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Parasites are endangered by the conservation of their hosts: Meta-analyses of the effect of host captivity on the odds of parasite infection

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ABSTRACT

Parasites are important drivers of ecosystem functions and play a key role in the maintenance of ecosystem health. However, parasites may be threatened by host conservation, as well as by host extinction. Captive management is of increasing importance for conserving threatened host species, but captivity represents a drastic environmental change that may in turn threaten parasites. To address this concern, we examined how host captivity affects the odds of parasite infection and identified which parasite life-history traits (particularly modes of transmission) are the strongest predictors of parasite decline. Data were collated from 45 studies examining parasite prevalence in both captive and free-range host populations across a total of 55 host and 158 parasite species. We performed meta-analyses of these studies and found that overall, the odds of infection by parasites were not different between host populations in captive and free-range environments. However, the odds of infection by helminths were lower in captivity. Parasites with indirect life cycles, especially helminths with complex life cycles and vector-borne protozoa, also had lower odds of infecting hosts in captivity. Finally, parasites transmitted through the environment with direct life cycles, particularly environmentally-transmitted helminths, had lower odds of infecting hosts in captivity. Parasite losses in captivity are likely caused by the use of antiparasitic drugs, and the biotic and abiotic differences between captive and free-range environments. If the goals of activities such as captive breeding are to re-establish self-sustaining ecosystems, then conservation efforts need to include both hosts and their parasites in captive management programs.

1. Introduction

The world is currently experiencing its sixth mass extinction event (Regnier et al., 2015; Ceballos et al., 2015; Ceballos et al., 2017). With hundreds of species becoming extinct each year through anthropogenic causes (Ceballos et al., 2017), conservation efforts to save the most threatened species are of increasing importance. To date, such efforts have mainly focused on large, charismatic megafauna (Albert et al., 2018), some of which depend on captivity for persistence (Mysterud et al., 2007). However, these species comprise only a small percentage of overall biodiversity, with the majority of biodiversity contained in groups that are less charismatic, more obscure and more neglected by conservation efforts, including symbiotic organisms such as parasites (Windsor, 1997; Gompper and Williams, 1998; Marcogliese, 2005; Dunn et al., 2009).

Parasites are integral parts of every ecosystem; they regulate host

populations, they contribute to energy flow through the many links in food webs, and they are a major component of biodiversity (Lafferty et al., 2006; Dobson et al., 2008; Sato et al., 2011; Hatcher et al., 2012). Despite their importance, parasite extinction risks and their potential impacts on ecosystem health have rarely been studied and are poorly described. Since they co-evolve with their hosts, parasites are especially vulnerable to co-extinction. Co-extinction occurs when a parasite, dependent on its host, becomes extinct as a result of the host's extinction, and this is thought to be one of the most common ways in which biodiversity is lost (Koh et al., 2004). Unfortunately, as well as being threatened by co-extinction events per se, parasites can even become extinct before their hosts, as a direct consequence of host decline (de Castro and Bolker, 2005). In addition, conservation efforts to restore declining host populations can actually endanger parasite fauna (Windsor, 1997; Gompper and Williams, 1998; Gomez and Nichols, 2013; Rozsa and Vas, 2015). Here, we refer to this phenomenon as

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"conservation-driven extinction". Although conservation-driven extinction has been poorly studied, there are a number of examples of parasite extinctions due to host conservation efforts. For example, the lice Neotrichodectes sp. and Colpocephalum californici from the blackfooted ferret (Mustela nigripes) and the Californian condor (Gymnogyps californianus), respectively, went extinct when host captive breeding programs included de-lousing protocols (Gompper and Williams, 1998; Koh et al., 2004). Most estimates of parasite extinctions focus only on co-extinction risks in the wild, without considering the possibility that parasites may go extinct before their hosts due to natural or humandriven causes (Koh et al., 2004; Dunn et al., 2009; Cizauskas et al., 2017). Understanding how methods used in host conservation impact parasite fauna and determining which factors contribute to parasite survival or demise are important next steps in conserving parasites and thus, maintaining wider ecosystem function (Gompper and Williams, 1998; Viney and Graham, 2013).

Captive animal management (e.g. zoos, captive breeding facilities, rehabilitation centres, and enclosures) is an important strategy for ensuring the survival of some endangered animals through raising public awareness (Balmford et al., 1995), providing opportunities for captive breeding programs, and supplementing natural populations (Kleiman, 1989). There are currently 38 animal species listed as extinct in the wild on the IUCN Red List of Threatened Species (IUCN, 2020), which survive only because of human intervention through captivity and captive breeding. Examples include the scimitar-horned oryx (*Oryx danmah*), the Hawaiian crow (*Corvus hawaiiensis*), the black softshell turtle (*Nilssonia nigricans*), the Polynesian tree snail (*Partula nodosa*), and the Socorro isopod (*Thermosphaeroma thermophilum*) (IUCN, 2020). Despite the growing number of animals destined for captivity, our understanding of how captivity affects associated fauna such as parasites is largely unexplored.

When a subset of hosts is transferred from a free-range/wild environment to captivity, some parasite species may be lost simply by chance because only uninfected hosts are taken (MacLeod et al., 2010), resulting in a new host population devoid of those parasites. This potential loss can be exacerbated by the already diminished parasite diversity associated with small populations of endangered hosts (Altizer et al., 2007). Even when parasites are successfully transferred to a captive environment, they may not survive in the new, unfamiliar conditions. In many ways, this is akin to the reduced diversity and abundance of parasites recorded for invasive species after they are introduced into a new environment (i.e. the enemy release hypothesis) (Keane and Crawley, 2002; Torchin and Mitchell, 2004; MacLeod et al., 2010). In captivity, the most obvious way in which parasites are lost is through direct parasite control, such as the use of antiparasitic drugs (Stringer and Linklater, 2014). Parasites can also be lost from captive populations indirectly, because of environmental differences experienced between captive and wild populations. For example, parasite survival may be affected through changes in host density, home range, the absence/change of intermediate hosts or vectors, or a change in the biotic or abiotic environment (Nunn et al., 2005; Krasnov et al., 2004; Lindenfors et al., 2007; Kutz et al., 2009; Wood et al., 2011). The magnitude of the effect that these variables will have on parasite survival is thought to be largely determined by the parasites' life-history traits (Thompson et al., 2018).

Most parasite extinction models examine the role that host-specificity could play in parasite co-extinctions, with disagreement on whether it is generalist or specialist parasites that suffer the most with host declines (Koh et al., 2004; Dunn et al., 2009; Strona, 2015; Strona and

Fattorini, 2016; Cizauskas et al., 2017). However, the effect of other life-history traits, such as mode of transmission, on parasite loss has been poorly studied (Thompson et al., 2018), especially in the context of captive management. The only other large-scale study comparing parasites of captive and free-range animals focuses on parasite richness in captive and wild primates, where it was found that total parasite species richness in captive primates was similar to the wild. However, the species compositions were almost entirely different, suggesting both loss of endemic parasites and a gain of foreign parasites in captivity (Herrera et al., 2019). In our current study, we ask whether there is a general tendency for hosts in captive environments to have lower odds of being infected by any parasite species compared to hosts in a freerange environment, and whether this tendency depends on parasite lifehistory traits. The magnitude of the decline of specific parasites may be determined by the combination of biotic and abiotic factors they are faced with in captivity that affect their transmission from host to host. We predicted that the odds of infection by parasites with indirect modes of transmission will be lower for hosts in a captive environment than in a free-range environment, because of the potential for these transmission pathways to be disrupted in captivity. Conversely, we predicted that the odds of infection by parasites which are transmitted by direct host to host contact will be higher for hosts in captivity because increased host density in captive facilities may facilitate transmission.

2. Methods

2.1. Data selection and inclusion criteria

Data for meta-analyses were compiled from studies of parasites in any terrestrial host animal species that were examined in both a captive (fenced enclosures including zoos, reserves, research colonies, captivebreeding facilities, or rehabilitation/rescue centres) and free-range (living in a wild free-range environment) environment. Both microparasites and macroparasites were selected for this study. Microparasites included viruses, bacteria, and protozoa, whereas macroparasites included helminths (nematodes, cestodes, trematodes, and acanthocephalans) as well as arthropods (ectoparasites such as fleas and ticks). We searched Web of Science, selecting 'all databases' using the terms "captiv* AND (wild OR "free-range" OR "free range" OR "free-living" OR "free living") AND (parasit*) AND compar* NOT parasitoid NOT freshwater NOT aquatic". Only terrestrial hosts were selected to remove the possible confounding factor that an aquatic environment might introduce when examining different modes of transmission. We expect parasite transmission to differ between the two environments, especially vector-borne and environmentally transmitted parasites. Within 2064 articles spanning through the years 1980 to 2019 inclusively, only 303 papers were selected for detailed inspection because they examined parasite infections for host populations in both captive and free-range environments. From these, 45 articles provided suitable data on parasite prevalence (used to calculate odds ratios, see below) from the same host species in both a captive and free-range environment, where sample collection was comparable for both population types. Unfortunately, most of the studies do not describe where the captive populations originated from, so we were unable to confirm that captive populations originated from the free-range populations with which they were compared.

Parasite prevalence was often based on molecular work, morphology, and/or serology, depending on the parasite species in question. We included data from studies based on serology because previous

spread

Table 1 Definitions for each parasite mode of transmission. Note that our definition of "complex life cycle" excludes vector-borne transmission.

| Direct (one host in life cycle) Parasites with direct life cycles require only one type of host to reproduce and complete their life cycle. | | | | | |
|--|---|--|--|--|--|
| Host contact Environmental contact | Close transmission between hosts via biting, scratching, aerosols, exchange of bodily fluids. This often includes bacteria and viruses. Ingestion of faecal matter or urine via contaminated environment, food or water. This includes many gastrointestinal nematodes and protozoa through a contaminated environment. | | | | |
| Indirect (two or more ho | sts in life cvcle) | | | | |

| Parasites with indirect life cycles require two or more types of hosts to reproduce and complete their life cycle. | | | | |
|--|--|--|--|--|
| Vector-borne | Transmission by a biting arthropod that carries the parasite. This often involves parasites found in the blood, e.g. protozoa such as trypanosomes and | | | |
| | Plasmodium spp., and even some nematodes. | | | |
| Complex life cycle | Transmission through ingestion (transmission) of an infected intermediate host (host infected with a larval, non reproductive perceite form) or | | | |

Complex life cycle Transmission through ingestion (trophic transmission) of an infected intermediate host (host infected with a larval, non-reproductive parasite form) or via free-living infectious stages. Examples include many helminths (trematodes, cestodes, acanthocephalans, and even some nematodes) and protozoa.

large-scale analyses found that discarding this type of data did not affect the results (Olival et al., 2017; Pandit et al., 2018) and is acceptable even when examining parasite richness (Herrera et al., 2019). We excluded studies if parasite prevalence was estimated based on the number of samples and not individual animals, or if multiple host species were pooled together. Data consisted of parasite taxonomy (based on contemporary literature), and host taxonomy, based on contemporary literature and corrected with TimeTree (Hedges et al., 2006). TimeTree is an up-to-date tool for building phylogenetic trees, consisting of thousands of published studies with up-to-date phylogenetic data (Hedges et al., 2006). Data also consisted of sample type (blood, faeces, etc.), captivity type (fenced enclosures including zoos, reserves, research colonies, captive-breeding facilities, or rehabilitation/rescue centres), total number of hosts examined in the captive and free-range environments, and number of infected hosts found in each environment. Mode of transmission (Table 1) for each parasite species was determined separately by comparison with a previously compiled database, the Global Mammal Parasite Database (GMPD) (Nunn and Altizer, 2005; Stephens et al., 2017). When the parasite was not listed in the GMPD, we searched the literature for a description of its life cycle and mode of transmission (in some cases, parasites utilized more than one transmission mode). Otherwise, for all other modes of transmission, when data were unavailable for a specific parasite species, we used the mode of transmission that is typical for that taxonomic group (at the genus or family level). When a study examined the same parasite species across multiple host species, or when multiple parasite species were examined in a single host species, each host-parasite association was considered as a unique case in our analysis. Finally, while we acknowledge that host-specificity is an important parasite life-history trait when studying parasite extinction, we have not included this trait in our study because determining host-specificity is not straightforward (Poulin et al., 2011).

2.2. Determining phylogenetic signal

A phylogenetic signal measures whether there is a tendency for closely related species to show a more similar response due to their evolutionary relatedness (Muenkemueller et al., 2012). To determine whether the relationship between the odds of parasite infection and environment was influenced by host phylogeny, we calculated Pagel's lambda (Pagel, 1999), which ranges from 0 to 1. Values closer to 1 indicate that closely related taxa show a more similar response, and

values close to 0 mean that closely related taxa do not show a more similar response. A phylogenetic tree was constructed for host species using TimeTree (Kumar et al., 2017). In R version 3.5.2 (R Core Team, 2018), we used the match.phylo.data() function from package picante v 1.8 (Kembel et al., 2010) to match our odds ratios to the species on the phylogenetic tree and calculate Pagel's lambda using the phylosig() function from the phytools v 0.6-99 package (Revell, 2012). Since we had multiple odds ratios for the same parasite species, we bootstrapped our Pagel's lambda so that each host was represented only once in the dataset; for each bootstrap, the parasite selected was randomly resampled with replacement. This was done 1000 times to account for any possible combinations of hosts and parasites. Since the phylogenetic signal was high (mean Pagel's $\lambda = 0.362, 95\%$ CI: 0.333–0.390), we can assume that host phylogeny had an effect on the relationship between odds of infection and environment and we therefore performed phylogenetic meta-analyses (Lajeunesse, 2009; Chamberlain et al., 2012) to account for host phylogeny. Although we did not make phylogenetically independent contrasts for parasites because robust phylogenies were not available for all parasite taxa, we undertook separate analyses for the major taxonomic groups.

2.3. Meta-analysis procedures

All meta-analyses were performed with the OpenMEE software (Wallace et al., 2017). We used a random effects model, which allows for different true effect sizes in different studies, because of the differences across studies (sampling method, geographic location, and host and parasite species). Since our data were binary for the predictor variable (captive and free-range) and consisted of number of infected hosts versus the number of uninfected hosts, we calculated odds ratios for each parasite (in each host species, if there were multiple host species examined) in each study as a measure of effect size. An odds ratio greater than 1 means that the odds of infection in captive host populations are higher, and less than 1 means that they are lower than in free-range host populations. Because of multiple comparisons (see below), and because corrections for multiple testing in meta-analyses are not universally agreed upon (Borenstein et al., 2009; Schmidt and Hunter, 2015), we opted for a more conservative approach by setting $\alpha = 0.01$ to reduce the chances of committing a Type I error (i.e. confidence intervals were set to 99%), which is recommended for analyses that may contribute to future policy decisions (Borenstein et al., 2009).

Table 2

The total number of parasite species (n = 158), counting unknown parasite species as unique, organized by taxonomic group and mode of transmission. Direct life cycles include parasites that utilize exclusively host-contact, exclusively environmental contact and parasites utilizing both modes of transmission, so the total number of species is greater than the two sub-categories combined. The same applies to indirect transmission methods.

| Taxonomic group | Number of species (% of total) | Mode of transmission | | | | | | | |
|-----------------|--------------------------------|----------------------|------------------------------|-----------------------------------|----------|------------------------------|--------------------------------|--|--|
| | | Direct | Exclusively host- contact | Exclusively environmental contact | Indirect | Exclusively vector- borne | Exclusively complex life cycle | | |
| Helminth | 65 (41.1%) | 47 | 0 | 46 | 18 | 0 | 18 | | |
| Protozoa | 43 (27.2%) | 24 | 0 | 5 | 19 | 9 | 7 | | |
| Bacteria | 41 (26.0%) | 38 | 10 | 7 | 3 | 3 | 0 | | |
| Virus | 4 (2.5%) | 4 | 2 | 0 | 0 | 0 | 0 | | |
| Arthropod | 5 (3.2%) | 4 | 0 | 3 | 1 | 0 | 1 | | |
| Total | 158 | 117 | 12 | 61 | 41 | 12 | 26 | | |



Fig. 1. Odds ratios (with confidence intervals) from meta-analyses examining the odds of infection by parasites in captive vs. free-range hosts, both over all examined studies, and for different taxa. Values below 1 mean lower odds of infection for hosts in captivity and values above 1 mean higher odds of infection for hosts in captivity. Odds are different if the confidence interval does not overlap with 1.

We initially examined the odds of infection in captive and freerange host populations over all parasites, then separately for helminths, protozoa, and bacteria. The effect of captivity on viruses and arthropods were not analyzed separately due to a small study sample size for each, but these groups were included in other analyses. Separate analyses were then performed for parasites with different modes of transmission (direct life cycle, host contact, environmental contact, indirect life cycle, vector-borne, and complex life cycle). Analyses for direct life cycles included parasites with both host contact and environmental contact and similarly, indirect life cycle analyses included both vectorborne parasites and those with complex life cycles. If a parasite utilized more than one mode of transmission (e.g. host contact and environmental contact), then it was included for analysis at the level of the highest category (i.e. direct life cycles in this case), but not for analysis at the level of the lowest category (e.g. not included in either hostcontact or environmental contact analyses). Where sample sizes permitted (5 or more host-parasite associations, to reduce the chances of a false positive result), we undertook separate analyses for helminths and



Fig. 2. Odds ratios (with confidence intervals) from meta-analyses examining the odds of infection by parasites in captive vs. free-range hosts for parasites with different modes of transmission. Direct transmission is composed of host-contact and environmental, and indirect transmission is composed of vector and complex life cycle. Values below 1 mean lower odds of infection for hosts in captivity and values above 1 mean higher odds of infection for hosts in captivity. Odds are different if the confidence interval does not overlap with 1.

protozoa with different modes of transmission.

3. Results

From the 45 selected studies investigating parasitism in both captive and free-range host populations, there were 86 parasite species identified. However, an additional 72 parasite taxa that were not identified to species level were also included; we have treated these as 72 separate species, but it is possible that some of them could have been repeats of the 86 identified species (Table 2). In total, there were 222 host-parasite associations (Appendix Table 1). Parasite taxa spanned 17 phyla, 26 classes, 41 orders, 71 families, and 84 genera. The most common parasite order in host-parasite associations was Rhabditida (n = 41), followed by Eucoccidiorida (n = 23), Enterobacterales (n = 17), Strongylida (n = 15), Amoebida (n = 13), and Trypanosomatida (n = 11). The most common genera were Entamoeba (n = 13), Ta*chygonetria* (n = 10), *Cryptosporidium* (n = 5), and *Balantidium* (n = 7). The genus could not be determined for 21 parasites, so they were classified to the lowest possible taxonomic level. The most common modes of transmission were environmental contact (n = 73) and complex life cycles (n = 39) (Table 2).

Across the 45 studies, there were 55 host species spanning 4 classes, 15 orders, 30 families, and 49 genera. The most common host orders in host-parasite associations were Primates (n = 102), Testudines

(n = 28), Squamata (n = 16), Carnivora (n = 13), Accipitriformes (n = 12), and Artiodactyla (n = 11). The most common families were Hominidae (n = 36), Testudinidae (n = 28), Lemuridae (n = 26), and Cercopithecidae (n = 20).

Henceforth, all differences in odds of infection are significant unless stated otherwise. Over all taxonomic groups and across all modes of transmission, there was no difference in the odds of hosts being infected in captivity compared to hosts being infected in a free-range environment (Fig. 1, Appendix Table 1). However, by separating parasite groups, we found that captive hosts had 2.71 times lower odds of being infected by helminths (Appendix Fig. 1), but there was no difference in the odds of infection by protozoa (Appendix Fig. 2) and bacteria in captive and free-range environments (Fig. 1, Appendix Table 1).

Stratifying by modes of transmission, the odds of infection by parasites with indirect life cycles were 2.57 times lower in captivity, whereas there was no difference in the odds of infection by parasites with direct life cycles in the captive and free-range environments (Fig. 2, Appendix Table 1). Comparing the different modes of transmission in more detail, captivity had the largest effect on environmentally transmitted parasites with direct life cycles, with hosts in captivity having 2.30 times lower odds of infection (Appendix Fig. 3). There was also a non-significant trend for lower odds of infection by vector-borne parasites with indirect life cycles in captivity (3.80 times lower odds) (Fig. 2, Appendix Table 1, Appendix Fig. 4). Further, there



Taxa

Fig. 3. Odds ratios (with confidence intervals) from meta-analyses examining the odds of infection by parasites in captive vs. free-range hosts for helminth and protozoan parasites with different modes of transmission. Values below 1 mean lower odds of infection for hosts in captivity and values above 1 mean higher odds of infection for hosts in captivity. Odds are different if the confidence interval does not overlap with 1.

was no difference in the odds of infection by parasites transmitted by direct host-host contact, or with indirect, complex life cycles (Appendix Fig. 5) in the two environments (Fig. 2, Appendix Table 1).

When different modes of transmission were examined separately for helminths and protozoa, the odds of infection by helminths with direct life cycles and environmental transmission were 2.70 times lower in captivity (Fig. 3, Appendix Table 1). Similarly, the odds of infection by helminths with indirect, complex life cycles were 3.40 times lower in captivity (Fig. 3, Appendix Table 1). Among protozoa, vector transmission was the only important mode of transmission, with hosts in captivity having 5.74 times lower odds of infection by vector-borne protozoa (Fig. 3, Appendix Table 1) while there was no difference in the odds of infection by protozoa with indirect, complex life cycles in captive and free-range environments.

4. Discussion

Overall, there was no difference in the odds of infection by parasites for hosts in a captive or free-range environment. However, the environment type may have affected some parasite taxa and not others. For example, while there was no difference in the odds of infection by bacteria or protozoa, helminths had lower odds of infecting hosts in captivity. The odds of infection were not just influenced by parasite taxa, but by the mode of transmission as well. As predicted, hosts in

captivity had lower odds of being infected by parasites with indirect life cycles, and this was especially true for helminths with complex life cycles and vector-borne protozoa. We also predicted that hosts in captivity would have higher odds of infection by parasites with direct life cycles but instead, we found that the odds of infection by parasites with direct life cycles did not differ between the two environments. This was largely due to parasites with transmission depending on host-contact because the odds of infection by these parasites were not different in the two environments and there was a lot of variation associated with this sub-group. However, the odds of infection by parasites with direct life cycles and environmental transmission were lower in captivity, especially for environmentally transmitted helminths. Overall, our results show that the mode of transmission does indeed play a role in how parasites respond to captivity, but there may also be other, taxon-specific factors that influence the odds of parasite infection in a captive environment.

4.1. Climate and geography

Animals in captivity often undergo significant changes in their environment, which may have implications for host-parasite associations, particularly for vector-borne parasites and parasites with complex life cycles, where free-living stages require a period of development in the environment. A change in abiotic factors such as geography or climate can also change the biotic factors of an area, such as the composition of definitive or intermediate hosts, vectors, as well as parasites (Nunn et al., 2005; Krasnov et al., 2004; Lindenfors et al., 2007; Kutz et al., 2009; Wood et al., 2011; Eriksson et al., 2020). Indeed, hosts in foreign, non-native ranges sometimes lose nearly half of their usual parasite species in the new environment (MacLeod et al., 2010). Our results for helminths and vector-borne protozoa are consistent with the hypothesis that parasites with more complex modes of transmission may be more prone to extinction because of a change in environment (Koh et al., 2004; Dobson et al., 2008; Rohr et al., 2011; Poulin and Morand, 2014). This could occur because of the direct effects of climatic variables, such as changes in temperature, light, UV radiation and moisture, on the survival of infective, free-living parasite stages (Pietrock and Marcogliese, 2003; Lafferty, 2009; O'Connor et al., 2006; Okulewicz, 2017), or because of the disruption of normal transmission pathways through the loss of vectors and intermediate hosts (Krasnov et al., 2004; Lindenfors et al., 2007; Kutz et al., 2009; Wood et al., 2011). In addition, since most captive animals in our study were held in close proximity to urban areas, urbanization itself may have had negative impacts on parasite transmission (Hess, 1994; Werner and Nunn, 2020). Urbanization brings with it pollution in the form of agricultural and industrial effluents, acidification, sewage, pesticides, and thermal pollution, which may all harm free-living stages of parasites (Pietrock et al., 2002; Marcogliese, 2005; Koprivnikar et al., 2006; Koprivnikar et al., 2007) and even intermediate hosts (Poulin, 1992; Lafferty, 1997; Milotic et al., 2018), potentially affecting parasites with complex life cycles (Werner and Nunn, 2020), particularly helminths.

The impact of captivity on vectors is still poorly understood and seems to be context-dependent. In some cases, there may be greater potential for the introduction of novel diseases when in captivity (Pung et al., 1998, Ratterree et al., 2003), as vectors may have a wider range of host species on which to feed (Tuten et al., 2012). In addition, the density of flying vectors can be higher in captivity than in the wild (Derraik et al., 2003; Bradley and Altizer, 2007). Despite some factors that seem to suggest a higher possibility of vector-borne pathogen transmission in captivity, there are four possible reasons as to why we found a non-significant trend for lower odds of infection by vectorborne parasites overall, but lower odds of infection by vector-borne protozoa. First, vector-borne parasites may experience a dilution effect in the presence of a high diversity of host species serving as decoys, and this can be especially important for zoos (Schmidt and Ostfeld, 2001; Ezenwa et al., 2006). Biting arthropod vectors are often generalists (Kettle, 1995), so the chances of a successful blood meal with the correct host become slimmer as the diversity of host species increases in captivity. Secondly, even when captive facilities are in a similar geographical area, the composition of flying vector species can differ (LaDeau et al., 2013; Heym et al., 2018) and different vectors may not always be capable of transmitting the same parasites (Kampen and Werner, 2015). Thirdly, a highly species-diverse vector population can lower the transmission of vector-born parasites (Chaves et al., 2011). Lastly, targeted or non-targeted parasite control may be causing the loss of non-flying ectoparasites serving as vectors, indirectly leading to a lower odds of infection by vector-borne parasites (Panayotova-Pencheva, 2016). The interplay between all these factors may be why we only saw a non-significant trend for lower odds of infection by vector-borne parasites, but did see lower odds of infection by vectorborn protozoa in captivity.

4.2. Parasite control

Other factors may also explain why we saw lower odds of infection by parasites, particularly with helminths, with both direct and indirect life cycles that were observed in our study. Parasite control, such as the administration of antiparasitic drugs, is likely the most direct cause of parasite loss. Drugs are routinely administered to captive animals to clear parasite infections and improve host health (Stringer and Linklater, 2014). This is particularly the case for endangered host species and those which are to be used in a captive breeding program, although there is not always a demonstrated improvement of host health from parasite control, in either captive or free-range populations (Pedersen and Fenton, 2015; Panavotova-Pencheva, 2016), Moreover, drugs are often non-specific and may affect more than one type of parasite. Ivermectin, a drug that targets both nematodes and some ectoparasites, has been used since 1981 as a cheap, effective anthelmintic and is commonly used to eradicate nematodes in captive animals (Campbell et al., 1984; Panayotova-Pencheva, 2016). Some ectoparasites are capable of transmitting vector-borne parasites, and their reduction through the use of non-specific drugs may be another reason why we may see a loss of vector-borne parasites, although we cannot draw this direct conclusion from our study. For captive ruminants, it is common for ivermectin treatment to be administered as frequently as every 2-3 months (Isaza et al., 1990) because of the perception that environmentally transmitted helminths (often nematodes) pose a major threat for captive animals (Kahn et al., 2005). Quarantine procedures may exacerbate parasite loss from captive animals because quarantine often involves vaccinations, antiparasitic drug treatments and even barriers against vectors, in addition to animal isolation (Kahn et al., 2005; Backues et al., 2011). Vector control is also recommended outside of quarantine as an additional way of controlling vector-borne parasite transmission (Derrickson and Snyder, 1992; Tuten, 2011). Lastly, dung removal is common for the prevention of environmentally transmitted parasites (Fagiolini et al., 2010). Thus, direct parasite control may be a major driving factor behind our observed lower odds of infection in captivity for certain parasite types, especially helminths that may be targeted due to their high prevalence in captivity (Panayotova-Pencheva, 2013; Jorgensen, 2015) and not other parasites such as protozoa or bacteria.

4.3. Implications and future directions

In our study, we observed lower odds of infection by parasites with indirect life cycles and parasites transmitted via direct, environmental contact in captive hosts. This means that in captivity, hosts are less likely to be infected by parasites with these modes of transmission. As a group, helminths and vector-borne protozoa were most vulnerable in captivity. While we cannot draw direct conclusions about conservationdriven parasite extinction from these results, this pattern does suggest that bringing animals into captivity may result in reduced odds of infection by certain types of parasites, leading to potential losses of parasite diversity down the line. This may have implications for parasite extinction if captive animals are threatened and have low numbers left in the wild, or no wild populations at all, because any parasites lost due to captivity may not be replaceable. With the progression of the sixth mass extinction, captivity may be an increasingly common way to save host species while dooming parasites to extinction, if captive management practices stay the same. In addition, if captive animals and/or their progeny are released back into the wild to establish new

populations, the resulting 'restored' ecosystem will forever be devoid of the parasites that once existed and will thus never truly be restored. It is unclear how losing parasites may affect ecosystems on a larger scale (Wood and Johnson, 2015), but drawing from what is known on the effect of losing top predators, losing parasites could have similar cascading effects on the whole ecosystem (Polis et al., 2000; Ripple et al., 2016). However, unlike top predators, parasites are both consumers and prey items, and they regulate organisms in all trophic levels, including top predators themselves (Anaya-Rojas et al., 2019), so the effects of losing parasites could have even greater repercussions. Invasive animals may serve as an example of how losing some natural enemies could potentially have both ecological and economic consequences.

Although host conservation is evidently a contributing factor in parasite extinctions, it also presents a unique avenue for control and intervention. By incorporating parasites into conservation programs along with their hosts, there is an opportunity to control how parasites are treated as well. However, conserving parasites is risky, particularly in a captive environment where there is potential for harming captive animals. Firstly, stress associated with captivity can make animals more susceptible to infection, and under the wrong circumstances, parasites that are normally benign can become pathogenic (Mason, 2010). Secondly, confined areas may promote transmission of density-dependent parasites (Lyles and Dobson, 1993), and finally, there is also potential for infection by novel parasites to which hosts are naïve (Lyles and Dobson, 1993). It has been suggested that if the risk of host morbidity is low, and host health or fitness is unaffected by the presence of the parasite, and/or if keeping the parasite is beneficial in the long-term, then parasites should be conserved with the host (Stringer and Linklater, 2014). However, finding this balance is not an easy task, especially with the difficulty of trying to conserve parasites with indirect life cycles, as well as the difficulty of controlling instead of eradicating parasites. Our lack of understanding of these processes highlights the importance of further research needed to better understand how parasite conservation might work in captivity.

We are not alone in suggesting that parasites should be targets for conservation (Windsor, 1997; Koh et al., 2004; Gomez and Nichols, 2013; Dougherty et al., 2016) and there are several examples of host conservation programs that do take parasites into account. For example, a host-specific louse, *Felicola isidoroi*, from wild Iberian lynx (*Lynx pardinus*), has been transferred to lynx in a captive-breeding program to ensure the persistence of the louse (Perez et al., 2013).

Appendix A

Table 1

Tasmanian devil (Sarcophilus harrisii) management also includes provisions for conserving parasites in captivity (Wait et al., 2017), because the retention of parasites is thought to confer long-term benefits. These programs have recognized that, counterintuitively, parasite-free hosts can become highly susceptible to infection upon re-introduction into the wild, whereas hosts that retain their parasites may actually be more successful in the long term (van Oosterhout et al., 2007; Almberg et al., 2012) not just through strengthening the immune system, but also because elimination of some parasites (e.g. nematodes) could lead to an increased prevalence of other, more harmful parasites (e.g. coccidians) (Pedersen and Antonovics, 2013; Knowles et al., 2013; Northover et al., 2018). Retaining parasites in captivity may thus be not only beneficial for the host, but would also allow for later re-establishment of evolutionary and ecological processes, and ecosystem services in the wild (Marcogliese, 2004; Almberg et al., 2012), providing a more complete restoration of a given ecosystem.

CRediT author statement

Marin Milotic: Conceptualization, Methodology, Formal analysis, Writing - Original Draft, Investigation, Data Curation, Visualization. Alan Lymbery: Supervision, Project administration, Writing-Reviewing and Editing. Andrew Thompson: Supervision, Project administration, Writing- Reviewing and Editing. Jean-François Doherty: Methodology, Investigation, Writing - Review & Editing, Visualization. Stephanie Godfrey: Supervision, Project administration, Conceptualization, Methodology, Software, Writing- Reviewing and Editing

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Odds ratios (OR) with confidence intervals (CI) from meta-analyses examining the odds of infection by parasites in captive vs. free-range hosts for different parasites grouped by taxa and modes of transmission. Each host-parasite interaction counts as one 'study' and thus, some parasite species are repeated and the sample size is higher than shown in Table 1 in the main body of the manuscript. Values below 1 including the CI mean lower odds of infection for hosts in captivity and values above 1 including the CI mean higher odds of infection for hosts in captivity. Significant results are bolded.

| | Sample size | OR | 99% CI | Magnitude of effect | Р |
|--|-------------|---------|----------------|---|---------|
| Overall | 222 | 0.5177 | 0.1313-2.0401 | 1.93 times lower odds in captivity | 0.216 |
| Helminth | 85 | 0.3694 | 0.1643-0.8305 | 2.71 times lower odds in captivity | 0.002 |
| Protozoa | 72 | 0.5880 | 0.2925-1.1822 | 1.70 times lower odds in captivity | 0.050 |
| Bacteria | 56 | 1.6143 | 0.8147-3.1200 | 1.61 times higher odds in captivity | 0.071 |
| Direct | 159 | 0.6449 | 0.1073-3.8772 | 1.55 times lower odds in captivity | 0.529 |
| Host contact | 15 | 1.4331 | 0.2922-7.0287 | 1.43 times higher odds in captivity | 0.560 |
| Environmental | 73 | 0.4380 | 0.2519-0.7616 | 2.30 times lower odds in captivity | 0.001 |
| Indirect | 63 | 0.3891 | 0.1912-0.7919 | 2.57 times lower odds in captivity | < 0.001 |
| Vector | 20 | 0.2632 | 0.0656-1.0556 | 3.80 times lower odds in captivity | 0.013 |
| Complex life cycle | 39 | 0.5804 | 0.0786-4.2855 | 1.72 times lower odds in captivity | 0.483 |
| Helminth - direct (same as environmental) | 57 | 0.3720 | 0.1593-0.8688 | 2.70 times lower odds in captivity | 0.003 |
| Helminth - indirect (same as complex life cycle) | 24 | 0.2954 | 0.0891-0.9795 | 3.40 times lower odds in captivity | 0.009 |
| Protozoa – direct | 37 | 1.5067 | 0.0331-68.6414 | 1.50 times higher odds in captivity | 0.782 |
| Protozoa –environmental | 5 | 1.2613 | 0.0962-16.5403 | 1.26 times higher odds in captivity | 0.816 |
| Protozoa –indirect | 35 | 0.3705 | 0.0582-2.3588 | 2.70 times lower odds in captivity | 0.167 |
| Protozoa – complex life cycle | 14 | 10.9928 | 0.0421-23.4267 | 11 times higher odds in captivity | 0.995 |
| Protozoa - vector | 17 | 0.1741 | 0.0360-0.8418 | 5.74 times lower odds of infection in captivity | 0.004 |



Fig. 1. Forest plot of odds ratios (rectangles) and confidence intervals (bars) for helminth species. Dashed line and diamond show the odds ratio and confidence intervals for all helminth species. Size of the points corresponds to the weight placed on individual 'studies'.

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| Studies | I | Estimate (| % C.I.) | |
|--|-----------|------------|--------------|----------|
| Cryptosporidium andersoni | 36.7087 | (2.5647, | 525.4164) | _ |
| Plasmodium_simium | 0.0864 | (0.0094, | 0.7956) | |
| Trypanostomatid | 0.0317 | (0.0010, | 0.9621) | |
| Toxoplasma gondii | 20.5263 | (1.1730, | 359.1979) | |
| Babesia kiwiensis | 0.0071 | (0.0001, | 0.5521) | e |
| Trypanostomatid -2 | 0.0469 | (0.0010. | 2,2979) | |
| Toxoplasma gondii-2 | 2.4810 | (0.6450. | 9.5437) | |
| Carvospora spp | 0.2549 | (0.0035. | 18,3607) | |
| Sarcocystis spp | 0.3137 | (0.0625 | 1.5743) | |
| Babesia rossi | 1.4222 | (0.3318. | 6.0970) | |
| Babesia_10331 | 0.0121 | (0.0008. | 0.1922) | |
| Trypanosoma cruzi | 0.0505 | (0,0009 | 2 7069) | |
| Trypanosoma_cruzi | 0.0305 | (0.0003, | 0 7787) | |
| Entempole histolution/dispor/monkovakii/puttelli | 4 4296 | (0.0002, | 226 1011) | |
| Entamoeba_histolytica/dispar/moskovskii/nuttaili | 4.4280 | (0.0585, | 1 2527) | |
| Balanudum_coli | 0.3914 | (0.1222, | 1.2557) | |
| | 0.4464 | (0.1516, | 1.3143) | |
| Entamoeba_histolytica | 0.6282 | (0.1642, | 2.4035) | |
| Leishmania_chagasi | 1.5455 | (0.0201, | 119.0973) | |
| Neospora_caninum | 0.1846 | (0.0169, | 2.0129) | |
| Toxoplasma_gondii-3 | 0.4167 | (0.0426, | 4.0727) | |
| Haemogregarina_fitzsimonsi | 0.1795 | (0.0031, | 10.2949) | |
| Toxoplasma_gondii-4 | 1.5217 | (0.0270, | 85.6309) | |
| Hepatozoon_sp. | 0.0340 | (0.0008, | 1.4339) | |
| Sarcocystis_neurona | 0.0023 | (0.0000, | 0.1707) | |
| Coccidia spp. | 0.3434 | (0.0413, | 2.8544) | _ |
| Entamoeba sp. | 0.3889 | (0.0462 | 3.2741) | |
| Toxoplasma gondii-5 | 129 8000 | (2.0130 | 8365 98271 | |
| Balantidium coli-2 | 46 2000 | (1 1130 | 1916 1531 | |
| Dalantigium_coll-2 | 10.2000 | (1.1139, | 750.1001) | |
| naemogreganna_mzsimonsi-2 | 12.5000 | (0.2061, | /58.1832) | |
| Balantiolum_coll-3 | 0.0180 | (0.0004, | 0.7277) | |
| Cryptosporidium_sp. | 1.9505 | (0.0111, | 343.4341) | |
| Entamoeba_coli-2 | 4.0833 | (0.1686, | 98.9009) | |
| Entamoeba_polecki | 14.6632 | (0.2907, | 739.5428) | |
| Giardia_sp. | 64.6104 | (1.5241, | 2738.9255) | |
| Giardia_duodenalis | 4.5614 | (1.0191, | 20.4163) | |
| Toxoplasma_gondii-6 | 0.1452 | (0.0470, | 0.4485) | |
| Hepatozoon_ursi | 0.7778 | (0.0358, | 16.9013) | |
| Leucocytozoon_marchouxi | 1.0821 | (0.5298, | 2.2099) | |
| Haemogregarina_lygosomarum | 0.0338 | (0.0007, | 1.5502) | |
| Hepatozoon_sp2 | 0.1591 | (0.0146, | 1.7311) | |
| Balantidium_coli-4 | 3408.8310 | (85.9752, | 135156.6874) | |
| Balantidium_coli-5 | 1.6241 | (0.7239. | 3.6436) | |
| Entamoeba coli-3 | 0.5556 | (0.2244 | 1.3755) | |
| Entamoeba histolytica-2 | 1.0303 | (0.4151 | 2.5572) | |
| Balantidium coli-6 | 0.0759 | (0.0190 | 0.30281 | |
| Chilomastiv sp | 1 6000 | (0.0150, | 0.3020) | |
| Entamocha en 2 | 1.5909 | (0.3007, | 0.2024) | |
| Entantoeba_sp2 | 3.0519 | (0.7280, | 12./942) | |
| Gairdia_sp. | 1.8224 | (0.0261, | 127.1430) | |
| Balantidium_sp. | 0.2378 | (0.1002, | 0.5643) | -■-1 |
| Blastocystis_sp. | 0.6556 | (0.2151, | 1.9982) | |
| Endolimax_nana | 1.5818 | (0.2701, | 9.2621) | |
| Entamoeba_coli-4 | 0.0949 | (0.0369, | 0.2442) | |
| Entamoeba_hartmanni | 0.1628 | (0.0434, | 0.6116) | |
| Entamoeba_histolytics/dispar | 0.0305 | (0.0059, | 0.1580) | |
| Entamoeba_sp3 | 0.3154 | (0.1066, | 0.9334) | |
| Giardia_sp2 | 0.5000 | (0.0586, | 4.2649) | |
| Iodamoeba buetschlii | 1.0261 | (0.1062. | 9.9175) | |
| Cryptosporidium parvum | 0.7472 | (0.0108 | 51,6355) | |
| Cryptosporidium muris | 2.8239 | (0.0609 | 131.0251) | |
| Encenhalitozoon son | 0 0800 | (0,0012 | 5 52871 | |
| Enteropytozoon bionousi | 0.0000 | (0.0012, | 0 1175 | |
| Enterocytozoon_bieneusi | 110 2000 | (11.6520 | 9.44/5) | |
| | 110.2000 | (11.0530, | 1042.1407) | |
| rypanosoma_cruzi-2 | 0.1077 | (0.0014, | 8.2652) | |
| Trypanostomatid4 | 0.0500 | (0.0009, | 2.8181) | |
| Trypanosoma_cruzi-3 | 0.0502 | (0.0006, | 3.9631) | |
| Trypanostomatid5 | 0.3846 | (0.0053, | 27.8166) | |
| Trypanosoma_cruzi-4 | 1.1765 | (0.0279, | 49.5550) | |
| Trypanostomatid6 | 0.7500 | (0.0608, | 9.2513) | |
| Cryptosporidium_sp_Tasmanian devil genotype | 0.1148 | (0.0281, | 0.4687) | I |
| Giardia sp3 | 0.0233 | (0.0005. | 1.0550) | |
| Haemogregarina fitzsimonsi-3 | 10.0645 | (1.3233 | 76.5450) | |
| Haemogregarina parvula | 2.6774 | (0.0385 | 186.22921 | |
| nacinogreganna_parvaid | 2.0774 | (0.0000) | 100.2292) | - |
| Overall (P = 0.0502) | 0.5880 | (0.2925, | 1.1822) | |
| | | | | |

0 0 0 0 0 0 0.010.02 0.060.16 0.59 1.59 6.37 31.83 159.15 636.6 3182.98 31829.85 Odds Ratio (log scale)

Fig. 2. Forest plot of odds ratios (rectangles) and confidence intervals (bars) for protozoan species. Dashed line and diamond show the odds ratio and confidence intervals for all protozoan species. Size of the points corresponds to the weight placed on individual 'studies'.

| Studies | Es | stimate | (% C.I.) | | |
|--|---------|------------------|--------------|-----------------|---------|
| Bacillus son | 4.5000 | (0.0701. | 288,9757) | | |
| Cryptosporidium andersoni | 36.7087 | (2.5647, | 525.4164) | | |
| Kalicephalus_costatus | 1.5746 | (0.0229, | 108.3695) | | |
| Kalicephalus_inermis | 0.9118 | (0.3465, | 2.3992) | | |
| Bacillus_spp2 | 0.4222 | (0.0052, | , 34.0638) | | |
| Strongyle_sp. | 0.0297 | (0.0006, | , 1.5378) | | |
| Strongyloides_sp. | 0.0857 | (0.0039, | , 1.8818) | | |
| Oesopnagostomum_sp. | 0.2952 | (0.0898, | , 0.9706) | | |
| | 0.2982 | (0.0991, | 0.8973) | | |
| Trichuris trichiura | 0.6984 | (0.2424. | 2.0126) | | |
| Ascarid sp.1 | 1.0947 | (0.1139, | 10.5226) | | |
| Oxyuroid_sp | 0.9000 | (0.0426, | 18.9996) | | |
| Strongyle_sp.1 | 0.0447 | (0.0057, | 0.3492) | | |
| Strongyle_sp.2 | 1.0947 | (0.1139, | , 10.5226) | | |
| Trichurid_sp | 0.1843 | (0.0040, | , 8.5530) | | |
| Bacillus_sp. | 11.3333 | (0.4960, | , 258.9414) | | _ |
| Coccidia spp | 0.3434 | (0.0413) | 2.8544) | | |
| Strongyle spp. | 0.0196 | (0.0005, | 0.8466) | | |
| Strongyloides_sp2 | 0.0530 | (0.0012, | 2.3134) | | - |
| Amblyomma_dubitatum | 0.4103 | (0.0541, | 3.1110) | | |
| Amblyomma_sp. | 0.3896 | (0.0475, | 3.1939) | | |
| Aeromonas_sp. | 57.3544 | (1.3453, | , 2445.1428) | | |
| Cryptosporidium_sp. | 1.9505 | (0.0111, | , 343.4341) | | |
| Klebsiella_oxytoca | 0.9783 | (0.1888, | , 5.0684) | | |
| Klebslella_sp. Pseudomonas, fluorescens | 0.0194 | (0.0504, | , //./525) | | |
| Pseudomonas_nuorescens | 0.1208 | (0.0003) | 5.3418) | | |
| Passalurus ambiguus | 1.1379 | (0.1642, | 7.8853) | | |
| Trichostrongylus_retortaeformis | 0.0116 | (0.0007, | 0.1873) | | _ |
| Odontacarus_lygosomae | 0.0001 | (0.0000, | 0.0164) | | |
| Oesophagostomum_sp2 | 0.0659 | (0.0241, | , 0.1804) | | |
| Strongyloides_fuelleborni-2 | 0.1229 | (0.0469, | 0.3219) | | |
| Trichostrongylus_sp2 | 0.2476 | (0.0933, | , 0.6568) | | |
| Trichuris_trichiura-2 | 0.7980 | (0.3281, | , 1.9409) | | |
| Ascalis_sp2 Mammomonogamus_sp | 0.4422 | (0.0824) | 2.3732) | | |
| Spirurida sp. | 0.1824 | (0.0088, | 3.7872) | | |
| Strongylida_sp. | 0.8333 | (0.2513, | 2.7640) | | |
| Strongyloides_sp3 | 4.9867 | (1.3819, | 17.9948) | | |
| Trichuris_sp. | 1.8246 | (0.4515, | , 7.3733) | | |
| Ascaris_sp3 | 1.5570 | (0.0228, | , 106.5360) | | |
| Hookworm | 0.0119 | (0.0017, | , 0.0822) | | |
| Strongyloides_sp4 | 0.4130 | (0.1801, | 0.9498) | | |
| Trichuris sp -2 | 0.4821 | (0.1141. | 2.0379) | | |
| Cryptosporidium muris | 2.8238 | (0.0609, | 131.0251) | | |
| Deletrocephalus_cesarpintoi | 0.1040 | (0.0016, | 6.8004) | | |
| Deletrocephalus_dimidiatus | 1.6667 | (0.0918, | 30.2600) | | |
| Dicheilonema_rheae | 0.0154 | (0.0002, | 1.0060) | | |
| Paradeletrocephalus_minor | 0.0255 | (0.0004, | , 1.5534) | | |
| Procyrnea_uncinipenis | 33.0000 | (1.0851, | , 1003.6283) | | |
| Cryptosporidium sp. Tasmanian devil genotype | 0.1148 | (0.1407) | 0.4687) | | |
| Alaeuris numidica | 0.5201 | (0.1451, | 1.8649) | | |
| Angusticaecum_holopterum | 15.7200 | (0.3260, | , 758.0984) | | |
| Ascarid_sp.2 | 0.0059 | (0.0001, | 0.2432) | | |
| Mehdiella_microstoma | 0.4322 | (0.0512, | 3.6466) | | |
| Mehdiella_stylosa | 0.2684 | (0.0481, | , 1.4991) | | |
| Mehdiella_uncinata | 1.3039 | (0.3174, | , 5.3569) | | |
| Oxyurold_sp-2 | 0 3378 | (0.3270, 0.0721) | 1 5830) | | |
| Tachygonetria_dentata | 0.4880 | (0.1692. | 1.4076) | | |
| Tachygonetria longicollis | 0.3895 | (0.1312, | 1.1563) | | |
| Tachygonetria_macrolaimus | 0.5190 | (0.1345, | 2.0032) | | |
| Tachygonetria_numidica | 1.0069 | (0.2101, | 4.8248) | | |
| Tachygonetria_palearticus | 2.5263 | (0.2269, | 28.1235) | | |
| Tachygonetria_pusilla | 0.1905 | (0.0252, | 1.4390) | | |
| racnygonetria_robusta | 0.2308 | (0.0300, | , 1.755) | | |
| Tachygonetria_seusa Tachygonetria_seurati | 5.1316 | (0.2503 | 105.2016) | | |
| Thaparia thapari | 4.9259 | (0.0711. | 341.0543) | | |
| | | | | | |
| Overall (P = 0.0001) | 0.4380 | (0.2519 | , 0.7616) | | |
| | | | | | |
| | | | | 0 0 0 0 0 0 0 0 | 0 0 0 0 |



0 0 0 0 0 0 0 0 0 0 0 0.01 0.03 0.1 0.26 1.042.61 10.43 52.15 260.75 1043 Odds Ratio (log scale)

Fig. 3. Forest plot of odds ratios (rectangles) and confidence intervals (bars) for environmentally transmitted species. Dashed line and diamond show the odds ratio and confidence intervals for all environmentally transmitted species. Size of the upoints corresponds to the weight placed on individual 'studies'.



Fig. 4. Forest plot of odds ratios (rectangles) and confidence intervals (bars) for vector-borne species. Dashed line and diamond show the odds ratio and confidence intervals for all vector-borne species. Size of the points corresponds to the weight placed on individual 'studies'.

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| Studies | E: | stimate (| % C.I.) | |
|------------------------------|----------|-----------|------------|---|
| Toxoplasma_gondii | 20.5263 | (2.3253, | 181.1901) | · · · · · · · · · · · · · · · · · · · |
| Toxoplasma_gondii-2 | 2.4810 | (0.8901, | 6.9155) | ∎ |
| Caryospora_spp. | 0.2549 | (0.0098, | 6.6034) | |
| Ophidascaris_spp. | 0.8333 | (0.3343, | 2.0776) | — — |
| Porocephalus_spp. | 2.0167 | (0.5341, | 7.6140) | |
| Renifer_heterocoelium | 1.4137 | (0.3570, | 5.5985) | |
| Rhabdias_vellardi | 0.9062 | (0.4292, | 1.9133) | — — |
| Sarcocystis_spp. | 0.3137 | (0.0919, | 1.0705) | |
| Capillaria_sp. | 0.2348 | (0.0102, | 5.4058) | |
| Hymenolepis_sp. | 0.0228 | (0.0011, | 0.4637) | e |
| Prosthenorchis_elegans | 12.7647 | (0.5872, | 277.4624) | |
| Leishmania_chagasi | 1.5455 | (0.0567, | 42.1472) | |
| Neospora_caninum | 0.1846 | (0.0300, | 1.1370) | |
| Toxoplasma_gondii-3 | 0.4167 | (0.0735, | 2.3613) | _ |
| Haemogregarina_fitzsimonsi | 0.1795 | (0.0082, | 3.9098) | _ |
| Toxoplasma_gondii-4 | 1.5217 | (0.0709, | 32.6698) | |
| Hepatozoon_sp. | 0.0340 | (0.0020, | 0.5859) | |
| Anoplocephala_sp. | 7.0000 | (0.2730, | 179.5017) | |
| Fasciola_sp. | 0.0937 | (0.0052, | 1.6943) | - |
| Paramphistomum_sp. | 0.2962 | (0.0146, | 6.0066) | |
| Toxoplasma_gondii-5 | 129.8000 | (5.4527, | 3089.8543) | |
| Haemogregarina_fitzsimonsi-2 | 12.5000 | (0.5499, | 284.1202) | |
| Prosthenorchis_elegans-2 | 0.1523 | (0.0153, | 1.5132) | |
| Prosthenorchis_elegans-3 | 1.2948 | (0.0688, | 24.3606) | |
| Prosthenorchis_elegans-4 | 0.9281 | (0.0941, | 9.1541) | |
| Andrya_spp | 0.2119 | (0.0098, | 4.5786) | _ |
| Dicrocoelium_dendriticum | 0.1111 | (0.0058, | 2.1458) | |
| Toxoplasma_gondii-6 | 0.1452 | (0.0615, | 0.3424) | |
| Hepatozoon_ursi | 0.7778 | (0.0747, | 8.0954) | |
| Dicrocoeliidae_sp. | 0.5963 | (0.0116, | 30.7830) | |
| Dicrocoelium_sp. | 0.5146 | (0.0101, | 26.2508) | |
| Hymenolepis_sp2 | 0.0699 | (0.0036, | 1.3764) | |
| Capillaria_venteli | 0.1040 | (0.0043, | 2.5030) | |
| Chapmania_tauricolis | 0.0400 | (0.0018, | 0.9005) | |
| Houttuynia_struthionis | 0.1040 | (0.0043, | 2.5030) | _ |
| Haemogregarina_fitzsimonsi-3 | 10.0645 | (2.1495, | 47.1243) | |
| Haemogregarina_parvula | 2.6774 | (0.1061, | 67.5394) | |
| Overall (P = 0.1672) | 0.6690 | (0.3783, | 1.1834) | |
| | | | | 0 0 0.01 0.01 0.02 0.06 0.11 0.22 0.56 1.12 2.24 5.59 11.19 55.93 223.73559.32 2237 Odds Ratio (log scale) |

Fig. 5. Forest plot of odds ratios (rectangles) and confidence intervals (bars) for parasites with complex life cycles. Dashed line and diamond show the odds ratio and confidence intervals for all parasites with complex life cycles. Size of the points corresponds to the weight placed on individual 'studies'.

Appendix B. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.biocon.2020.108702.

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