

Review

# A Review of *Strongyloides* spp. Environmental Sources Worldwide

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**Abstract:** *Strongyloides* spp. are parasitic nematodes that are transmitted through the environment and are capable of causing disease. These nematodes affect an estimated 3–300 million humans worldwide. Identifying the environmental reservoirs of *Strongyloides* spp. is essential for the development of appropriate control strategies. This systematic literature review examined all published studies that identified *Strongyloides stercoralis*, *Strongyloides fuelleborni*, *Strongyloides fuelleborni kellyi*, and *Strongyloides* spp. from an environmental source. Most studies detected the nematode from dog and primate fecal samples. Other environmental sources identified were ruminants, cats, rodents, insects, water, soil, as well as fruit and vegetables. Most studies used microscopy-based identification techniques; however, several employed molecular-based techniques, which have become increasingly popular for the detection of *Strongyloides* spp. A limitation identified was a lack of studies that comprehensively screened all potential environmental samples in a region. Future research should undertake this holistic screening process to identify which environmental reservoirs pose the greatest significance to human health. Potential controls can be identified through the identification of environmental sources. Understanding where *Strongyloides* spp. is commonly found within the environment of endemic areas will inform environmental control strategies to reduce this neglected disease.

**Keywords:** *Strongyloides* spp.; *Strongyloides stercoralis*; *Strongyloides fuelleborni*; strongyloidiasis; environmental reservoirs

## 1. Introduction

Strongyloidiasis is a disease caused by parasitic nematodes of the genus *Strongyloides*. Within this genus, three species, *Strongyloides stercoralis*, *Strongyloides fuelleborni*, and *Strongyloides fuelleborni kellyi* are known to parasitize humans [1,2].

*S. stercoralis*, *S. fuelleborni*, and *S. fuelleborni kellyi* are capable of autoinfecting the host. This occurs after adult female parthenogenic nematodes within the infected human shed eggs. These eggs develop to larvae that are passed within the stool. A certain number burrow through the wall of the large intestine, thereby reinfecting the body. Infected individuals can have a low-level undetected infection for many years [3]. When this auto-infective life cycle becomes uncontrolled in immunocompromised, young, and elderly patients, a disseminated infection can develop. Disseminated infection occurs when the parasite travels throughout the body. This can result in sepsis, bacterial meningitis, or gastrointestinal hemorrhage [4]. The mortality rate from a disseminated infection and its comorbidities is estimated to be 80% [3]. The larvae that are passed within the stool are then capable of completing a free-living cycle, in which they molt twice to develop into filariform larvae. These infective filariform larvae are capable of then reinfecting humans, where they can be involved with the autoinfection cycle again [5].

Both *S. stercoralis* and *S. fuelleborni* are able to complete their life cycle within animals such as canids, primates, and insects. Animal species-specific strains of *S. stercoralis* unable to infect humans have been identified [6]. This ability for the nematode to reproduce within other animals indicates that all infected animals' feces may pose an infection threat to humans.

After excretion in the stool, larvae can survive and reproduce within the environment, and environmental sources contaminated with larvae can cause reinfection. Although *Strongyloides* spp. are classified as soil-transmitted helminths, locations that harbor *Strongyloides* spp. within the environment, with the exception of soil, have not been investigated holistically [7,8]. By reviewing and collating all reported environmental sources of *S. stercoralis*, *S. fuelleborni*, and *S. fuelleborni kellyi*, environmental interventions can be implemented.

We need a better understanding of the environmental sources of *Strongyloides* spp.; resistance to the current anthelmintic drugs has been observed in other *Strongyloides* spp. [9]. Both environmental and clinical control of *Strongyloides* spp. is essential [10]. The aim of this review is to identify all research reporting *S. stercoralis*, *S. fuelleborni*, *S. fuelleborni kellyi*, and *Strongyloides* spp. within environmental sources worldwide.

## 2. Results

One thousand two hundred and twenty-two papers were retrieved from SCOPUS and Web of Science using the search terms identified as suitable, as seen in Table 1, with 174 articles identified as eligible for inclusion.

*S. stercoralis* was identified in 35% of all studies and *S. fuelleborni* in 10% of all studies; both *S. stercoralis* and *S. fuelleborni* were identified in 1% of all studies. *S. fuelleborni* and *Strongyloides* spp. were identified in 0.5% of studies, and genus-level identification was identified in 55% of all studies, as seen in Table A1. *S. fuelleborni kellyi* was not identified within any papers.

The most commonly identified reports of *Strongyloides* spp. were within primates (26% of all published works), and dogs (14% of all published works), as seen in Table A1. Other animals identified as environmental sources included cats, ruminants, rodents, and insects. Water, soil, as well as fruit and vegetables were all also identified as containing *Strongyloides* spp.

Fifty percent of all studies identifying *Strongyloides* spp. within primate populations identified the larvae to genus level only. *S. fuelleborni* was the next most frequently identified species at 40%. Parasitic infections were identified more frequently in terrestrial primates than arboreal primates [11,12]. Most studies (80%) employed microscopy, as seen in Table A1. Proximity to human populations and increased interaction with human populations was also frequently reported in infected populations [13,14]. Captive primates treated with anthelmintic drugs were also reported as carriers of *Strongyloides* spp. [15]. Sample size ranged from 7 to 3349, and prevalence within primate studies ranged from <1% to 100%, as seen in Table A1.

Domestic and stray dogs were the second most commonly identified source. Fourteen percent of all studies identifying *Strongyloides* spp. were within dogs, with sample sizes ranging from 35 to 879 and prevalence ranged from <1% to 45%, as seen in Table A1.

All studies reporting incidences of *Strongyloides* spp. within ruminant farming animals only identified *Strongyloides* to the genus level, as seen in Table A1.

Studies identifying rodents as a source of *Strongyloides* spp. accounted for 5% of the published works. Studies identified *Rattus rattus*, *Rattus norvegicus*, *Mus musculus*, *Dasyprocta*, and *Hydrochoerus hydrochaeris* as carriers of *Strongyloides* spp. [16–22]. Sample sizes for rodent-based studies ranged from 10 to 502. The prevalence ranged from 10% to 97%, as seen in Table A1.

Studies identifying insects within the order Diptera as a source of *Strongyloides* spp. accounted for 2% of the published works, as seen in Table A1. Identified insects within this order included flies of the genus *Musca* spp. and *Lucilia* spp. All studies identifying *Strongyloides* spp. within Diptera identified it from sites within the continent of Africa [23–25]. The sample sizes ranged from 5000 to 9950, and prevalence was between <1% and 2%.

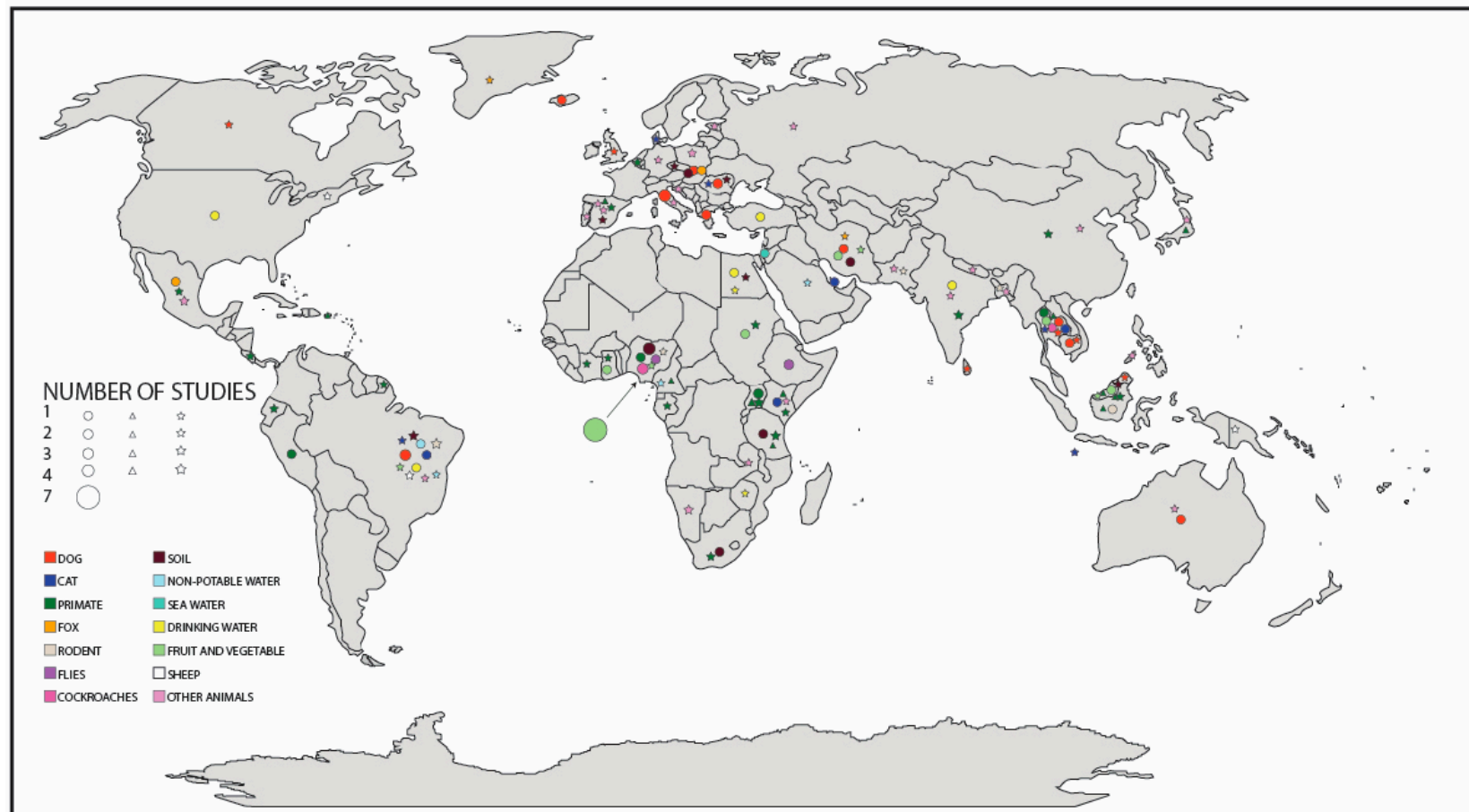
Insects within the order Blattodea were identified in 2% of all studies, as seen in Table A1. Identified insects within this order include cockroaches from the genus *Periplaneta* spp. and *Blattella* spp. Four of the five identified studies reported *Strongyloides* spp. within populations of Blattodea in Africa. The remaining study identified *Strongyloides* spp. in Blattodea in Thailand. All studies identified infected insects within housing and food preparation areas [26–29]. The sample sizes of studies identifying insects within the order Blattodea ranged from 70 to 920, with the prevalence ranging from 1% to 81%.

Half (50%) of published works identifying parasitic contamination of vegetables and fruits found *S. stercoralis* upon leafy, rough-surfaced vegetables such as lettuces, cabbage, celery, spinach, and carrot [30–37]. The sample sizes for fruit and vegetable-based studies ranged from 36 to 1130, with prevalence ranging from <1% to 46%.

Countries where *Strongyloides* spp. was identified in soils in public areas included Spain, Iran, Malaysia, Nigeria, Brazil, the Czech Republic, Slovakia, and Romania, as seen in Figure 2 [38–47]. Geophagy, the purposeful consumption of soils, was also commonly identified as a factor in infection from soil-based sources.

Studies identifying environmental sources of *S. stercoralis*, *S. fuelleborni*, and *Strongyloides* spp. are distributed across the world. Areas with a large amount of research included Europe, Africa, and South East Asia, as seen in Figure 1. Areas lacking research include Oceania, and the Americas, as seen in Figure 1. Many published studies identified *Strongyloides* spp. within temperate regions as opposed to tropical regions, as seen in Figure 1.

Microscopy was the most commonly used identification technique (90%). However, molecular detection was more common in recent publications. For example, in 2018, 6 of the 14 papers identified employed molecular-based techniques; however, in 2011, 1 of 11 papers published used molecular-based techniques, as seen in Table A1.



**Figure 1.** Map displaying the global distribution of all reported environmental cases of *Strongyloides stercoralis*, *Strongyloides fuelleborni*, and *Strongyloides* spp. Where circles are representative of *Strongyloides stercoralis*, diamonds are representative of *Strongyloides fuelleborni*, and stars are representative of *Strongyloides* spp. The size of each shape is mapped to the number of studies published in that country. Location of shapes does not represent exact location of study, but country in which the study was completed. Colored fill of shapes was assigned to a single source and is consistent across all helminth species.

### 3. Discussion

#### 3.1. Animals

Primates and domesticated or feral dogs (canids) adapt well to association with human settlements and cohabitation with humans, indicating the potential for transmission to humans. Contamination with feces from domesticated or synanthropic primates and dogs may lead to other environmental sources, such as water and soil, becoming reservoirs of *Strongyloides* spp. capable of causing infection. Most studies found in this review were based on primate and dog investigation, suggesting that these animals preferentially live closely with and benefit from humans. This habitual closeness presents a chance for environmental transmission of *Strongyloides* spp.

##### 3.1.1. Canids

Studies that report parasites found in canid feces frequently investigate multiple parasites such as *Ancylostoma* spp., *Giardia* spp., and *Strongyloides* spp. These studies have often found low levels of *S. stercoralis* within otherwise highly parasitically infected populations [40,48–56]. Infection occurs more frequently in canids when they are living stray. This might be a result of exposure to infective *Strongyloides* spp. larvae occurring more frequently to these dogs than dogs living within homes [57]. Mass drug administration (MDA) to stray dogs has been implemented successfully for the control of rabies; accordingly, it may be an option for the control of *Strongyloides* spp. [10]. Isolated or infrequent anthelmintic treatment increases infection rates and so considered treatment must be implemented [10,58]. Studies identifying canid feces as containing *Strongyloides* spp. commonly also screened the samples for other parasites. Sample sizes ranged from 35 to 3465. The highest prevalence was reported by Beknazarova et al. [59] who screened 35 canine fecal samples from Australia, of which 49% were positive for *Strongyloides* spp. This low sample size with a high positivity rate in comparison with other studies is representative of the inconsistent fecal shedding of *Strongyloides* spp. as well as the endemic location of the study. The lowest prevalence was reported by Ardelean et al. [60] with 1% of 3465 samples positive from dogs within Romania. Strongyloidiasis was observed most commonly in dogs three to six months of age in this study. This variance based on age and study location may be further impacted by the detection method. Ardelean et al. [60] reported high levels of *Ancylostomidae* spp. which is morphologically similar to *Strongyloides* spp., therefore making reliable identification with microscopy alone difficult.

##### 3.1.2. Primates

Areas sparsely populated by humans increase roaming in primates due to the attractive food sources but offer a low threat from the decreased human numbers. More frequent entry to communities in search of food potentially increases the numbers of *Strongyloides* spp.-infected primate feces within these sparsely populated communities [13,14]. Terrestrial *Papio* primates were likely to excrete *Strongyloides* spp. larvae; however, arboreal *Cercopithecus neglectus* were less likely [11,12]. This may be due to less frequent contact with soil containing *Strongyloides* spp. larvae. The impact of human populations upon forests has led to an increased chance of interaction between humans and potentially infected primates. Hasegawa et al. [61] observed that degraded forest increased the chance of roaming and transfer of parasites.

Captive primates present an infection risk to handlers because anthelmintic treatment has been observed to not eliminate *Strongyloides* spp. larvae shedding within feces [15]. This may be due to the introduction of new individuals to groups, a phenomenon also observed within wild individuals [15]. This indicates the value in introducing physical environmental controls beyond anthelmintic drugs, especially in communities exposed to roaming wild primates.

Tourist sanctuaries provide an ideal environment for contact between primates and humans. Environmental controls such as fecal contamination removal can decrease helminthic infection in both primates and humans without interfering with natural behaviors [62]. *Strongyloides* spp. is unable to

transfer either from animal to human or from human to human directly [63]. This further supports the importance of clearing feces because contact with the animals does not cause infection; however, contact with fecal matter can cause infection. Larger groups, such as those within tourist sanctuaries, are generally associated with higher parasitic species richness. Some variation of infection can be expected based on food availability and stress levels [64].

Studies of primates had sample sizes ranging from 7 to 3349, with prevalence also ranging from <1% to 100%. Prevalence within primate populations was reported to be higher than in canine populations. Hasegawa et al. [61] reported 100% prevalence within seven gorilla and chimpanzees from Uganda; whereas Li et al. [65] screened 3349 fecal samples and identified a prevalence rate of 6%. This variation in prevalence may be due to the inconsistent shedding of *Strongyloides* spp. larvae. Li et al. [65] employed microscopy whereas Hasegawa et al. [61] employed molecular techniques, which may account for differentiation in prevalence.

### 3.1.3. Ruminants

*Strongyloides* spp. has also been found within the feces of ruminants used in western farming settings including pigs, sheep, and cattle. All studies identifying *Strongyloides* spp. within farm-associated ruminants only identified the parasite to the species level [66,67]. These may have been genus specific, such as the pork threadworm, *Strongyloides ransomi*, or the more general *Strongyloides papillosis*. All studies used microscopy, a technique that can have low success in identifying *Strongyloides* spp. to species level. These recorded observations indicate the potential for infected ruminant feces to provide an environmental source of *Strongyloides* spp.

### 3.1.4. Rodents

Rodents are known to carry a range of communicable diseases. *Strongyloides* spp. has been found in several rodent species, including common house rats, and non-synanthropic rodents such as *Hydrochoerus hydrochaeris*. *S. stercoralis* has been identified in house rat feces in East Java, Indonesia, using microscopy [20]. The area in which *S. stercoralis* was identified in house rat feces is an area with poor sanitation and hygiene. People reported a large house rat population within these areas [20]. In such cases, where a zoonotic pathogen is identified, control of the offending carrier can be employed. The sample sizes of rodents were low in comparison with other sources, with the highest sample size being 502 [19]. The highest prevalence was within a population of *Rattus norvegicus* within a Brazilian slum [17]. The rodents sampled within this study had particularly high levels of infection with helminths; in all except five, helminths were present within their feces [17]. This prevalence of 97% from a sample size of 299 is representative of animals living within an area highly contaminated by human waste.

### 3.1.5. Insects

Increasing urbanization has allowed for synanthropic dependence to increase within insect populations. Densely urbanizing areas lead to an increase in available food for insects, and areas with poor sanitation and hygiene practices attract disease-carrying insects such as those within the order Blattodea (cockroaches) and Diptera (flies). Filth flies present a source of helminth transmission. Their preference for consuming wet, rotting substances indicates a high probability for the consumption and carriage of *Strongyloides* spp. Carriage of *Strongyloides* spp. has been observed on the external body of flies despite frequent preening and cleaning [68]. Fetene and Worku [23] identified *S. stercoralis* within *Chrysomya rufifacies*, *Musca sorbens*, and *Lucilia cuprina*. *C. rufifacies* were identified largely within butcheries and defecating grounds; *M. sorbens* was found more frequently within the market collection sites. Furthermore, *Musca domestica*, a species always found in association with humans, has been observed to carry *Strongyloides* spp. [24]. The presence of these flies within human food areas presents a potential transmission route for *Strongyloides* spp. larvae. Prevalence was higher in the internal structures of flies than on the external surface of flies [25]. This observation is further supported by

the preference of these flies for consumption of wet substances. Insects within the order Blattodea, commonly known as cockroaches, also present a transmission source. Parasite prevalence has been found to be associated with housing type. Low-cost housing with pit latrines as well as housing in close proximity to dumpsites was reported to contain higher levels of carrier cockroaches [26,28,29]. Through the introduction of environmental controls such as fly screens or nets, movement of carrier insects can be decreased [27]. Sample sizes for both orders were high. Studies found low prevalence with the exception of Morenikeji et al. [28] who reported 81% in 70 cockroaches.

### 3.2. Water

Contamination of water is also a potential source of helminth transferal. Pollution of water sources with human and agricultural waste can render water sources unsuitable for use as drinking and irrigation water. In areas where water access is limited, contaminated water may be employed for these uses [69]. Waste stabilization ponds, chlorination, or activated sludge treatment systems may be suitable approaches for reducing helminth levels; however, many studies monitoring wastewater treatment methods have provided contradictory results [70–73]. Some studies identified standard treatment techniques as adequate for removing larvae; however, others did not. Frequent monitoring of treated waste water is important because treated water has been identified as containing higher than acceptable levels of helminths including *Strongyloides* spp. [74]. To date, studies have focused on the helminth burden of treated water instead of comparing treated with untreated levels. Through focusing on untreated and treated waters from the same area, reduction in burden levels of treated water may be better understood.

Untreated water used for drinking can contain *Strongyloides* spp., particularly when water is sourced from storm water or collected rainwater [75]. According to one study, when water runoff moves into drinking water sources such as rivers, it can carry *Strongyloides* spp. larvae with it [75]. Bore and ground-water contamination can also occur and has been identified [76,77]. Jonnalagadda and Bhat [77] found that improper washing of vessels used to collect and store water can lead to helminth contamination. Implementation of appropriate washing and sanitation education in areas with high contamination risk may decrease incidences of infection.

Prevalence of *Strongyloides* spp. within non-potable water was higher than in potable water; this was expected because most sources of non-potable water were collected from wastewater treatment facilities [71]. The prevalence of *Strongyloides* spp. within non-treated wastewater was between 40–100%. Treated waste water intended for use on crops for human consumption had a much lower prevalence (2%); however, it was still observed to be present, supporting the importance of monitoring water intended for reuse [70].

### 3.3. Fruit and Vegetables

The rough nature of green, leafy vegetables surfaces means that adhesion of parasitic larvae and eggs occurs easily when these vegetables are either washed with contaminated water or come into contact with contaminated human fecal-based fertilizers (i.e., night soil) [30]. Studies identified *S. stercoralis* contamination most frequently within leafy, rough-surfaced vegetables such as lettuces, cabbage, celery, spinach, and carrot [30–37]. This correlation may be due to these vegetables growing close to or in the ground, which may lead to increased contamination from fertilizers [78,79]. Market vendors commonly wash vegetables prior to purchase, and consumption of raw vegetables such as salad leaves is frequently noted [31,79,80]. There is an increasing focus on the study of vegetables, washing water, and farm soil to determine where in the food chain parasites are being introduced [33].

Prevalence of *Strongyloides* spp. within fruit and vegetable samples was generally low, ranging from <1% to 46%. Ogbolu et al. [81] found *S. stercoralis* in 46% of fresh vegetables sold at open markets in Nigeria. The application of night soils and untreated wastewater is common within low-income nations may have led to the high level of prevalence [81]. Lower prevalence was also reported within

Nigeria, between <1% and 19%. This variation may be due to differences in handling of samples, treatment during farming, and cross contamination [30,31].

### 3.4. Soil

Increasing urbanization has led to an ever-increasing amount of waste. Modern waste includes not only fecal waste but waste produced in the form of rubbish. Dumpsites and landfills are commonly employed to deal with this large amount of waste; *Strongyloides* spp. contamination can occur throughout the nearby environments. Dumps and landfills pose a transmission risk due to the ability of *Strongyloides* spp. larvae to survive effectively in the soil [82].

Contamination of soils with animal feces within public recreation areas also presents a transmission source. High levels of soil-transmitted helminths were reported in public area soils such as parks in Spain, Iran, Malaysia, Nigeria, Brazil, the Czech Republic, Slovakia, and Romania [38–47].

The texture and chemistry of soil also plays a role in the prevalence of *Strongyloides* spp. larvae. Moisture levels in soils increases the incidence of rhabditiform larvae developing into filariform larvae [83]. This requirement for moisture is supported by the findings of a study of helminth larvae during the wet season, which found that no larvae were located during the dry season despite contamination [39]. High sand and silt content soils favor the survival of *Strongyloides* spp. and other helminth larvae. This is due to the high porosity of these soils, which allows larvae to move effectively through the soils towards sources of nutrition and moisture [84].

*Strongyloides* spp. is transmitted from soil-based sources to humans through skin-to-soil contact; however, the behavior of purposefully ingesting soil known as geophagy can also lead to soil-based infections. Geophagy is culturally accepted and common in sub-Saharan Africa. This behavior is common in pregnant women; *S. stercoralis* infections have been observed, along with other soil-transmitted helminth infections, in these women [85,86]. Geophagy may be undertaken as a method for diet supplementation in low-income areas. Notably, these areas are more likely to have helminth-contaminated soil, which leads to an increased chance of infection.

Prevalence of *Strongyloides* spp. within soil was between 1% and 20%. Ivoke et al. [85] screened 797 pregnant women for parasitic infections related to geophagy. The prevalence of infection was 1% within this cohort. This low prevalence is likely due to picking soils specifically for consumption. Higher prevalence was observed in soils sampled in soil directly from areas densely populated with poor health infrastructure [41].

### 3.5. PCR and Microscopy

Identification of *Strongyloides* spp. nematodes can be undertaken using several methods. These fall into either techniques involving the identification of *Strongyloides* spp. larvae using a microscope or molecular-based techniques. Microscopy presents several problems but it accounts for most larval identification-based techniques (90%) as presented in this literature review. This study did not exclude papers based on year; accordingly, this overrepresentation of microscopy is likely a result of the recent introduction of polymerase chain reaction (PCR) techniques. Recent papers have increasingly employed PCR as accessibility to the equipment increases. In 2018, 5 of the 14 papers published employed molecular-based techniques; in contrast, in 2011, only 1 of 11 studies published employed molecular-based techniques, as seen in Table A1. This increasing use of molecular-based techniques is expected, and its use will allow for more accurate identification of species of *Strongyloides* spp. The strengths of microscopy include that it can be employed within the field or where resources are limited; however, microscopy alone cannot reliably differentiate *S. stercoralis* from *S. fuelleborni*. The reliance on microscopy-based techniques is hazardous because both species are morphologically similar [34]. Molecular techniques allow for the accurate identification of *Strongyloides* spp. to the species level; however, set up of molecular protocols can be expensive. Each technique has strengths and weaknesses; when looking at all published works, a consideration of the identification techniques allows for more accurate assessment of reports.



### 3.6. Global Distribution

Globally, published research has mainly focused in countries within Africa, Europe, and South East Asia. Commonly, *Strongyloides* spp. is reported as a tropical disease; however, *Strongyloides* spp. was often also reported in temperate regions such as Europe, as seen in Figure 1 [83,87]. This may be due to a lack of resources within low-income nations, leading to an overrepresentation of the generally higher income countries within Europe. Australia and the Americas both lacked studies looking at the environmental sources of *Strongyloides* spp. (Figure 1). This indicates a need for more research into the environmental transmission of *S. stercoralis*, *S. fuelleborni*, and *Strongyloides* spp. within these areas.

## 4. Materials and Methods

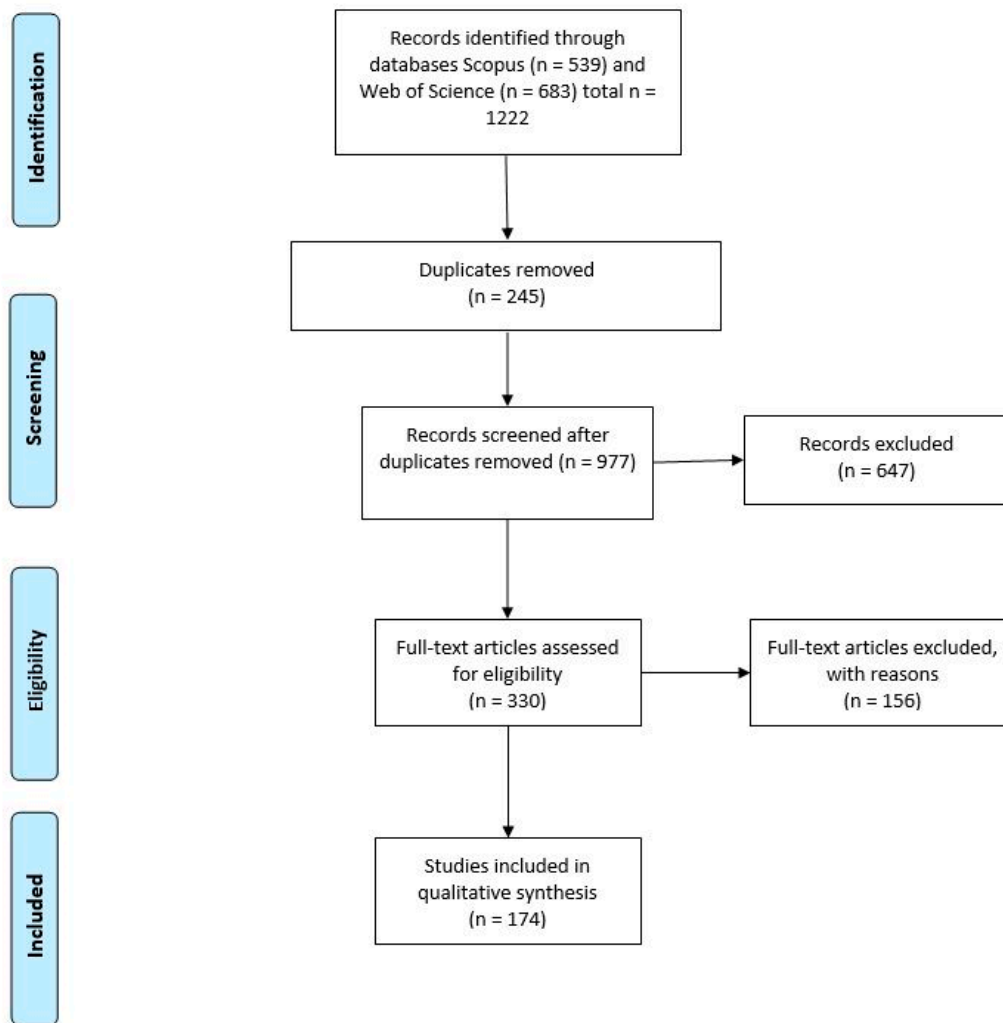
This systematic literature review is based on an adapted version of the PRISMA statement. This tool allows for the transparent and reliable reporting of evidence. A systematic search of the databases Scopus and Web of Science was undertaken, and all articles published prior to 2019 were included. Key words used in searches included *Strongyloides* spp., strongyloidiasis, tap water, soil, insect, zoonotic, and waste, as seen in Table 1. A search strategy was developed to ensure a transparent and complete literature review of all identified environmental sources of *Strongyloides* spp. was completed. This strategy is as follows; All non-English documents were excluded from the search.

To be included, published data must have reported *Strongyloides* spp. in one of the three spp. capable of human infection or to the genus level because these studies cannot be excluded as identifying disease-causing *Strongyloides* spp. The document must have reported this presence within an environmental source. Documents were excluded if they were reviews, reports of humans with *Strongyloides* spp. infection with no mention of contributing environmental source, or lab-based studies, as seen in Figure 2.

First, all titles and abstracts of all papers were manually reviewed to ensure the papers met inclusion criteria. If it was unclear from titles and abstracts if papers met the criteria, they were included for full text review. Papers that were unclear were included. Papers were then read as full text and compared against inclusion and exclusion criteria. Articles that met these criteria were included in the study. All papers included in the study had key points extracted and recorded including the environmental source reported, species of *Strongyloides* spp. observed, detection method used, and the country from which the sample was taken.

**Table 1.** Complete search strategy and all key words used to identify relevant literature.

| Search Terms Employed to Identify Relevant Literature   |
|---|
| <i>Strongyloides</i> OR Strongyloidiasis OR " <i>Strongyloides stercoralis</i> " OR " <i>S. stercoralis</i> " OR " <i>Strongyloides fuelleborni</i> " OR " <i>S. fuelleborni</i> " OR " <i>Strongyloides fuelleborni kellyi</i> " OR " <i>S. fuelleborni kellyi</i> "   |
| AND   |
| "Tap Water" OR "Potable water" OR Water OR Soil OR Dirt OR sediment OR synanthropic OR "synanthropic insect" OR Insect OR " <i>Musca domestica</i> " OR flies OR " <i>Musca vetustissima</i> " OR <i>Sarcophagidae</i> OR " <i>Chrysomya megacephala</i> " OR " <i>Musca sorbens</i> " OR " <i>Lucilia cuprina</i> " OR " <i>Calliphora vicina</i> " OR " <i>Blattella germanica</i> " OR " <i>Periplaneta Americana</i> " OR Cockroach OR dog OR " <i>Canis lupis</i> " OR zoonotic OR Monkey OR "septic tank" OR waste OR wastewater OR rubbish OR trash OR environment |



**Figure 2.** Flow diagram representing the search strategies used (based on the PRISMA statement reporting guidelines for systematic literature reviews) showing an overview of the retrieved articles and the total articles identified as eligible.

## 5. Conclusions

Although *Strongyloides* spp. is considered a soil-transmitted helminth, there are several environmental sources that can potentially provide a route of transmission of the disease. Understanding the potential sources, combined with the adoption of environmental controls for *Strongyloides* spp. is likely to decrease transmission and therefore infections. Animals such as dogs, primates, and insects, as well as soil, water, and fruit and vegetables have all been reported to contain *Strongyloides* spp. larvae, capable of perpetuating infection within humans who have come into contact. Future research is needed to undertake a holistic screening of all environmental sources within endemic areas to identify those which pose the greatest significance to human health. By understanding the established and recorded environmental reservoirs of *S. stercoralis*, *S. fuelleborni*, and *S. fuelleborni kellyi*, better environmental controls can be implemented.

**Author Contributions:** M.A.F.W., H.W., and K.E.R. designed and participated in review design. M.A.F.W. drafted and edited the manuscript, H.W. corrected and contributed to the manuscript, K.E.R. corrected and contributed to the manuscript. All authors approved of the final manuscript.

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**Conflicts of Interest:** The authors declare no conflict of interest.

## Appendix A

**Table A1.** Summary of all reports, and studies identifying *S. stercoralis*, *S. fuelleborni*, *S. fuelleborni kellyi*, and *Strongyloides* spp. within environmental sources worldwide.

| Species Parasite                 | Prevalence | Sample Size | Detection Method | Country          | Reference                          | Source |
|----------------------------------|------------|-------------|------------------|------------------|------------------------------------|--------|
| <i>Strongyloides stercoralis</i> | 1%         | 3465        | Microscopy       | Romania          | (Ardelean et al., 2005) [60]       | Dog    |
| <i>Strongyloides stercoralis</i> | 49%        | 35          | Molecular        | Australia        | (Beknazarova et al., 2017) [59]    | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 3208        | Microscopy       | Iceland          | (Eydal and Skirnisson 2016) [88]   | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 215         | Microscopy       | Brazil           | (Ferreira et al., 2006) [89]       | Dog    |
| <i>Strongyloides</i> spp.        | <1%        | 457         | Microscopy       | Canada           | (Gaunt and Carr 2011) [90]         | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 181         | Microscopy       | Brazil           | (Goncalves et al., 2007) [91]      | Dog    |
| <i>Strongyloides stercoralis</i> | 87%        | 88          | Molecular        | Cambodia         | (Jaleta et al., 2017) [6]          | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 879         | Microscopy       | Greece           | (Kostopoulou et al., 2017) [48]    | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 189         | Microscopy       | Thailand         | (Leelayoova et al., 2009) [49]     | Dog    |
| <i>Strongyloides stercoralis</i> | 45%        | 171         | Microscopy       | Brazil           | (Martins et al., 2012) [58]        | Dog    |
| <i>Strongyloides stercoralis</i> | 4%         | 52          | Microscopy       | Romania          | (Mircean et al., 2012) [92]        | Dog    |
| <i>Strongyloides</i> spp.        | 5%         | 175         | Microscopy       | Malaysia         | (Noor Azian et al., 2008) [40]     | Dog    |
| <i>Strongyloides stercoralis</i> | 2%         | 281         | Microscopy       | Greece           | (Papazahariadouet al., 2007) [50]  | Dog    |
| <i>Strongyloides stercoralis</i> | 2%         | 272         | Microscopy       | Italy            | (Paradies et al., 2017) [93]       | Dog    |
| <i>Strongyloides</i> spp.        | 11%        | 90          | Microscopy       | Sri Lanka        | (Perera et al., 2013) [57]         | Dog    |
| <i>Strongyloides stercoralis</i> | 6%         | 174         | Microscopy       | Iran             | (Razmi et al., 2009) [52]          | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 239         | Microscopy       | Italy            | (Riggio et al., 2013) [53]         | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 639         | Microscopy       | Italy            | (Sauda et al., 2018) [55]          | Dog    |
| <i>Strongyloides</i> spp.        | 15%        | 94          | Microscopy       | Cambodia         | (Schär et al., 2014) [87]          | Dog    |
| <i>Strongyloides stercoralis</i> | 10%        | 60          | Microscopy       | Slovakia         | (Štrkolcová et al., 2017) [45]     | Dog    |
| <i>Strongyloides</i> spp.        | 2%         | 171         | Microscopy       | England          | (Wright et al., 2016) [56]         | Dog    |
| <i>Strongyloides stercoralis</i> | <1%        | 463         | Microscopy       | Italy            | (Zanzani et al., 2014) [94]        | Dog    |
| <i>Strongyloides</i> spp.        | 2%         | 197         | Microscopy       | Thailand         | (Pumidonming et al., 2016) [51]    | Dog    |
| <i>Strongyloides stercoralis</i> | 18%        | 824         | Microscopy       | Qatar            | (Abu-Madi et al., 2007) [95]       | Cat    |
| <i>Strongyloides</i> spp.        | 47%        | 28          | Microscopy       | Christmas Island | (Adams et al., 2008) [96]          | Cat    |
| <i>Strongyloides</i> spp.        | 54%        | 37          | Microscopy       | Brazil           | (Lima et al., 2017) [97]           | Cat    |
| <i>Strongyloides</i> spp.        | 3%         | 414         | Microscopy       | Romania          | (Mircean et al., 2010) [98]        | Cat    |
| <i>Strongyloides stercoralis</i> | 14%        | 173         | Microscopy       | Brazil           | (Monteiro et al., 2016) [99]       | Cat    |
| <i>Strongyloides stercoralis</i> | 44%        | 103         | Microscopy       | Kenya            | (Njuguna et al., 2017) [100]       | Cat    |
| <i>Strongyloides</i> spp.        | <1%        | 300         | Microscopy       | Thailand         | (Rojekittikhun et al., 2014) [101] | Cat    |

Table A1. Cont.

| Species Parasite  | Prevalence   | Sample Size | Detection Method         | Country       | Reference                           | Source  |
|---|--|-------------|--------------------------|---------------|-------------------------------------|---------|
| <i>Strongyloides stercoralis</i>                                      | 21%  | 38          | Microscopy               | Thailand      | (Sedionoto and Anamnart 2018) [102] | Cat     |
| <i>Strongyloides</i> spp.   | 99.10%   | 99          | Microscopy               | Denmark       | (Takeuchi-Storm et al., 2015) [103] | Cat     |
| <i>Strongyloides fuelleborni</i>                                      | UNK  | UNK         | Molecular and Microscopy | Japan         | (Arizono et al., 2012) [13]         | Primate |
| <i>Strongyloides</i> spp.   | 41.44%   | 41          | Microscopy               | Uganda        | (Bezjian et al., 2008) [11]         | Primate |
| <i>Strongyloides</i> spp.   | 37%  | 24          | Microscopy               | French Guiana | (De Thoisy et al., 2001) [14]       | Primate |
| <i>Strongyloides</i> spp.   | 21%  | 125         | Microscopy               | India         | (Ekanayake et al., 2006) [104]      | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 28%  | 293         | Microscopy               | Uganda        | (Gillespie et al., 2004) [105]      | Primate |
| <i>Strongyloides fuelleborni</i> and <i>Strongyloides stercoralis</i> | <1% <i>S. stercoralis</i> , 4% <i>S. fuelleborni</i> | 2103        | Microscopy               | Uganda        | (Gillespie et al., 2005) [106]      | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 84%  | 153         | Microscopy               | Tanzania      | (Gillespie et al., 2010) [107]      | Primate |
| <i>Strongyloides fuelleborni</i> and <i>Strongyloides</i> spp.        | 11% <i>S. fuelleborni</i> , 15% <i>S. spp.</i>       | 27          | Microscopy               | Spain         | (Gomez et al., 1996) [15]           | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 23%  | 401         | Microscopy               | Japan         | (Gotoh 2000) [108]                  | Primate |
| <i>Strongyloides fuelleborni</i> and <i>Strongyloides stercoralis</i> | 100%   | 7           | Molecular                | Uganda        | (Hasegawa et al., 2016) [61]        | Primate |
| <i>Strongyloides</i> spp.   | 88%  | 96          | Microscopy               | Ecuador       | (Helenbrook et al., 2015) [64]      | Primate |
| <i>Strongyloides</i> spp.   | 4%   | 238         | Microscopy               | Uganda        | (Hodder and Chapman 2012) [109]     | Primate |
| <i>Strongyloides</i> spp.   | 7%   | 40          | Microscopy               | Kenya         | (Karere and Munene 2002) [12]       | Primate |
| <i>Strongyloides</i> spp.   | 41%  | 624         | Microscopy               | Borneo        | (Klaus et al., 2018) [62]           | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 32%  | 652         | Microscopy               | Borneo        | (Klaus et al., 2017) [110]          | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 57%  | 141         | Microscopy               | Puerto Rico   | (Knezevich et al., 1998) [111]      | Primate |
| <i>Strongyloides</i> spp.   | 43%  | 686         | Microscopy               | Tanzania      | (Kooriyama et al., 2012) [112]      | Primate |
| <i>Strongyloides</i> spp.   | 74%  | 3142        | Microscopy               | Côte d'Ivoire | (Kouassi et al., 2015) [113]        | Primate |
| <i>Strongyloides</i> spp.   | 13%  | 366         | Microscopy               | India         | (Kumar et al., 2018) [114]          | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 44% <i>S. fuelleborni</i> , 4% <i>S. spp.</i>        | 25          | Microscopy               | Malaysia      | (Kuze et al., 2010) [115]           | Primate |
| <i>Strongyloides fuelleborni</i>                                      | 95%  | 20          | Molecular and Microscopy | Indonesia     | (Labes et al., 2011) [116]          | Primate |

Table A1. Cont.

| Species Parasite  | Prevalence | Sample Size | Detection Method | Country           | Reference                                 | Source  |
|---|------------|-------------|------------------|-------------------|---|---------|
| <i>Strongyloides</i> spp.   | 37%        | 59          | Microscopy       | Ethiopia          | (Legesse and Erko 2004) [117]             | Primate |
| <i>Strongyloides</i> spp.   | 5%         | 222         | Microscopy       | Belgium           | (Leveck et al., 2007) [118]               | Primate |
| <i>Strongyloides</i> spp.   | 6%         | 3349        | microscopy       | China             | (Li et al., 2017) [65]                    | Primate |
| <i>Strongyloides stercoralis</i>                                  | 6%         | 46          | Microscopy       | Nigeria           | (Mafuyai et al., 2013) [119]              | Primate |
| <i>Strongyloides</i> spp.   | 50%        | 134         | Microscopy       | Costa Rica        | (Maldonado-Lopez et al., 2014) [120]      | Primate |
| <i>Strongyloides</i> spp.   | 77%        | 78          | Microscopy       | Ecuador           | (Martin-Solano et al., 2017) [121]        | Primate |
| <i>Strongyloides</i> spp.   | 17%        | 53          | Microscopy       | Uganda            | (Matsubayashi et al., 1992) [122]         | Primate |
| <i>Strongyloides fuelleborni</i>                                  | 58%        | 432         | Molecular        | Uganda            | (McLennan et al., 2017) [123]             | Primate |
| <i>Strongyloides</i> spp.   | 84%        | 121         | Microscopy       | Uganda            | (Muehlenbein et al., 2005) [124]          | Primate |
| <i>Strongyloides fuelleborni</i>                                  | 45%        | 315         | Microscopy       | Kenya             | (Munene et al., 1998) [125]               | Primate |
| <i>Strongyloides fuelleborni</i>                                  | 21%        | 297         | Microscopy       | Kenya             | (Muriuki et al., 1998) [126]              | Primate |
| <i>Strongyloides</i> spp.   | 76%        | 83          | Microscopy       | Costa Rica        | (Parr et al., 2013) [127]                 | Primate |
| <i>Strongyloides</i> spp.   | 13%        | 366         | Microscopy       | Tanzania          | (Petrasova et al., 2010) [128]            | Primate |
| <i>Strongyloides</i> spp.   | 44%        | 130         | Microscopy       | Tanzania          | (Petrzelkova et al., 2010) [129]          | Primate |
| <i>Strongyloides stercoralis</i>                                  | 15%        | 86          | Microscopy       | Peru              | (Phillips et al., 2004) [130]             | Primate |
| <i>Strongyloides</i> spp.   | 43%        | 47          | Microscopy       | Gabon             | (Pouillevet et al., 2017) [131]           | Primate |
| <i>Strongyloides fuelleborni</i>                                  | 6%         | 125         | Microscopy       | Cameroon          | (Pourrut et al., 2011) [132]              | Primate |
| <i>Strongyloides</i> spp.   | 53%        | 55          | Microscopy       | Ghana             | (Ryan et al., 2012) [133]                 | Primate |
| <i>Strongyloides</i> spp.   | 8%         | 420         | Molecular        | Mexico            | (Solorzano-Garcia and de Leon 2017) [134] | Primate |
| <i>Strongyloides fuelleborni</i>                                  | 39%        | 243         | Molecular        | Thailand and Laos | (Thanchomnang et al., 2018) [135]         | Primate |
| <i>Strongyloides</i> spp.   | 35%        | 283         | Microscopy       | India             | (Tiwari et al., 2017) [136]               | Primate |
| <i>Strongyloides stercoralis</i>                                  | 31%        | 135         | Microscopy       | Thailand          | (Wenz-Mucke et al., 2013) [137]           | Primate |
| <i>Strongyloides</i> spp.   | 24%        | 272         | Microscopy       | South Africa      | (Wren et al., 2015) [138]                 | Primate |
| <i>Strongyloides</i> spp.   | 24%        | 332         | Microscopy       | South Africa      | (Wren et al., 2016) [139]                 | Primate |
| <i>Strongyloides fuelleborni</i><br>and <i>Strongyloides</i> spp. | UNK        | 14          | Molecular        | Malaysian Borneo  | (Frias et al., 2018) [140]                | Primate |
| <i>Strongyloides</i> spp.   | 29%        | 64          | Microscopy       | Brazil            | (De Souza et al., 2012) [66]              | Sheep   |
| <i>Strongyloides</i> spp.   | 8%         | 165         | Microscopy       | Papua New Guinea  | (Koinari et al., 2013) [141]              | Sheep   |
| <i>Strongyloides</i> spp.   | <1%        | 27          | Microscopy       | New England       | (MacGlaflin et al., 2011) [142]           | Sheep   |
| <i>Strongyloides</i> spp.   | UNK        | 1798        | Microscopy       | Brazil            | (McManus et al., 2009) [143]              | Sheep   |
| <i>Strongyloides</i> spp.   | 2%         | 275         | Microscopy       | Greenland         | (Andreassen et al., 2017) [144]           | Fox     |
| <i>Strongyloides</i> spp.   | 4%         | 22          | Microscopy       | Iran              | (Dalimi et al., 2006) [145]               | Fox     |

Table A1. Cont.

| Species Parasite                 | Prevalence | Sample Size | Detection Method | Country        | Reference                              | Source        |
|----------------------------------|------------|-------------|------------------|----------------|--|---------------|
| <i>Strongyloides stercoralis</i> | 16%        | 249         | Microscopy       | Mexico         | (Hernandez-Camacho et al., 2011) [146] | Fox           |
| <i>Strongyloides stercoralis</i> | 2%         | 1198        | Microscopy       | Slovakia       | (Miterpakova et al., 2009) [147]       | Fox           |
| <i>Strongyloides</i> spp.        | 65%        | 60          | Microscopy       | Pakistan       | (Afshan et al., 2013) [16]             | Rat           |
| <i>Strongyloides</i> spp.        | 97%        | 299         | Microscopy       | Brazil         | (Carvalho-Pereira et al., 2018) [17]   | Rat           |
| <i>Strongyloides</i> spp.        | 40%        | 25          | Microscopy       | Brazil         | (Lima et al., 2017) [97]               | Rat           |
| <i>Strongyloides</i> spp.        | 13%        | 76          | Microscopy       | Bangladesh     | (Fuehrer et al., 2012) [18]            | Rat           |
| <i>Strongyloides</i> spp.        | 10%        | 502         | Microscopy       | Nigeria        | (Isaac et al., 2018) [19]              | Mouse and rat |
| <i>Strongyloides stercoralis</i> | 53%        | 98          | Microscopy       | Indonesia      | (Prasetyo et al., 2016) [20]           | House rat     |
| <i>Strongyloides</i> spp.        | 10%        | 10          | Microscopy       | Brazil         | (Souza et al., 2015) [21]              | Capybaras     |
| <i>Strongyloides</i> spp.        | 10%        | 31          | Microscopy       | Brazil         | (Gioia-Di Chiacchio et al., 2014) [22] | Capybaras     |
| <i>Strongyloides stercoralis</i> | 2%         | 6530        | Microscopy       | Ethiopia       | (Fetene and Worku 2009) [23]           | Flies         |
| <i>Strongyloides stercoralis</i> | <1%        | 9950        | Microscopy       | Ethiopia       | (Getachew et al., 2007) [24]           | Flies         |
| <i>Strongyloides stercoralis</i> | 2%         | 5000        | Microscopy       | Nigeria        | (Umeche 1989b) [25]                    | Flies         |
| <i>Strongyloides stercoralis</i> | 12%        | 749         | Microscopy       | Nigeria        | (Adenusi et al., 2018) [26]            | Cockroaches   |
| <i>Strongyloides stercoralis</i> | 1%         | 920         | Microscopy       | Thailand       | (Chamavit et al., 2010) [27]           | Cockroaches   |
| <i>Strongyloides stercoralis</i> | 81%        | 70          | Microscopy       | Nigeria        | (Morenikeji et al., 2016) [28]         | Cockroaches   |
| <i>Strongyloides stercoralis</i> | UNK        | 234         | Microscopy       | Nigeria        | (Tatfeng et al., 2005) [29]            | Cockroaches   |
| <i>Strongyloides stercoralis</i> | 2%         | 125         | Microscopy       | Nigeria        | (Adesewa and Morenikeji, 2017) [82]    | Soil          |
| <i>Strongyloides</i> spp.        | 3%         | 625         | Microscopy       | Spain          | (Dado et al., 2012) [38]               | Soil          |
| <i>Strongyloides</i> spp.        | 8%         | 120         | Microscopy       | Egypt          | (Etewa et al., 2016) [83]              | Soil          |
| <i>Strongyloides stercoralis</i> | 1%         | 797         | Microscopy       | Nigeria        | (Ivoke et al., 2017) [85]              | Geophagy      |
| <i>Strongyloides stercoralis</i> | 2%         | 1078        | Microscopy       | Tanzania       | (Kawai et al., 2009) [86]              | Geophagy      |
| <i>Strongyloides stercoralis</i> | 3%         | 112         | Microscopy       | Iran           | (Motazedian et al., 2006) [39]         | Soil          |
| <i>Strongyloides</i> spp.        | 7%         | 182         | Microscopy       | Malaysia       | (Noor Azian et al., 2008) [40]         | Soil          |
| <i>Strongyloides stercoralis</i> | 20%        | 102         | Microscopy       | Nigeria        | (Ogbolu et al., 2011) [41]             | Soil          |
| <i>Strongyloides</i> spp.        | 5%         | 2520        | Microscopy       | Brazil         | (Rocha et al., 2011) [42]              | Soil          |
| <i>Strongyloides</i> spp.        | 2%         | 500         | Microscopy       | Czech Republic | (Valkounova 1982) [43]                 | Soil          |
| <i>Strongyloides</i> spp.        | 3%         | 125         | Microscopy       | Brazil         | (Mandarino-Pereira et al., 2010) [44]  | Soil          |
| <i>Strongyloides stercoralis</i> | 14%        | 14          | Microscopy       | Slovakia       | (Strkolcova et al., 2017) [45]         | Soil          |

Table A1. Cont.

| Species Parasite   | Prevalence                                     | Sample Size | Detection Method | Country      | Reference                          | Source             |
|--|--|-------------|------------------|--------------|------------------------------------|--------------------|
| <i>Strongyloides stercoralis</i>                               | 12%  | 17          | Microscopy       | South Africa | (Sumbele et al., 2014) [84]        | Soil               |
| <i>Strongyloides</i> spp.                                      | 4%   | 45          | Microscopy       | Romania      | (Tudor 2015) [46]                  | Soil               |
| <i>Strongyloides stercoralis</i>                               | 6%   | 150         | Microscopy       | Nigeria      | (Umeche 1989a) [47]                | Soil               |
| <i>Strongyloides</i> spp.                                      | 6%   | 16          | Microscopy       | Brazil       | (da Silva et al., 2014) [148]      | Soil               |
| <i>Strongyloides</i> spp.                                      | UNK  | 8           | Microscopy       | Cameroon     | (Aghaindum and Landry, 2019) [149] | Non-potable water  |
| <i>Strongyloides</i> spp.                                      | 40% - 100%                                     | 100         | Microscopy       | Saudi Arabia | (Bolbol 1992) [69]                 | Non-potable water  |
| <i>Strongyloides stercoralis</i>                               | 2%%  | UNK         | Microscopy       | Brazil       | (Bastos et al., 2008) [70]         | Non-potable water  |
| <i>Strongyloides</i> spp.                                      | 100%   | 3           | Microscopy       | Brazil       | (Cutolo et al., 2006) [71]         | Non-potable water  |
| <i>Strongyloides stercoralis</i>                               | 19%  | 52          | Microscopy       | Palestine    | (Hilles et al., 2014) [150]        | Seawater           |
| <i>Strongyloides stercoralis</i>                               | 1%   | 85          | Microscopy       | Turkey       | (Bakir et al., 2003) [151]         | Drinking water     |
| <i>Strongyloides fuelleborni</i> and <i>Strongyloides</i> spp. | 11% <i>S. fuelleborni</i> , 15% <i>S. spp.</i> | 9950        | Microscopy       | Zimbabwe     | (Dalu et al., 2011) [76]           | Drinking water     |
| <i>Strongyloides</i> spp.                                      | UNK  | UNK         | Microscopy       | Egypt        | (El Shazly et al., 2003) [75]      | Drinking water     |
| <i>Strongyloides stercoralis</i>                               | 7%   | 80          | Microscopy       | Egypt        | (El-Badry et al., 2018) [152]      | Drinking water     |
| <i>Strongyloides stercoralis</i>                               | 81%  | 16          | Microscopy       | Brazil       | (Freitas et al., 2017) [153]       | Drinking water     |
| <i>Strongyloides stercoralis</i>                               | 51%  | 232         | Microscopy       | India        | (Jonnalagadda and Bhat 1995) [77]  | Drinking water     |
| <i>Strongyloides stercoralis</i>                               | 100%   | UNK         | Microscopy       | USA          | (Klotz et al., 1992) [154]         | Drinking water     |
| <i>Strongyloides stercoralis</i>                               | UNK  | UNK         | Molecular        | Malaysia     | (Zeehaida et al., 2011) [155]      | Fruit & vegetables |
| <i>Strongyloides stercoralis</i>                               | <1%  | 1130        | Microscopy       | Nigeria      | (Adamu et al., 2012) [30]          | Fruit & vegetables |

Table A1. Cont.

| Species Parasite                 | Prevalence | Sample Size | Detection Method | Country  | Reference                      | Source             |
|----------------------------------|------------|-------------|------------------|----------|--------------------------------|--------------------|
| <i>Strongyloides stercoralis</i> | <1%        | 960         | Microscopy       | Nigeria  | (Adenusi et al., 2015) [31]    | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 10%        | 150         | Microscopy       | Nigeria  | (Amaechi et al., 2016) [78]    | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 7%         | 190         | Microscopy       | Nigeria  | (Amuta et al., 2017) [32]      | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 7%         | 240         | Microscopy       | Nigeria  | (Dada et al., 2015) [33]       | Fruit & vegetables |
| <i>Strongyloides</i> spp.        | 1%         | 453         | Microscopy       | Iran     | (Fallah et al., 2016) [34]     | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 36%        | 360         | Microscopy       | Ghana    | (Kudah et al., 2018) [35]      | Fruit & vegetables |
| <i>Strongyloides</i> spp.        | 13%        | 108         | Microscopy       | Brazil   | (Luz et al., 2017) [156]       | Fruit & vegetables |
| <i>Strongyloides</i> spp.        | 19%        | 199         | Microscopy       | Nigeria  | (Maikai et al., 2012) [157]    | Fruit & vegetables |
| <i>Strongyloides</i> spp.        | 11%        | 36          | Microscopy       | Malaysia | (Matyusof et al., 2017) [80]   | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 1%         | 260         | Microscopy       | Sudan    | (Mohamed et al., 2016) [36]    | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 10%        | 265         | Microscopy       | Thailand | (Punsawad et al., 2019) [37]   | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 46%        | 120         | Microscopy       | Nigeria  | (Ogbolu et al., 2009) [81]     | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 14%        | 140         | Microscopy       | Iran     | (Madadi 2010) [158]            | Fruit & vegetables |
| <i>Strongyloides stercoralis</i> | 19%        | 80          | Microscopy       | Nigeria  | (Ohaeri and Unogu 2011) [79]   | Fruit & vegetables |
| <i>Strongyloides</i> spp.        | 7%         | 15          | Microscopy       | Zambia   | (Berentsen et al., 2012) [159] | Other animals      |
| <i>Strongyloides</i> spp.        | 5%         | 272         | Microscopy       | Nepal    | (Bista et al., 2017) [160]     | Other animals      |



Table A1. Cont.

| Species Parasite          | Prevalence | Sample Size | Detection Method | Country           | Reference                             | Source        |
|---------------------------|------------|-------------|------------------|-------------------|---------------------------------------|---------------|
| <i>Strongyloides</i> spp. | 100%       | 1           | Microscopy       | Brazil            | (Cardia et al., 2016) [161]           | Other animals |
| <i>Strongyloides</i> spp. | 4%         | 432         | Microscopy       | Spain             | (Cordon et al., 2008) [162]           | Other animals |
| <i>Strongyloides</i> spp. | 40%        | 52          | Microscopy       | Russia            | (González et al., 2007) [163]         | Other animals |
| <i>Strongyloides</i> spp. | 2%         | 956         | Microscopy       | India             | (Gupta et al., 2018) [164]            | Other animals |
| <i>Strongyloides</i> spp. | <1%        | 1005        | Microscopy       | Germany           | (Hallinger et al., 2018) [165]        | Other animals |
| <i>Strongyloides</i> spp. | 31%        | 42          | Microscopy       | Japan             | (Hasegawa et al., 2017) [166]         | Other animals |
| <i>Strongyloides</i> spp. | <1%        | 400         | Microscopy       | Croatia           | (Hermosilla et al., 2017) [167]       | Other animals |
| <i>Strongyloides</i> spp. | 64% - 99%  | 990         | Microscopy       | Mexico            | (Hu et al., 2018) [168]               | Other animals |
| <i>Strongyloides</i> spp. | 4%         | 821         | Microscopy       | China             | (Huang et al., 2014) [169]            | Other animals |
| <i>Strongyloides</i> spp. | 15%        | 2280        | Microscopy       | Pakistan          | (Khan et al., 2010) [67]              | Other animals |
| <i>Strongyloides</i> spp. | UNK        | 6           | Microscopy       | Namibia           | (Kumba et al., 2003) [170]            | Other animals |
| <i>Strongyloides</i> spp. | 36%        | 58          | Microscopy       | Poland            | (Mizgajska-Wiktor et al., 2010) [171] | Other animals |
| <i>Strongyloides</i> spp. | 67%        | 12          | Microscopy       | Mexico            | (Mukul-Yerves et al., 2014) [172]     | Other animals |
| <i>Strongyloides</i> spp. | 57%        | 201         | Microscopy       | Estonia           | (Oja et al., 2017) [173]              | Other animals |
| <i>Strongyloides</i> spp. | 47%        | 383         | Microscopy       | Mexico            | (Ojeda-Robertos et al., 2017) [174]   | Other animals |
| <i>Strongyloides</i> spp. | 7%         | 6           | Molecular        | Iberian Peninsula | (Perera et al., 2013) [175]           | Other animals |

Table A1. Cont.

| Species Parasite          | Prevalence | Sample Size | Detection Method | Country     | Reference                       | Source        |
|---------------------------|------------|-------------|------------------|-------------|---------------------------------|---------------|
| <i>Strongyloides</i> spp. | 3%         | 468         | Microscopy       | Poland      | (Pilarczyk et al., 2015) [176]  | Other animals |
| <i>Strongyloides</i> spp. | 17%        | 86          | Microscopy       | Bangladesh  | (Rahman et al., 2018) [177]     | Other animals |
| <i>Strongyloides</i> spp. | 3%         | 1883        | Microscopy       | Italy       | (Rinaldi et al., 2009) [178]    | Other animals |
| <i>Strongyloides</i> spp. | 44%        | 163         | Microscopy       | Portugal    | (Rosalino et al., 2006) [179]   | Other animals |
| <i>Strongyloides</i> spp. | 45%        | 82          | Microscopy       | Australia   | (Turni and Smales 2001) [180]   | Other animals |
| <i>Strongyloides</i> spp. | UNK        | UNK         | Microscopy       | Namibia     | (Turner et al., 2010) [181]     | Other animals |
| <i>Strongyloides</i> spp. | UNK        | UNK         | Microscopy       | Namibia     | (Turner et al., 2012) [182]     | Other animals |
| <i>Strongyloides</i> spp. | <1%        | 213         | Microscopy       | Kenya       | (VanderWaal et al., 2014) [183] | Other animals |
| <i>Strongyloides</i> spp. | 74%        | 243         | Microscopy       | Philippines | (Ybanez et al., 2018) [184]     | Other animals |

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