Molecular prevalence and phylogenetic analysis of theileria annulata and trypanosoma evansi in cattle in northern tunisia. *Vet Med Sci* 2018; **4**: 17–25.

534 Salvatore A D., Galuppi R. Molecular evidence of leishmania infantum in ixodes ricinus ticks from dogs and cats, in italy. *Vet Ital* 2014; **50**: 307–12.

535 Salzer P J. S., Gillespie TR. Impact of anthropogenic disturbance on native and invasive trypanosomes of rodents in forested uganda. *Ecohealth* 2016; **13**: 698–707.

536 Santaella O J., Quinnell RJ. Leishmania (viannia) infection in the domestic dog in chaparral, colombia. *Am J Trop Med Hyg* 2011; **84**: 674–80.

537 Sarquis C-C O., Lima MM. Eco-epidemiology of chagas disease in northeastern brazil: Triatoma brasiliensis, t. Pseudomaculata and rhodnius nasutus in the sylvatic, peridomestic and domestic environments. *Parasitol Res* 2012; **110**: 1481–5.

538 Sastre F N., Altet L. Detection of leishmania infantum in captive wolves from southwestern europe. *Vet Parasitol* 2008; **158**: 117–20.

539 Sazmand E A., Joachim A. Molecular identification of hemoprotozoan parasites in camels (camelus dromedarius) of iran. *Iran J Parasitol* 2016; **11**: 568–73.

540 Selmi MBS R.Dhibi. Evidence of natural infections with trypanosoma, anaplasma and babesia spp. In military livestock from tunisia. *Tropical Biomedicine* 2019; **36**: 742–57.

541 Shadomy W S. V., Chappell CL. Combined use of enzyme-linked immunosorbent assay and flow cytometry to detect antibodies to trypanosoma cruzi in domestic canines in texas. *Clin Diagn Lab Immunol* 2004; **11**: 313–9.

542 Sharbatkhori S M., Parvizi P. Molecular variation in leishmania parasites from sandflies species of a zoonotic cutaneous leishmaniasis in northeast of iran. *J Vector Borne Dis* 2014; **51**: 16–21.

543 Sharma BK A.Sharma. Incidence of haemoprotozoan infection in canines in and around mathura. *Veterinary Practitioner* 2011; **12**: 149–50.

544 Silbermayr L K., Solkner J. A novel qPCR assay for the detection of african animal trypanosomosis in trypanotolerant and trypanosusceptible cattle breeds. *PLoS Negl Trop Dis* 2013; **7**: e2345.

545 Silva Rde R C., Alves LC. Detection of antibodies against leishmania infantum in cats (felis catus) from the state of pernambuco, brazil. *Rev Soc Bras Med Trop* 2014; **47**: 108–9.

546 Simo S G., Asonganyi T. Identification of different trypanosome species in the mid-guts of tsetse flies of the malanga (kimpese) sleeping sickness focus of the democratic republic of congo. *Parasit Vectors* 2012; **5**: 201.

547 Singh P N., Kumar R. A comparative evaluation of parasitological, serological and DNA amplification methods for diagnosis of natural trypanosoma evansi infection in camels. *Vet Parasitol* 2004; **126**: 365–73.

548 Singla D L. D., Ba MS. Conventional and molecular diagnosis of haemo-protozoan infectionsin cattle and equids from republic of guinea and india. *Indian Journal of Animal Research* 2017; **52**. DOI:10.18805/ijar.v0iOF.6988.

549 Sobrino F R., Gortazar C. Characterization of widespread canine leishmaniasis among wild carnivores from spain. *Vet Parasitol* 2008; **155**: 198–203.

550 Solano-Gallego L L., Breitschwerdt E. A serological study of exposure to arthropod-borne pathogens in dogs from northeastern spain. *Vet Res* 2006; **37**: 231–44.

551 Solano-Gallego M L., Ferrer L. Prevalence of leishmania infantum infection in dogs living in an area of canine leishmaniasis endemicity using PCR on several tissues and serology. *J Clin Microbiol* 2001; **39**: 560–3.

552 Solano-Gallego R L., Trotta M. Detection of leishmania infantum DNA mainly in rhipicephalus sanguineus male ticks removed from dogs living in endemic areas of canine leishmaniosis. *Parasit Vectors* 2012; **5**: 98.

553 Spada C E., Proverbio D. Prevalence of leishmania infantum and co-infections in stray cats in northern italy. *Comp Immunol Microbiol Infect Dis* 2016; **45**: 53–8.

554 Sumbria S D., Bal MS. Equine trypanosomosis in central and western punjab: Prevalence, haemato-biochemical response and associated risk factors. *Acta Trop* 2014; **138**: 44–50.

555 Sumbria S D., Kaur P. Comparative seroprevalence and risk factor analysis of trypanosoma evansi infection in equines from different agro-climatic zones of punjab (india). *Rev Sci Tech* 2017; **36**: 971–9.

556 Sun G K., Chen JP. Prevalence of canine leishmaniasis in beichuan county, sichuan, china and phylogenetic evidence for an undescribed leishmania sp. In china based on 7SL RNA. *Parasit Vectors* 2012; **5**: 75.

557 Szpeiter F B. B., Marcili A. Bat trypanosomes from tapajos-arapiuns extractive reserve in brazilian amazon. *Rev Bras Parasitol Vet* 2017; **26**: 152–8.

558 Tabar A M. D., Roura X. Vector-borne infections in cats: Molecular study in barcelona area (spain). *Vet Parasitol* 2008; **151**: 332–6.

559 Tadesse A, Tsegaye B. Bovine trypanosomosis and its vectors in two districts of bench maji zone, south western ethiopia. *Trop Anim Health Prod* 2010; **42**: 1757–62.

560 Tafese M W., Fentahun T. Prevalence of bovine trypanosomosis and its vectors in two districts of east wollega zone, ethiopia. *Onderstepoort J Vet Res* 2012; **79**: E1–4.

561 Kante Tagueu F S., Simo G. Prevalence of sodalis glossinidius and different trypanosome species in glossina palpalis palpalis caught in the fontem sleeping sickness focus of the southern cameroon. *Parasite* 2018; **25**: 44.

562 Tamay-Segovia B-D Paulino, Retana-Guiascón OG. Presence of virginia opossum (didelphis virginiana) and pic (triatoma dimidiata) infected with trypanosoma cruzi in urban areas: Preliminary evaluation in the city of campeche, mexico. *Austral journal of veterinary sciences* 2017; **49**: 35–8.

563 Tanczos B B., Farkas R. First record of autochthonous canine leishmaniasis in hungary. *Vector Borne Zoonotic Dis* 2012; **12**: 588–94.

564 Tehseen J Sonia, Qamar MF. Field investigation of trypanosoma evansi and comparative analysisof diagnostic tests in horses from bahawalpur, pakistan. *Turkish Journal of Veterinary and Animal Sciences* 2017; **41**: 288–93.

565 Tomas-Perez K M., Fisa R. First report of natural infection in hedgehogs with leishmania major, a possible reservoir of zoonotic cutaneous leishmaniasis in algeria. *Acta Trop* 2014; **135**: 44–9.

566 Tonelli T G. B., Andrade Filho JD. Leishmania (viannia) braziliensis infection in wild small mammals in ecotourism area of brazil. *PLoS One* 2017; **12**: e0190315.

567 Tono F Rafi Rabecca, Ibitoye EB. Presence of trypanosome species and anemic status of dogs in zuru, nigeria. *Macedonian Veterinary Review* 2015; **38**: 217–22.

568 Toz E S. O., Ozbel Y. [An epidemiological study on canine leishmaniasis (CanL) and sand flies in northern cyprus]. *Turkiye Parazitol Derg* 2013; **37**: 107–12.

569 Toz NE S. O.Sakru. Serological and entomological survey of zoonotic visceral leishmaniasis in denizli province, aegean region, turkey. *New Microbiologica* 2009; **32**: 93–100.

570 Trindade NA de A C. N. D.da Cunha. Cunha. Immunofluorescent antibody test (IFAT) for trypanosoma cruzi in dogs from urban and rural areas of pelotas, RS. *Boletim De Industria Animal* 2015; **72**: 111–6.

571 Tsakmakidis A Iota, Diakou A. Leishmania infection in rodents in greece. *Trop Med Int Health* 2017; **22**: 1523–32.

572 Valadas M S., Gennari SM. Occurrence of antibodies anti-neospora caninum, anti-toxoplasma gondii, and anti-leishmania chagasi in serum of dogs from para state, amazon, brazil. *Parasitol Res* 2010; **107**: 453–7.

573 Valkiūnas I G., Shapoval AP. High prevalence of blood parasites in hawfinch coccothraustes coccothraustes. *Journal of Natural History* 2003; **37**: 2647–52.

574 Valkiunas I G., Causey D. Additional observations on blood parasites of birds in costa rica. *J Wildl Dis* 2004; **40**: 555–61.

575 Valkiunas S G., Smith TB. Further observations on the blood parasites of birds in uganda. *J Wildl Dis* 2005; **41**: 580–7.

576 Villagran JA de D M. E.Martinez-Ibarra. Pathological alterations and prevalence of trypanosoma cruzi in opossums from western mexico. *Boletin De Malariologia Y Salud Ambiental* 2011; **51**: 87–8.

577 Villena G-P F. E., Ampuero JS. First report of trypanosoma cruzi infection in salivary gland of bats from the peruvian amazon. *Am J Trop Med Hyg* 2018; **99**: 723–8.

578 Dohlen C von A. R., Sharma RN. Prevalence of antibodies against visceralizing leishmania spp. In brown rats from grenada, west indies. *Vet World* 2018; **11**: 1321–5.

579 Votypka P J., Petrzelkova KJ. An unexpected diversity of trypanosomatids in fecal samples of great apes. *Int J Parasitol Parasites Wildl* 2018; **7**: 322–5.

580 Voyvoda ST H.Pasa. Prevalence of leishmania infantum and dirofilaria immitis infection in dogs in aydin province and the town of selcuk, izmir, turkey. *Turkish Journal of Veterinary & Animal Sciences* 2004; **28**: 1105–11.

581 Wang H J. Y., Chen HT. The prevalence of canine leishmania infantum infection in western china detected by PCR and serological tests. *Parasit Vectors* 2011; **4**: 69.

582 Wong SM Y. Y., Dumonteil E. Molecular epidemiology of trypanosoma cruzi and triatoma dimidiata in costal ecuador. *Infect Genet Evol* 2016; **41**: 207–12.

583 Yabsley MJ, Noblet GP. Seroprevalence of trypanosoma cruzi in raccoons from south carolina and georgia. *J Wildl Dis* 2002; **38**: 75–83.

584 Yefi-Quinteros M-SM E., Cattan PE. Trypanosoma cruzi load in synanthropic rodents from rural areas in chile. *Parasit Vectors* 2018; **11**: 171.

585 Zanet S S., Ferroglio E. Epidemiology of leishmania infantum, toxoplasma gondii, and neospora caninum in rattus rattus in absence of domestic reservoir and definitive hosts. *Vet Parasitol* 2014; **199**: 247–9.

586 Zangooie MK F.Ganjali. Molecular detection of trypanosoma evansi based on ITS1 rDNA gene in camelus dromedarius in sistan region, iran. *Tropical Biomedicine* 2018; **35**: 1140–7.

587 Zhang G J. R., Chen JP. Molecular detection, identification and phylogenetic inference of leishmania spp. In some desert lizards from northwest china by using internal transcribed spacer 1 (ITS1) sequences. *Acta Trop* 2016; **162**: 83–94.

588 Zhao Y G. H., Wang HF. Epidemiological investigation of asymptomatic dogs with leishmania infection in southwestern china where visceral leishmaniasis is intractable. *Korean J Parasitol* 2016; **54**: 797–801.

589 Zivicnjak M T., Baric-Rafaj R. A seroepidemiologic survey of canine visceral leishmaniosis among apparently healthy dogs in croatia. *Vet Parasitol* 2005; **131**: 35–43.

590 Zivicnjak FK T.Martinkovic. Serological and entomological studies of canine leishmaniosis in croatia. *Veterinarski Arhiv* 2011; **81**: 99–110.

591 Zoghlami C Z., Zhioua E. Interaction between canine and human visceral leishmaniases in a holoendemic focus of central tunisia. *Acta Trop* 2014; **139**: 32–8.

592 Ollerton J, Winfree R, Tarrant S. How many flowering plants are pollinated by animals? *Oikos* 2011; **120**: 321–6.

593 Gallai N, Salles J-M, Settele J, Vaissière BE. Economic valuation of the vulnerability of world agriculture confronted with pollinator decline. *Ecological Economics* 2009; **68**: 810–21.

594 Morse R, Calderone N. The value of honey bees as pollinators of u.s. Crops in 2000. *Bee Cult* 2000; **128**: 1–5.

595 Cameron SA, Sadd BM. Global trends in bumble bee health. *Annual Review of Entomology* 2020; **65**: 209–32.

596 Mallinger HRAG Rachel E. AND Gaines-Day. Do managed bees have negative effects on wild bees?: A systematic review of the literature. *PLOS ONE* 2017; **12**: 1–32.

597 Fischer B, Taborsky B, Dieckmann U. Unexpected patterns of plastic energy allocation in stochastic environments. *The American Naturalist* 2009; **173**: E108–20.

598 Alonso S, Dohoo I, Lindahl J, Verdugo C, Akuku I, Grace D. Prevalence of tuberculosis, brucellosis and trypanosomiasis in cattle in tanzania: A systematic review and meta-analysis. *Animal Health Research Reviews* 2016; **17**: 16–27.

599 Pollitt LC, MacGregor P, Matthews K, Reece SE. Malaria and trypanosome transmission: Different parasites, same rules? *Trends in Parasitology* 2011; **27**: 197–203.

600 Schmidt KA, Ostfeld RS. Biodiversity and the dilution effect in disease ecology. *Ecology* 2001; **82**: 609–19.

601 Halsey S. Defuse the dilution effect debate. *Nature Ecology & Evolution* 2018; **3**. DOI:10.1038/s41559-018-0764-3.

602 Wood CL, Lafferty KD. Biodiversity and disease: A synthesis of ecological perspectives on lyme disease transmission. *Trends in Ecology & Evolution* 2013; **28**: 239–47.

603 Barribeau S, Sadd B, Plessis L, *et al.* A depauperate immune repertoire precedes evolution of sociality in bees. *Genome Biology* 2015; **16**: 83.

604 Evans JD, Aronstein K, Chen YP, *et al.* Immune pathways and defence mechanisms in honey bees apis mellifera. *Insect Molecular Biology* 2006; **15**: 645–56.

Table1. ***Summary of all included studies based on parasite groupings***

Trypanosomatid groups	Parasite grouping	Host order	Infected hosts	Geographic distribution	systematic studies	meta-analysis studies	Kmeta	sig	pooled estimate (ci.il, ci.ul)	SE	pooled prevalence
'jaculum'_spp.	monoxenous_spp.	Hemiptera	Insects {True bugs}	South America	1	1	4	***	0.563 (0.227, 0.889)	0.170	28.2
Agomonas_spp.	monoxenous_spp.	Diptera	Insects {flies}	South and Central America, Africa	1	1	3		0.123 (-0.271, 0.521)	0.202	0.9
Blastocrithidia_spp.	monoxenous_spp.	Hemiptera, Chiroptera	Insects {True bugs}, none_insects {bats}	South and North America	3	3	5	*	0.234 (0.039, 0.429)	0.100	4.62
Crithidia_bombi	monoxenous_spp.	Hymenoptera	Insects {bees}	South and North America, Europe	18	18	80	***	0.569 (0.475, 0.663)	0.048	23.7
Crithidia_expoeki	monoxenous_spp.	Hymenoptera	Insects {bees}	North America	2	2	10		0.569 (0.474, 0.664)	0.0483	28.7
Crithidia_mellificae,_Lotmaria_passim	monoxenous_spp.	Hymenoptera	Insects {bees}	Europe, South and North Amarica , Asia and Africa	7	7	7	***	0.149 (0.10, 0.394)	0.125	1.53
Crithidia_mexicana	monoxenous_spp.	Hymenoptera	Insects {bees}	North America	1	1	8	.	0.335 (-0.002, 0.673)	0.171	10.0
Crithidia_spp.	monoxenous_spp.	Hymenoptera, Diptera	Insects {bees, flies}	North America, Europe, Asia	3	3	8	*	0.286 (0.073, 0.499)	0.108	7.3
fish_trypanosomes	dixenous_spp.	Acipenseriformes	none_insects {fish}	Europe	2	2	2	***	0.729 (0.449, 1.01)	0.143	44.36
Herpetomonas_spp.	monoxenous_spp.	Diptera	Insects {flies}	South America	1	1	1		0.244(-0.176, 0.624)	0.204	4.26
Leishmania_amazonensis	dixenous_spp.	Diptera	Insects {flies}	South America	1	1	1		0.174 (-0.166, 0.513)	0.173	2.30
Leishmania_braziliensis	dixenous_spp.	Diptera, Carnivora	Insects {flies}, none_insects {dogs}	South and North America and Asia	12	7	7	***	0.308 (0.165, 0.4450)	0.073	8.54
Leishmania_donovani	dixenous_spp.	Diptera, Carnivora and others	Insects {flies}, none_insects {dogs, and multiple other hosts}	Asia and Africa	5	3	3	*	0.272 (0.040, 0.503)	0.118	6.56
Leishmania_guyanensis	dixenous_spp.	Diptera, Carnivora	Insects {flies}, none_insects {dogs}	South America	2	1	2	*	0.357 (0.0418, 0.671)	0.161	11.6
Leishmania_infantum	dixenous_spp.	Diptera, Carnivora, Chiroptera and others	Insects {flies}, none_insects {dogs, cats, rodents, equids, bats, oppossums, other animals}	South and North America, Europe, Africa, Asia	119	41	45	***	0.359 (0.298, 0.421)	0.031	11.8
Leishmania_major	dixenous_spp.	Diptera, Carnivora, Rodentia and others	Insects {flies}, none_insects {dogs, cats, rodents, birds, other animals}	South America, Asia, Africa	14	5	9	**	0.252 (0.0926, 0.412)	0.082	5.60
Leishmania_mexicana	dixenous_spp.	Carnivora, Chiroptera, Rodentia	none_insects {rodents, bats,	South and North America	4	2	2	***	0.444 (0.195, 0.692)	0.127	18.0

			dogs}								
Leishmania_spp.	dixenous_spp.	Diptera, Carnivora, Rodentia and others	insects{flies}, none_insects {dogs, cats, rodents, other animals}	South America, Africa, Europe	62	30	57	***	0.335 (0.267, 0.403)	0.035	10.2
Leishmania_tropica	dixenous_spp.	Diptera, Carnivora	insects{flies}, none_insects {dogs, cats}	Asia and Africa	5	4	4	.	0.182 (-0.002, 0.367)	0.094	2.60
Leishmania_turanica	dixenous_spp.	Rodentia	none_insects {rodents}	Asia and Africa	1	NA	NA		NA	NA	NA
Leptomonas_spp.	monoxenous_spp.	Siphonaptera, Hemiptera	Insects {true bugs, fleas}	South America	2	2	5	.	0.241 (-0.02, 0.503)	0.134	5.04
Lotmaria_passim	monoxenous_spp.	Hymenoptera	Insects {bees}	South and North America, Asia and Africa	8	8	11	***	0.549 (0.393, 0.705)	0.080	26.8
monoxenous_spp.	monoxenous_spp.	Hymenoptera, Hemiptera	Insects {bees, true bugs}	Asia	2	2	2	***	0.567 (0.239, 0.896)	0.168	28.5
Phytomonas_spp.	dixenous_spp.	Hemiptera	Insects {true bugs}	South America, Asia	3	3	6	**	0.253 (0.05, 0.455)	0.101	5.60
Trypanosoma_avium	dixenous_spp.	Siphonaptera, Passeriformes	Insects {fleas}, none_insects {birds}	Australia, Europe, North America	4	3	3	.	0.198 (-0.0214, 0.418)	0.112	3.26
Trypanosoma_brucei	dixenous_spp.	Diptera, Carnivora, Artiodactyla and others	Insects {flies}, none_insects {dogs, cattle, sheep, goats, equids and others}	Africa and Asia	40	25	43	***	0.161 (0.0943, 0.228)	0.034	1.90
Trypanosoma_chelodinae	dixenous_spp.	NA	none_insects {animals}	Australia	1	NA	NA		NA	NA	NA
Trypanosoma_congolense	dixenous_spp.	Diptera, Carnivora, Artiodactyla and others	Insects {flies}, none_insects {dogs, cattle, sheep, goats, equids and others}	Africa	58	38	78	***	0.261 (0.205, 0.318)	0.029	6.05
Trypanosoma_copemani	dixenous_spp.	NA	none_insects {animals}	Australia	1	1	1	.	0.373 (-0.0239, 0.770)	0.203	12.7
Trypanosoma_cruzi	dixenous_spp.	Hemiptera, Chiroptera, Carnivora	Insects {True bugs}, none_insects {dogs, cats, bats}	South, Central and n North America	50	33	39	***	0.357 (0.290, 0.423)	0.034	11.6
Trypanosoma_culicavium	dixenous_spp.	Diptera	Insects {flies}	Australia	1	1	2		0.218 (-0.114, 0.550)	0.169	4.14
Trypanosoma_dionisii	dixenous_spp.	Chiroptera	none_insects {bats}	South and North America	3	3	5	***	0.423 (0.227, 0.619)	0.100	16.30
Trypanosoma_equiperdum	dixenous_spp.	Perissodactyla	none_insects {equids}	Asia	1	1	1		0.224 (-0.173, 0.621)	0.203	4.30
Trypanosoma_evansi	dixenous_spp.	Artiodactyla, Perissodactyla and others	none_insects {equids, camels, dogs, cattle, goats, sheep, buffaloes and animals}	South America, Africa, Asia and Europe	63	32	46	***	0.339 (0.272, 0.405)	0.034	10.50
Trypanosoma_everetti	dixenous_spp.	Passeriformes	none_insects {birds}	Africa	1	1	1		0.0394 (-0.358, 0.437)	0.203	0.000
Trypanosoma_evotomys	dixenous_spp.	Rodentia	none_insects {rodents}	Europe	1	1	1	*	0.399 (0, 0.798)	0.204	14.60

Trypanosoma_giganteum	dixenous_spp.	NA	none_insects {animals}	Europe	1	NA	NA		NA	NA	NA
Trypanosoma_gilletti	dixenous_spp.	NA	none_insects {animals}	Australia	1	1	1		0.185 (-0.212, 0.582)	0.203	2.70
Trypanosoma_godfreyi	dixenous_spp.	Diptera, Artiodactyla	Insects {flies}, none_insects {pigs}	Africa	4	3	6	.	0.174 (-0.0044, 0.353)	0.091	2.34
Trypanosoma_lewisi	dixenous_spp.	Rodentia	none_insects {rodents}	Asia and Africa	2	2	2	***	0.511 (0.230, 0.792)	0.143	23.5
Trypanosoma_noyesi	dixenous_spp.	NA	none_insects {animals}	Australia	1	1	1		0.206 (-0.191, 0.603)	0.203	3.50
Trypanosoma_rangeli	dixenous_spp.	Hemiptera, Chiroptera	Insects {True bugs}, none_insects {bats}	North and South America	3	2	2		0.158 (-0.0816, 0.398)	0.122	1.80
Trypanosoma_simiae	dixenous_spp.	Siphonaptera, Artiodactyla, Perissodactyla	Insects {fleas}, none_insects {cattle, equids, pigs}	Africa	9	6.00	15	**	0.195 (0.067, 0.323)	0.065	3.08
Trypanosoma_spp.	dixenous_spp.	Diptera, Artiodactyla, Passeriformes, Rodentia, Hemiptera, Chiroptera, Acipenseriformesand others	Insects {True bugs, flies}, none_insects {cattle, rodents, bats, pigs, birds, fish, equids, and others}	South and North America, Europe, Africa, Asia and Australia	47	17	21	***	0.285 (0.192, 0.377)	0.05	7.25
Trypanosoma_theileri	dixenous_spp.	Artiodactyla	none_insects {cattle, animals}	South America, Africa	5	4	6	***	0.343 (0.182, 0.504)	0.082	10.7
Trypanosoma_tungarae	dixenous_spp.	Anura	none_insects {frogs}	South America	1	1	1	*	0.558 (0.133, 0.983)	0.217	27.7
Trypanosoma_vegrandis	dixenous_spp.	Chiroptera and others	none_insects {bats, animals}	Australia	3	1	1	*	0.438 (0.0413, 0.835)	0.203	17.5
Trypanosoma_vivax	dixenous_spp.	Diptera, Artiodactyla, Perissodactyla and others	Insects {flies}, none_insects {cattle, sheep, goats, camels, dogs, other animals}	Africa, South America	63	43	61	***	0.279 (0.225, 0.334)	0.028	7.00
Trypanosomatidae_spp.	mix	Diptera, Hemiptera, Siphonaptera, Chiroptera and others	Insects {true bugs, fleas, flies}, none_insects {reptiles, bats, rodents}	Europe, South America, Asia and Africa	15	12	15	***	0.423(0.305, 0.451)	0.06	16.372
Trypanozoon	dixenous_spp.	Diptera, Artiodactyla and others	Insects {flies}, none_inescts {animals, pigs, camels, dogs, cattle}	Africa	6	4	7		0.222 (0.0681, 0.376)	0.078	4.8

Parasite grouping as extracted from systematically (51 level) and quantitatively (47 level) included studies. Parasite groups ending with "spp." are trypanosomatids with no enough information to break them down to the exact parasite taxa/group. Systematic and quantitative summary of the main features are outlined in for each group.

Table2: ***Pooled prevalence for several subgroup analysis***

Analysis 1							
Host grouping	***k***	**pooled estimate (CI.lb, CI.ub)**	**Microscopic (%)**	**pooled estimate (CI.lb, CI.ub)**	**Molecular (%)**	**(t-test)**	**Sig**
Insects	313	0.409 (0.352, 0.466)	14.9	0.332 (0.282, 0.382)	9.64	0.0002	***
Non-insects	229	0.120 (0.361, 0.448)	0.642	0.405 (0.361, 0.448)	14.9	<.0001	***
Analysis 2							
Host grouping	***K***	**pooled estimate (CI.lb, CI.ub)**	**Dixenous (%)**	**pooled estimate (CI.lb, CI.ub)**	**Monoxenous (%)**	**(t-test)**	**Sig**
Insects	313	0.280 (0.228, 0.333)	6.61	0.483 (0.414, 0.552)	20.9	<.0001	***
Flies	155	0.232 (0.194 0.270)	4.80	0.173 (-0.0226, 0.244)	2.45	0.438	
Truebugs	33	0.357 (0.265, 0.449)	11.5	0.358 (0.170, 0.547)	11.6	0.991	
Analysis 3 *							
Parasite grouping	***K***	**pooled estimate (CI.lb, CI.ub)**	**Insects (%)**	**pooled estimate (CI.lb, CI.ub)**	**Non-insects (%)**	**(t-test)**	**Sig**
Dixenous spp	390	0.244 (0.216, 0.272)	5.51	0.316 (0.290, 0.342)	9.38	0.0001	***
Leishmania spp.	125	0.162 (0.114, 0.210)	2.02	0.397 (0.357, 0.438)	14.5	0.0001	***
Trypanosoma spp.[1]	226	0.208 (0.177, 0.240)	4.09	0.248 (0.219, 0.277)	5.85	0.0001	***
Trypanosoma cruzi	39	0.394 (0.285, 0.502)	14.51	0.294 (0.201, 0.388)	8.17	0.1731	
Analysis 4							
Bees Groups	***K***	**pooled estimate (CI.lb, CI.ub)**	**Wild (%)**	**pooled estimate (CI.lb, CI.ub)**	**Managed (%)**	**(t-test)**	**Sig**
All	123	0.554 (0.440, 0.668)	26.8	0.505 (0.207, 0.804)	22.2	0.754	
Honeybee	17	0.631 (0.448, 0.815)	34.2	0.481 (0.082, 0.880)	20.1	0.502	
Bumblebee	106	0.530 (0.398, 0.663)	24.4	0.527 (0.113, 0.941)	24.2	0.991	

*dixenous species with prevalence data from both insects and non-insects

[1] Prevalence data for *Trypanosoma cruzi* are not included here

All of the analysis were done using meta-regressions with random effect model and an appropriate nested random design.

K is the total prevalence data included in the analysis in each row.