Parasites & Vectors

REVIEW

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Cryptosporidium infections in terrestrial ungulates with focus on livestock: a systematic review and meta-analysis

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Abstract

Background: *Cryptosporidium* spp. are causative agents of gastrointestinal diseases in a wide variety of vertebrate hosts. Mortality resulting from the disease is low in livestock, although severe cryptosporidiosis has been associated with fatality in young animals.

Methods: The goal of this systematic review and meta-analysis was to review the prevalence and molecular data on *Cryptosporidium* infections in selected terrestrial domestic and wild ungulates of the families Bovidae (bison, buffalo, cattle, goat, impala, mouflon sheep, sheep, yak), Cervidae (red deer, roe deer, white-tailed deer), Camelidae (alpaca, camel), Suidae (boar, pig), Giraffidae (giraffes) and Equidae (horses). Data collection was carried out using PubMed, Scopus, Science Direct and Cochran databases, with 429 papers being included in this systematic analysis.

Results: The results show that overall 18.9% of ungulates from the investigated species were infected with *Cryptosporidium* spp. Considering livestock species (cattle, sheep, goats, pigs, horses and buffaloes), analysis revealed higher *Cryptosporidium* infection prevalence in ungulates of the Cetartiodactyla than in those of the Perissodactyla, with cattle (29%) being the most commonly infected farm animal.

Conclusions: Overall, the investigated domestic ungulates are considered potential sources of *Cryptosporidium* contamination in the environment. Control measures should be developed to reduce the occurrence of *Cryptosporidium* infection in these animals. Furthermore, literature on wild populations of the named ungulate species revealed a widespread presence and potential reservoir function of wildlife.

Keywords: Cryptosporidiosis, Livestock, Cattle, Sheep, Goat, Pig, Horse, Wildlife

Background

Cryptosporidium, the causative agent of cryptosporidiosis, is an ubiquitous protozoan parasite. It causes gastrointestinal disease in a wide variety of vertebrate hosts, including ungulates of the orders Artiodactyla and Perissodactyla, as well as humans. Several *Cryptosporidium* species are known to be zoonotic with animals as major reservoirs [1]. In resource-limited settings, cryptosporidiosis is a leading cause of diarrhoeal death in children younger than five years across the globe, only second to rotaviral enteritis [2]. Cryptosporidiosis is also a significant contributor to health care cost in developed countries. It is estimated that in the USA 748,000 cases of human cryptosporidiosis occur annually [3]. Residents of and travelers to developing countries may be at greater risk of infection due to poor water treatment and food sanitation [4, 5]. Cryptosporidiosis typically induces self-limiting diarrhea in immunocompetent individuals, but the infection can be severe and life-threatening in immunocompromised subjects [6]. It is one of the most important diseases in young ruminants, especially neonatal calves [7, 8]. The clinical presentation of

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cryptosporidiosis varies from asymptomatic to deadly, leading to important economic losses due to growth retardation, reduced productivity and mortality [9, 10]. Considering that an infected bovine calf can shed up to 1.1×10^8 oocysts per gram of feces at the peak of the infection, cattle (and very likely wild ruminants) are significant contributors of environmental *Cryptosporidium* oocysts [11, 12], causing water-borne [13–15] and food-borne [16, 17] diarrhea outbreaks in humans worldwide. The worldwide annual excretion of *Cryptosporidium* spp. oocysts by livestock has been calculated to be 3.2×10^{23} [18], with cattle being the host species causing most environmental contamination. Cattle are able to carry different species including *C. hominis* which implies an associated significant public health risk [19]. In addition, *Cryptosporidium* oocysts are infective at the time they are passed in feces and are highly resilient to a wide range of environmental factors including disinfection and water treatment processes. Moreover, low infection doses are sufficient to cause disease in suitable hosts, e.g. 10–100 oocysts are described to provoke diarrhea in humans [20, 21].

Over the past few decades, a major subject of debate and controversy in the epidemiology of *Cryptosporidium* is whether, and to what extent, domestic and wildlife species may act as natural reservoirs of human cryptosporidiosis [22, 23]. This is principally due to the fact that the genus *Cryptosporidium* encompasses nearly 40 valid species with marked differences in host range, among which over 10 (mainly *C. hominis*, *C. parvum* and *C. meleagridis*) have been reported in humans [24] with a variety of genotypes being zoonotic [1, 22, 25]. The public health significance of animal cryptosporidiosis varies greatly depending on factors such as geographical variation in prevalence and genotype distribution, seasonality, load of environmental contamination with oocysts and access to surface waters intended for human consumption or recreation [9, 26]. In particular, genotyping data from epidemiological surveys conducted globally indicate that infected calves are the major reservoir for zoonotic *C. parvum* in many areas [26, 27], with lambs, kids and foals being potential additional sources of *C. parvum* infection for humans in some areas of the world [28–31]. Pigs are only sporadically infected with zoonotic *Cryptosporidium* species and are therefore considered minor contributors to the zoonotic transmission of cryptosporidiosis in humans [32]. Adult livestock typically harbor low level and asymptomatic infections but are epidemiologically important as cryptic carriers of the parasite, enabling re-infections at the herd level. Little is known of the molecular epidemiology and transmission cycles of cryptosporidiosis in wild ungulates. However, recent surveys have revealed the presence of *C. parvum* in wild hoofed species including the American mustang (*Equus ferus caballus*) [33], Scottish roe deer (*Capreolus capreolus*) and red deer (*Cervus elaphus*) [34], and Spanish wild boars (*Sus scrofa scrofa*) [35], which may represent a threat to water quality and public health [34].

In the present study, we conducted a systematic review of publications on the prevalence of *Cryptosporidium* infections and *Cryptosporidium* species distribution in domestic and wild ungulates in order to ascertain the extent to which hoofed animals should be considered as relevant reservoirs of human infection.

Methods

Search strategy

To evaluate the prevalence of *Cryptosporidium* infection in hoofed animals, we performed a comprehensive review of literatures (full text or abstracts) published online. English databases including PubMed, Scopus, Science Direct and Cochran were searched for publications related to *Cryptosporidium* infection of animals worldwide, from 1984 to 2016. We used the following MeSH terms alone or in combination: "*Cryptosporidium*" or "cryptosporidiosis" and "prevalence" and "livestock" or "cattle" or "buffaloes" or "sheep" or "pigs" or "camels" or "alpacas" or "horses" or "ruminants" or "wildlife". To identify additional published articles, we used the PubMed option of "related articles" and checked the reference lists of the original and review articles. The more agricultural and veterinary focused database CAB abstracts was searched using the following search terms: "*Cryptosporidium*" or "cryptosporidiosis" and "prevalence" and "cattle" or "cows" or "calves" or "buffaloes" or "sheep" or "lambs" or "goats" or "kids" or "camels" or "alpacas" or "crias" or "llamas" or "pigs" or "piglets" or "horses" or "foals" or "deer" or "fawns" or "farm animals" or "ruminants" or "livestock" or "wildlife". A protocol for the literature review was devised (Fig. 1) in accordance with the PRISMA guidelines [36] (Additional file 1: Table S1).

Inclusion and exclusion criteria

As part of the eligibility for inclusion, titles that suggested the topic *Cryptosporidium* in domestic and wild hoofed animals were selected. The abstracts from the selected reference titles were reviewed by two independent reviewers to determine if the studies met the inclusion criteria and, if so, the entire articles were reviewed in full. If more than one report was published from the same study, only one was included. Exclusion criteria included studies only on human cryptosporidiosis or case reports. Studies on epidemiology of *Cryptosporidium* spp. in groups unrelated to hoofed animals, or studies presenting overall prevalence estimates, where samples were collected from the ground, and data from each animal

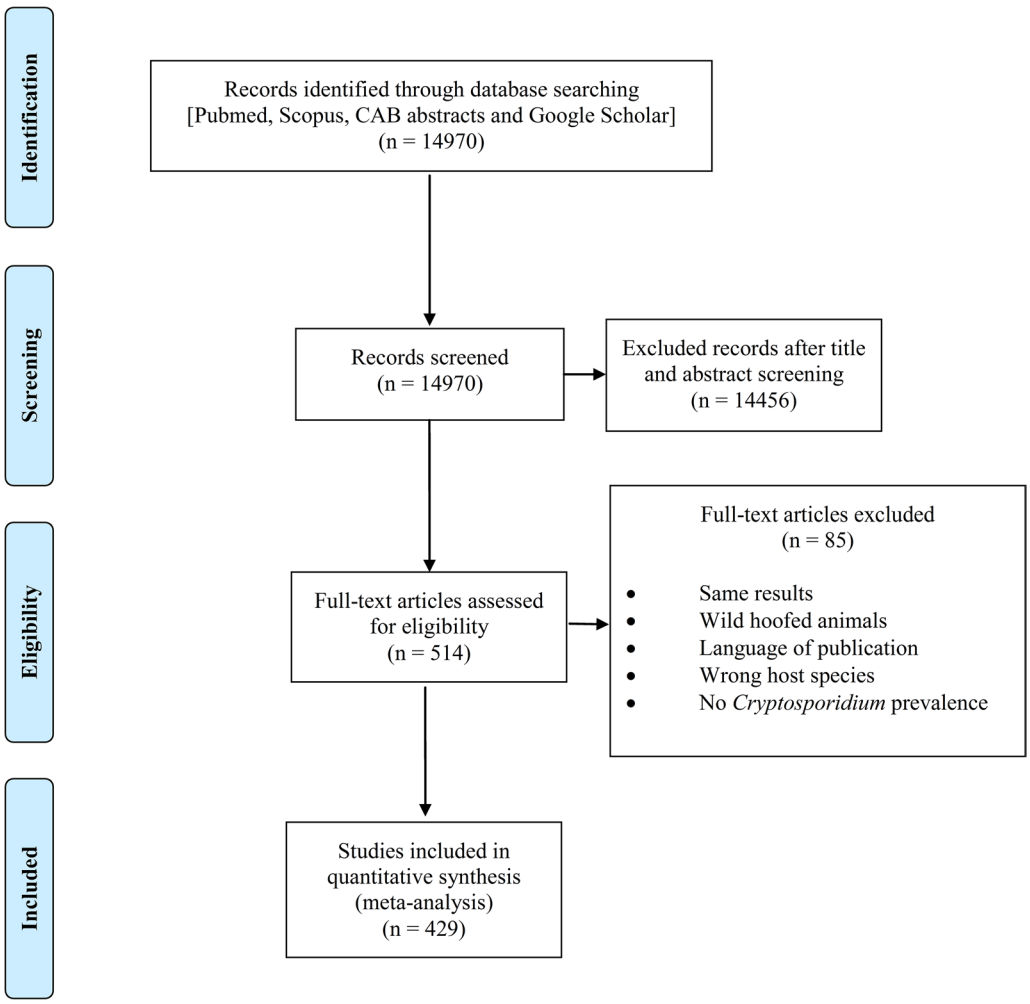

Fig. 1 Flow diagram describing the paper selection process according to PRISMA guidelines

were not independently retrievable, were also excluded. The language of data collection was limited to English. In order to provide contemporaneous and representative estimates, studies were excluded if they presented data collected prior to 1984. On several occasions, we contacted the authors for the collection of raw data.

Data extraction and tabulation

A data extraction form was used to collect the following data from each study: first author, year of publication, location of study, period of study, host species, age range, clinical signs (diarrhoeic *versus* non-diarrhoeic), population nature (e.g. domestic, captive or wild), total number of fecal samples, utilized detection method (conventional microscopy, CM; immunofluorescence antibody test, IFA; enzyme-linked immunosorbent assay, ELISA; immunochromatographic test, ICT; quantitative latex agglutination, QLAT; and polymerase chain reaction, PCR), number of *Cryptosporidium*-positive samples and identity of *Cryptosporidium* species and genotypes.

Retrieving sequences and phylogenetic analyses

To examine the genetic relationships among *Cryptosporidium* spp. (*C. hominis*, *C. felis*, *C. parvum*, *C. erinacei*, *C. xiaoi*, *C. ryanae*, *C. scrofarum*, *C. muris*, *C. andersoni*, *C. ubiquitum*, *C. bovis* and *C. suis*) in ungulates, a phylogenetic tree was constructed using the program Splits Tree v.4.0 based on the Neighbor-Net method and Median-Joining analysis of sequences

of the *18S* rRNA gene [37]. For this purpose, the sequences of the *18S* rRNA gene of these *Cryptosporidium* spp. were retrieved from the GenBank database in the FASTA format. These sequences were initially obtained from various herbivores, including cattle, buffaloes, yaks, camels, goats, sheep and deer, as well as pigs.

Meta-analysis

A meta-analysis was performed for studies describing *Cryptosporidium* infection prevalence in domestic animals that are common in many parts of the world, i.e. cattle, sheep, goats, buffaloes, horses and pigs. This analysis was performed to enhance knowledge on the potential role of livestock in zoonotic *Cryptosporidium*

Table 1 Summarized *Cryptosporidium* prevalence data for major domestic farmed animals. Data for wild populations of the given species not included (see for full datasets and other host species in Additional file 2: Table S2)

Host species	Region	No. of studies	Utilized diagnostic methods	Retrieved minimum prevalence (%)	Retrieved maximum prevalence (%)
Buffalo (*Bubalus bubalis*)	Africa	6	CM, PCR	1.3 (CM)	52.0 (CM)
	Asia	16	CM, ICT, PCR	3.6 (CM)	50.0 (CM)
	Australia	2	PCR	13.1 (PCR)	30.0 (PCR)
	Europe	1	ELISA	14.7 (ELISA)	
	South America	2	CM, PCR	9.4 (CM)	48.2 (PCR)
Cattle (*Bos taurus*)	Africa	29	CM, ELISA, PCR	0.5 (CM)	86.7 (CM)
	Asia	74	CM, ICT, IFA, PCR	1.5 (CM)	93.0 (CM)
	Australia	7	CM, IFA, PCR	3.6 (IFA)	73.5 (PCR)
	Europe	60	CM, ELISA, ICT, IFA, PCR, QLAT	0.0 (CM)	71.7 (CM)
	New Zealand	5	CM, IFA	2.6 (IFA)	21.2 (CM)
	North America	29	CM, IFA, PCR	1.1 (IFA)	78.0 (CM)
	South America	11	CM, ICT, PCR	3.0 (CM)	56.1 (CM)
Goat (*Capra hircus*)	Africa	10	CM, ELISA	0.0 (CM)	76.5 (ELISA)
	Asia	15	CM, ICT, IFA	0.0 (IFA)	42.9 (CM)
	Australia	1	PCR	4.4 (PCR)	
	Europe	22	CM, ELISA, IFA	0.0 (CM)	93.0 (IFA)
	North America	3	CM	20.0 (CM)	72.5 (CM)
	South America	3	CM	4.8 (CM)	100 (CM)
Sheep (*Ovis aries*)	Africa	10	CM, ELISA, PCR	1.3 (CM)	41.8 (ELISA)
	Asia	17	CM, ELISA, ICT, PCR	1.8 (CM)	66.6 (CM)
	Australia	7	PCR	2.2 (PCR)	81.3 (PCR)
	Europe	22	CM, IFA, ELISA	1.4 (CM)	100.0 (CM)
	North America	9	CM, IFA, PCR	20.0 (CM)	77.4 (PCR)
	South America	5	CM, PCR	0.0 (CM)	25.0 (PCR)
Pig (*Sus scrofa*)	Africa	5	CM, ELISA, IFA, PCR	13.6 (CM)	44.9 (ELISA)
	Asia	13	CM, IFA, PCR	0.4 (IFA)	55.8 (PCR)
	Australia	3	CM, PCR	0.3 (CM)	22.1 (PCR)
	Europe	13	CM, IFA, PCR	0.1 (CM)	40.9 (IFA)
	North America	6	CM, IFA	2.8 (ns)	19.6 (CM)
	South America	3	CM, PCR	0.0 (CM)	2.2 (PCR)
Horse (*Equus caballus*)	Africa	3	CM, PCR	0.0 (CM)	2.9 (PCR)
	Asia	7	CM, PCR	2.7 (PCR)	37.0 (CM)
	Europe	10	CM, ELISA, IFA, PCR	3.4 (PCR)	25.0 (IFA)
	New Zealand	2	CM	18.0 (CM)	83.3 (CM)
	North America	6	CM, IFA, PCR	0.0 (IFA/PCR[a])	17.0 (IFA)
	South America	7	CM	0.0 (CM)	100.0 (CM)

[a] Multiple studies revealed the same prevalence data

Abbreviation: ns, not stated

Table 2 Statistical analysis of *Cryptosporidium* infection prevalence in domestic ungulates using CM and PCR methods

Method/host	CM						PCR					
	Pooled (%)	OR (95% CI)	Heterogeneity			Publication bias	Pooled (%)	OR (95% CI)	Heterogeneity			Publication bias
			Q statistic	*df*	I^2 (%)	Egger bias (*P*-value)			Q statistic	*df*	I^2 (%)	Egger bias (*P*-value)
Cattle	22.5	19.6–25.6	11,038.9	127	98.8	10.51 ($P < 0.0001$)	29.1	23.1–35.6	1591.1	34	97.9	11.52 ($P < 0.0001$)
Sheep	20.7	15.2–26.8	1391.9	30	97.8	6.77 ($P = 0.0086$)	24.4	16.4–33.4	916.7	14	98.5	8.18 ($P = 0.014$)
Goat	18.7	12.36–26.2	1852.1	28	98.5	9.01 ($P = 0.0004$)	8.2	3.7–14.3	11.2	2	82.2	–
Pig	15.5	10.5–21.3	1545.4	21	98.6	12.42 ($P = 0.0485$)	22.6	13.7–33.0	99.8	5	95.0	2.36 ($P = 0.6452$)
Horse	13.8	6.6–22.9	621.6	16	97.4	6.71 ($P = 0.0002$)	4.7	2.0–8.4	22.5	4	82.3	3.67 ($P = 0.0452$)
Buffalo	18.6	11.1–27.4	991.4	17	98.3	8.76 ($P = 0.0004$)	26.0	12.2–42.8	152.4	4	97.4	9.28 ($P = 0.1434$)

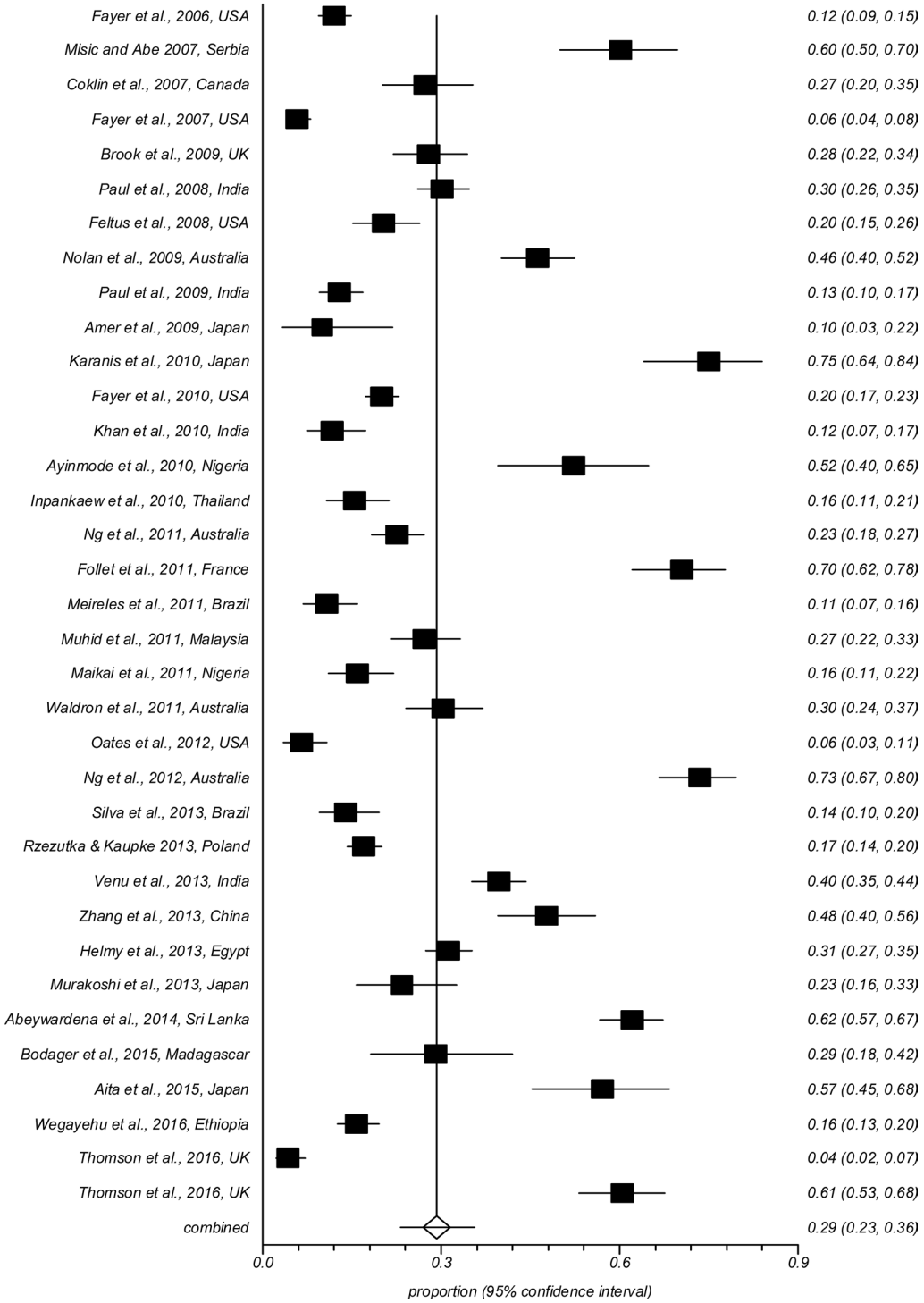

Fig. 2 Forest plot of prevalence of *Cryptosporidium* spp. infection in cattle using molecular methods (first author, year and country)

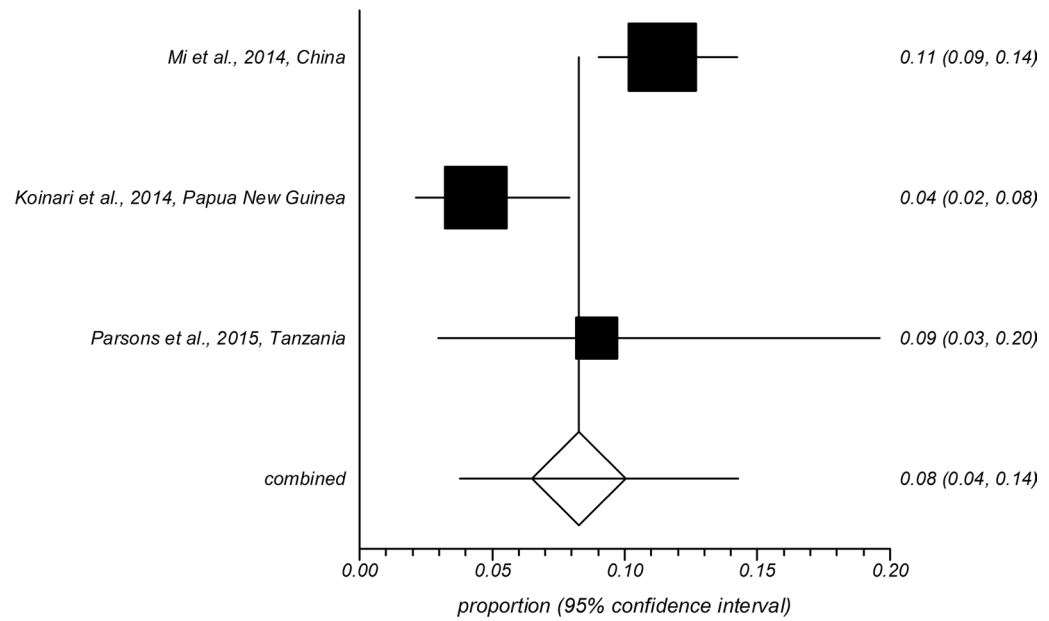

Fig. 3 Forest plot of prevalence of *Cryptosporidium* spp. infection in goats using molecular methods (first author, year and country)

transmission since these animals feature a close contact to humans. The pooled prevalence of *Cryptosporidium* infection as well as its 95% confidence interval (CI) was calculated for each study. A forest plot was generated to display the summarized results and heterogeneity among the included studies. To ensure comparable sensitivity of tests used in analyzed studies, only results from studies based on PCR as a diagnostic method were included. Studies using PCR methods only for molecular *Cryptosporidium* species/genotype identification but utilizing alternative diagnostic methods to determine prevalence were not included. The heterogeneity was expected in advance and statistical analyses including I^2 and Cochrane's Q test (with a significance level of $P<0.1$) were used to quantify these variations. The meta-analysis considering the random effects model [38] was performed using the Stats Direct statistical software (http://www.statsdirect.com).

Results

The initial database search retrieved 14,970 publications. The screening of these records enabled us to exclude 14,456 studies due to not meeting the inclusion criteria. Altogether, 514 studies were retained for further investigation. During the secondary assessment of these papers, another 85 were excluded because of one of the following reasons: other host species including wild hoofed animals; report of the same results as another paper published by the same author; and language of publication (e.g. Chinese, Spanish, etc.). Papers evaluating cryptosporidiosis in camels, yaks, donkeys, alpacas and llamas were excluded in the secondary analysis of data, as the meta-analysis focused on *Cryptosporidium* infection in cattle, sheep, goats, pigs, buffaloes and horses. Eventually, 429 studies which evaluated *Cryptosporidium* infection during three decades met our eligibility criteria and were retained for analysis (Fig. 1).

Different diagnostic procedures were used for the detection of *Cryptosporidium* oocysts to a varying extent in the different studies. The included publications featured CM examination ($n=371$), IFA ($n=107$), ELISA ($n=25$), ICT ($n=9$), quantitative latex agglutination (QLAT) ($n=1$) and polymerase chain reaction (PCR) ($n=99$) (Additional file 2: Table S2).

In total, 196,638 stool samples from Artiodactyla and Perissodactyla ungulates were evaluated, of which 37,206 (18.9%) subjects were positive for *Cryptosporidium* infection. Among the 196,638 stool samples, 90,744 were associated with the domestic hoofed animals (including camels, yaks, donkeys, alpacas and llamas), displaying a *Cryptosporidium* infection prevalence of 13.6% ($n=12,377$) (Table 1 and Additional file 2: Table S2).

All subsequent analyses included only the studies that focused on *Cryptosporidium* infection in cattle, sheep,

goats, pigs, buffaloes and horses ($n=429$). Among them, 201 provided data on cattle, 66 on sheep, 55 on goats, 39 on pigs, 37 on horses and 28 on buffaloes (Additional file 2: Table S2).

A total of 105,894 samples from 245 studies on common livestock, defined as cattle, sheep, goats, pigs, horses and buffaloes, were examined for *Cryptosporidium* infection, with 24,829 (23.4%) being positive for *Cryptosporidium* spp. using CM and PCR methods. Most of the studies were conducted on cattle ($n=163$) and sheep ($n=46$).

The pooled prevalence rates using the CM method were 22.5% (95% CI: 19.6–25.6%), 20.7% (95% CI: 15.2–26.8%), 18.7% (95% CI: 12.36–26.2%), 15.5% (95% CI: 10.5–21.3%), 13.8% (95% CI: 6.6–22.9%) and 18.6% (95% CI: 11.1–27.4%) for cattle, sheep, goats, pigs, horses and buffaloes, respectively (Table 2). The pooled prevalence rates using the PCR method were 29.1% (95% CI: 23.1–35.6%), 24.4% (95% CI: 16.4–33.4%), 8.2% (95% CI: 3.7–14.3%), 22.6% (95% CI: 13.7–33%), 4.7% (95% CI: 2–8.4%) and 26.0% (95% CI: 12.2–42.8%) for cattle, sheep, goats, pigs, horses and buffaloes, respectively (Table 2). Analysis of available data by regions (continents and New Zealand) showed a moderate geographical variation of observed prevalence (Table 1). Although diagnostic tests varied among regions, the observed prevalence mostly fell within the 5–30% range (Table 2). Regarding cattle, a considerably lower maximum prevalence was seen in New Zealand compared to other regions. *Cryptosporidium* prevalence in goat tended to be lower in Asia; however, only one study was available for Australia. For sheep it was the highest in the regions with most intensive sheep production, i.e. Australia, Europe and North America (Table 1). *Cryptosporidium* prevalence in pigs was the highest in Asia, Africa and Europe. In horses,

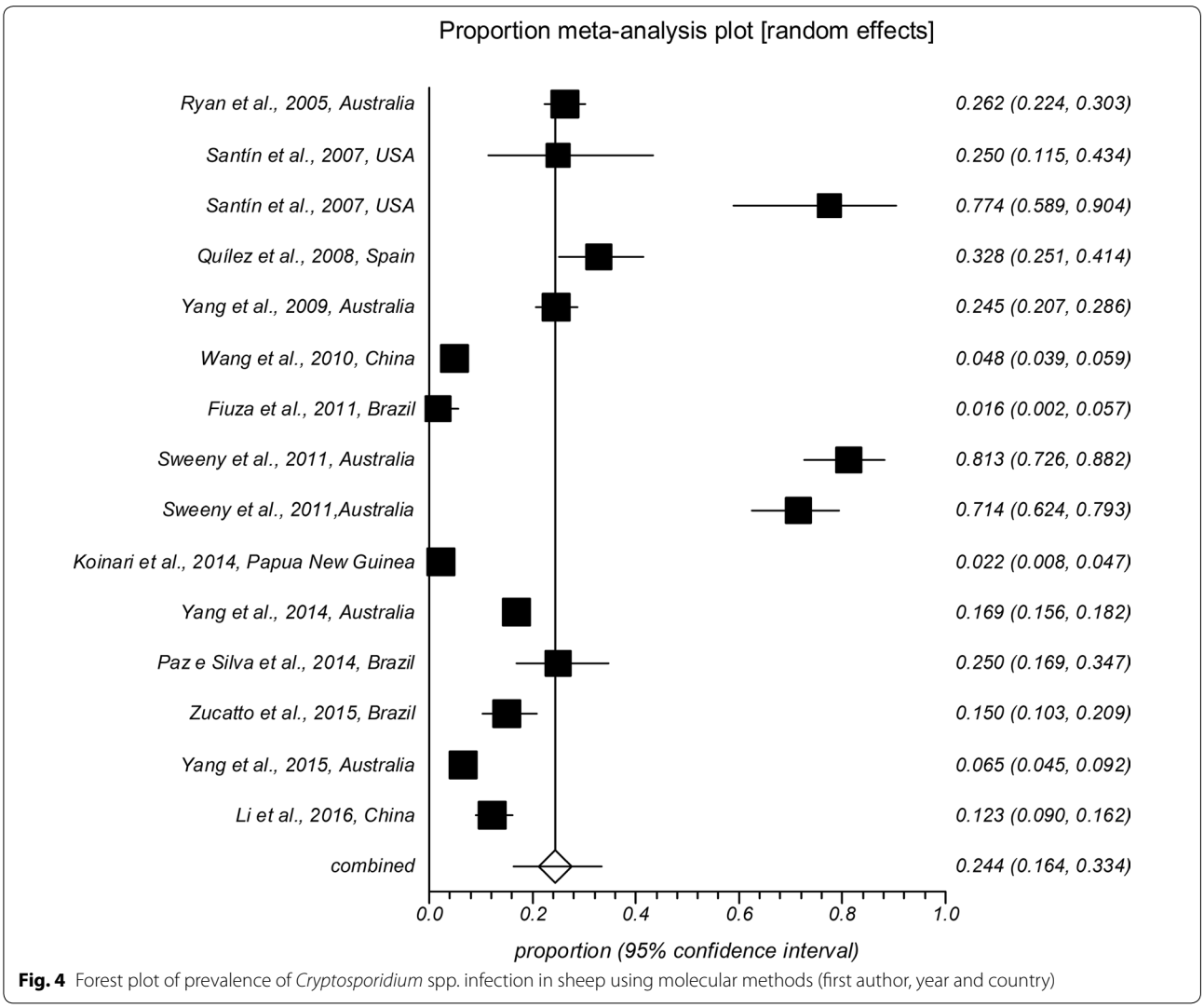

Fig. 4 Forest plot of prevalence of *Cryptosporidium* spp. infection in sheep using molecular methods (first author, year and country)

studies in South America reported the highest *Cryptosporidium* prevalence.

The forest plot diagrams of prevalence of *Cryptosporidium* infection in domestic hoofed animals derived from studies using a PCR method are shown in Figs. 2, 3, 4, 5, 6, 7. As forest plots show, there is a considerable variation of study numbers and observed prevalence in a given host species within each defined geographical region, even if only studies based on PCR methodology are included. Considering a wider range of studies, i.e. studies that use either CM or PCR (Table 2), cattle are most commonly infected globally while horses feature the lowest *Cryptosporidium* prevalence.

The highest and lowest prevalence rate of *Cryptosporidium* infection in domestic hoofed animals was observed in America (26%) and Africa (14%) continents, respectively (Table 3, Fig. 8). Among 53 countries with data, Canada (60%) showed the highest infection rate whereas China, Thailand and Germany (8%) had the lowest infection rate (Table 3, Fig. 8).

The distribution of *Cryptosporidium* species/genotypes by host and geographical region is summarized in Table 4. *Cryptosporidium parvum* (monoinfections 4172/10,583; 39.4%) and *C. andersoni* (monoinfections 1992/10,583; 18.8%) were the most commonly detected *Cryptosporidium* species (Table 4). A phylogenetic network was constructed based on sequences of *Cryptosporidium* spp. (Fig. 9) using the Neighbor-Net method. On the basis of this phylogenetic analysis, 10 clades (I, II, III, IV, V, VI, VII, VIII, IX and X) containing 12 *Cryptosporidium* spp. were identified (Fig. 9). Interestingly, *C. andersoni* and *C. muris* were placed together in Clade I, and *C. xiaoi* and *C. bovis* were both placed in Clade III. It further demonstrated a pairwise sister relationship between clades III and IV (clustering *C. xiaoi*, *C. bovis*, and *C. ryanae*), VI and VII (containing *C. ubiquitum* and *C. suis*) and VIII and IX (containing *C. hominis* and *C. erinacei*), respectively. Interestingly, the result of the phylogenetic analysis indicated that clades II (*C. scrofarum*), III (*C. bovis* and *C. xiaoi*) and IV (*C. ryanae*) could have originated from a common ancestor. The distribution of *Cryptosporidium* spp. in a wide range of domestic and wild ungulates is presented in Table 4. The *C. parvum* is the most common genotype in cattle (54.1%), goats (42.1%) and horses (40.2%), followed by *C. ryanae* in buffaloes (66.6%), *C. suis* in pigs (54.1%), and *C. xiaoi* in sheep (48.9%). In terms of transmission dynamics and clinical importance of zoonotic *Cryptosporidium* spp., *C. hominis*, *C. parvum*, *C. andersoni*, *C. bovis* and *C. ubiquitum* were identified in sheep/goats, cattle/goats/horses/pigs/sheep, cattle/camels/sheep/yaks, buffaloes/cattle/sheep/pigs/red deer and alpacas/buffaloes/cattle/goats/impalas/sheep/red deers, respectively (Table 4).

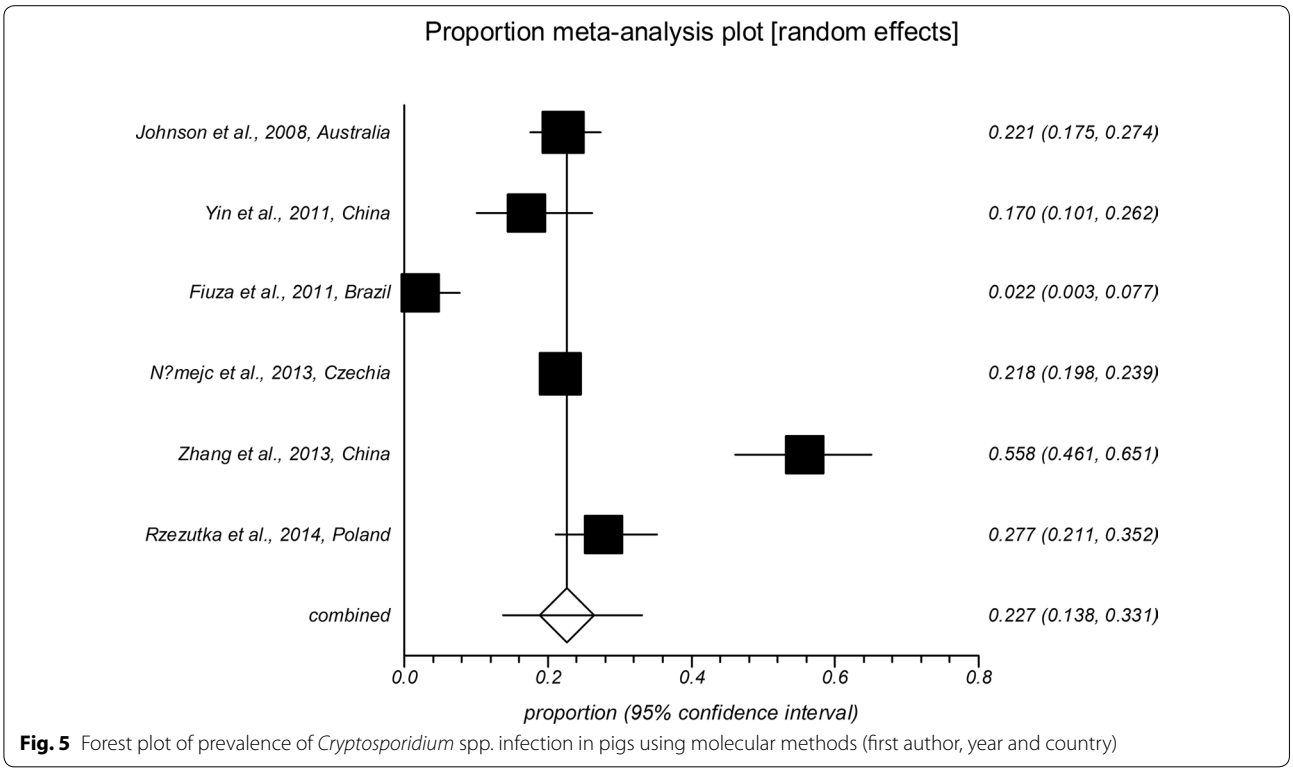

Fig. 5 Forest plot of prevalence of *Cryptosporidium* spp. infection in pigs using molecular methods (first author, year and country)

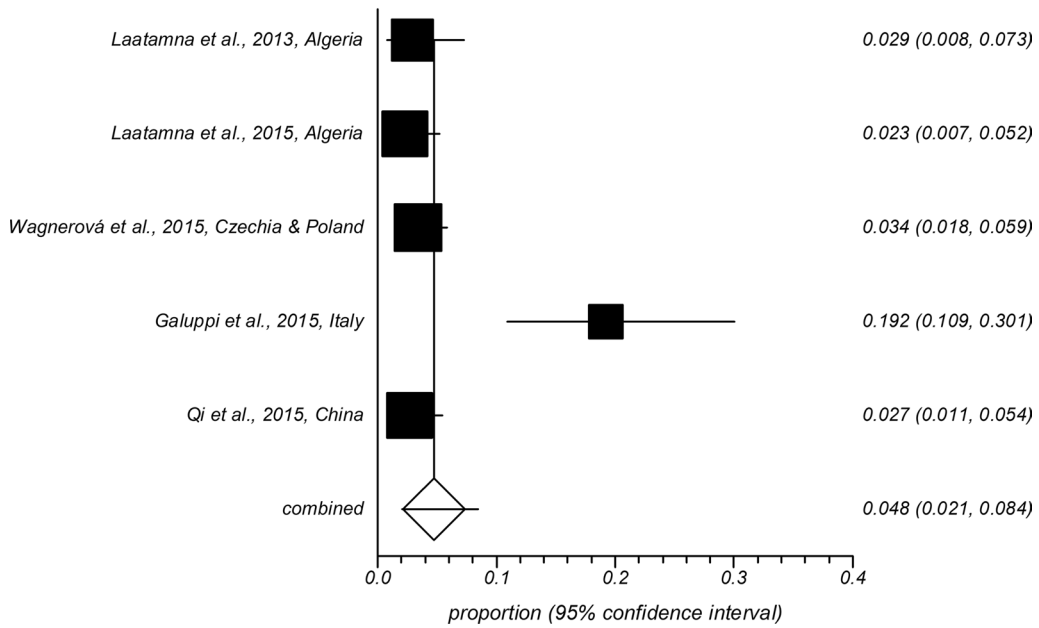

Fig. 6 Forest plot of prevalence of *Cryptosporidium* spp. infection in horses using molecular methods (first author, year and country)

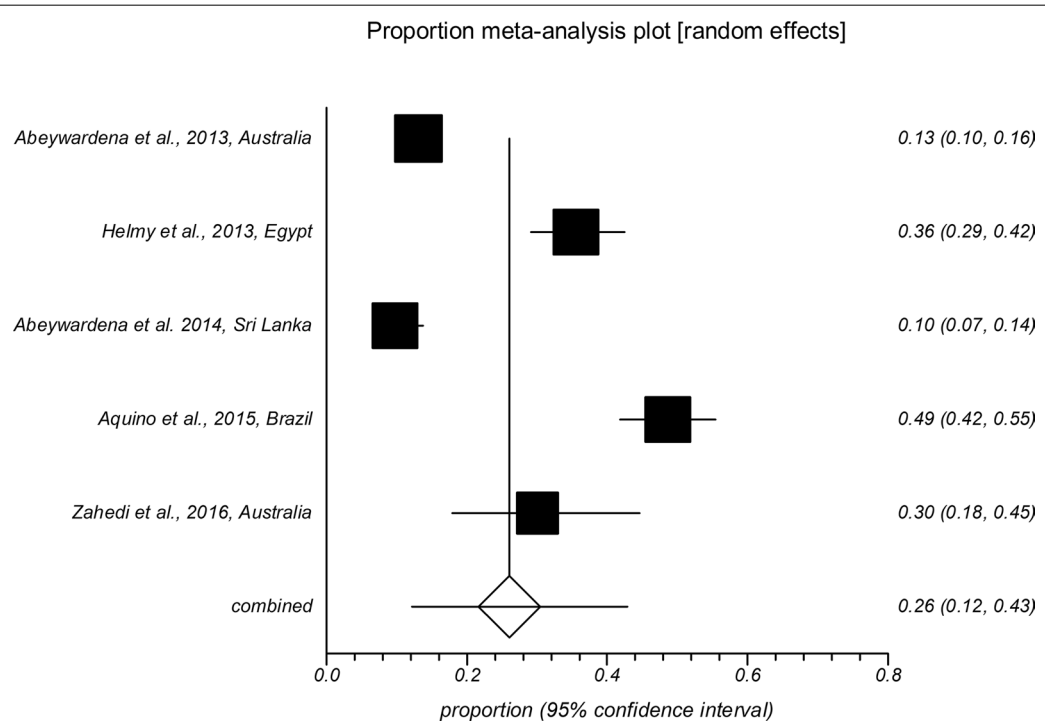

Fig. 7 Forest plot of prevalence of *Cryptosporidium* spp. infection in buffaloes using molecular methods (first author, year and country)

Table 3 The prevalence of *Cryptosporidium* infection in terrestrial ungulates (cattle, sheep, goat, pig, horse and buffalo) using conventional microscopic methods. Data are presented separately by continent and country

Continent	Country	Prevalence, pooled proportion (95% CI) (%)
Africa (43 studies; 17,424 samples)	Egypt	10 (4.44–19.32)
	Ethiopia	17 (7.15–30.13)
	Ghana	29[a]
	Kenya	15 (10.72–21.30)
	Malawi	18 (10.48–28.78)
	Nigeria	17 (13.07–22.33)
	South Africa	0.5[a]
	Tanzania	11 (1.59–29.29)
	Tunisia	14 (2.09–44.93)
	Total prevalence in Africa: 14 (11.12–18.31)	
America (37 studies; 15,860 samples)	Argentina	25 (18.83–33.58)
	Brazil	16 (5.82–30.23)
	Canada	60 (23.32–91.14)
	Chile	56[a]
	Costa Rica	11[a]
	Mexico	41 (31.81–52.23)
	Trinidad	32 (6.47–67.24)
	USA	11 (2.84–24.39)
	Total prevalence in America: 26 (18.41–34.67)	
Asia (90 studies; 37,458 samples)	Bangladesh	9 (2.93–20.36)
	China	8 (5.62–12.95)
	India	21 (16.02–28.47)
	Iran	16 (11.96–20.68)
	Iraq	17 (11.36–25.23)
	Japan	24 (0.02–72.52)
	Malaysia	24 (8.43–46.55)
	Myanmar	56[a]
	Nepal	35 (28.81–43.45)
	Pakistan	16 (9.05–25.96)
	South Korea	17 (11.53–23.57)
	Sri Lanka	28[a]
	Taiwan	35 (32.44–38.15)
	Thailand	8 (3.08–17.41)
	Vietnam	18[a]
	Total prevalence in Asia: 17 (14.94–20.30)	
Australia (4 studies; 923 samples)	Australia	23 (0.00–71.85)
	New Zealand	20 (15.42–25.92)
	Total prevalence in Australia: 21 (7.28–40.02)	
Europe (71 studies, 34,229 samples)	Austria	11[a]
	Czech Republic	17 (9.87–27.11)
	Denmark	33 (14.90–55.60)
	France	17 (2.56–41.08)
	Germany	8 (3.62–48.31)
	Greece	17 (9.87–27.11)
	Ireland	23 (3.84–52.25)
	Netherlands	60[a]
	Poland	11 (3.62–21.85)
	Portugal	17[a]

Table 3 (continued)

Continent	Country	Prevalence, pooled proportion (95% CI) (%)
	Romania	21 (15.02–27.97)
	Serbia	40 (31.95–49.48)
	Spain	29 (19.80–39.75)
	Sweden	8[a]
	Switzerland	55[a]
	Turkey	34 (19.82–50.61)
	UK	34 (0.59–85.50)
	Total prevalence in Europe: 23 (20.37–27.68)	

[a] One study was performed in these countries

Discussion

In this systematic review and meta-analysis, we found that 18.9% of the overall populations of the investigated ungulate species were infected with *Cryptosporidium* spp. Our study showed that although the prevalence of *Cryptosporidium* infection was higher in ungulates of the Cetartiodactyla than in Perissodactyla, the prevalence in the latter was not negligible and needs to be considered in terms of pathogen transmission and cycling. From the data collected and summarized on wild animals (as included in Table 4, and Additional file 2: Table S2), it is obvious that sylvatic cycles play a major role in *Cryptosporidium* transmission. Wild terrestrial ungulates are likely serving as important reservoir for the parasite, and certainly the infection of livestock and humans may occur by contact to wildlife feces. For meta-analysis, worldwide *Cryptosporidium* prevalence and species/genotype identity common livestock species have been scrutinized. Overall, *Cryptosporidium* prevalence in farmed animals is the highest in the Americas and Europe (Table 3) which could be attributed to the intensive farm animal production in these regions. More specifically, considering domestic farm animals, the pooled prevalence of equine *Cryptosporidium* infection was 4.7%, compared to the pooled prevalence of 29.1%, 26.0%, 24.4%, 22.6% and 8.2% in cattle, buffaloes, sheep, pigs and goats, respectively. Regarding the number of studies published for the different geographical regions, our analysis does not support under investigation of certain regions (e.g. Asia) as cause of a detection bias. This reinforces the suggestion that animal production intensity affects the prevalence of *Cryptosporidium* spp. Concentrated animal feeding operations (CAFOs) are most common in cattle and pigs. For example, in the USA, in 2002 more than 71% of all produced beef were derived from operations holding more than 5000 heads of cattle each. It is known that CAFOs pose a major problem due to the high amounts of manure that are released to the environment, facilitating potential pathogen transmission to humans, wildlife and other agricultural operations [39]. Furthermore, pathogen transmission within a CAFO seems much more likely than in more extensive farming systems. Accordingly, a high prevalence of *Cryptosporidium* was observed in animals from countries with many CAFO operations, especially in studies in Asia and Europe, with both regions harboring the majority of the commercial pig raising industry [40]. High prevalences in pigs in Africa may be attributed to the opposite effect of extensive farming with high exposure to environmental contamination. Other host animals displaying a high prevalence, such as buffaloes and sheep, are also generally kept in larger groups on commercial operations. The comparatively low prevalence rates in equines and goats may potentially result from smaller animal groups and free-range nature of the animal management.

Between wild and domestic animals, it appears that *Cryptosporidium* prevalence is lower in wild populations than in farmed populations in the same host species. For example, Zahedi et al. [41] reported *Cryptosporidium* infection rates of 30% in farmed buffalo but 12% in wild buffalo. This suggests that animal density and confinement to the same (contaminated) environment facilitate *Cryptosporidium* transmission in domestic animals, and there is no clear host species disposition in terms of general susceptibility to infection with the genus *Cryptosporidium* despite the observed variation in *Cryptosporidium* infection rates among host species (Table 4).

Cryptosporidiosis in ungulates, especially ruminants, has several economic and health implications. Cryptosporidiosis in neonatal calves can lead to profuse watery diarrhea, loss of appetite, lethargy, dehydration and even death, thus may require costly treatments [42]. Moreover, as shown in sheep and goats, cryptosporidiosis can exhibit long-term effects on the growth of animals [43, 44]. Additionally, infected calves can shed over 1×10^{10} oocysts each day, which can survive in the environments for months. The ingestion of very few oocysts can cause infection in susceptible hosts, including humans [23, 45].

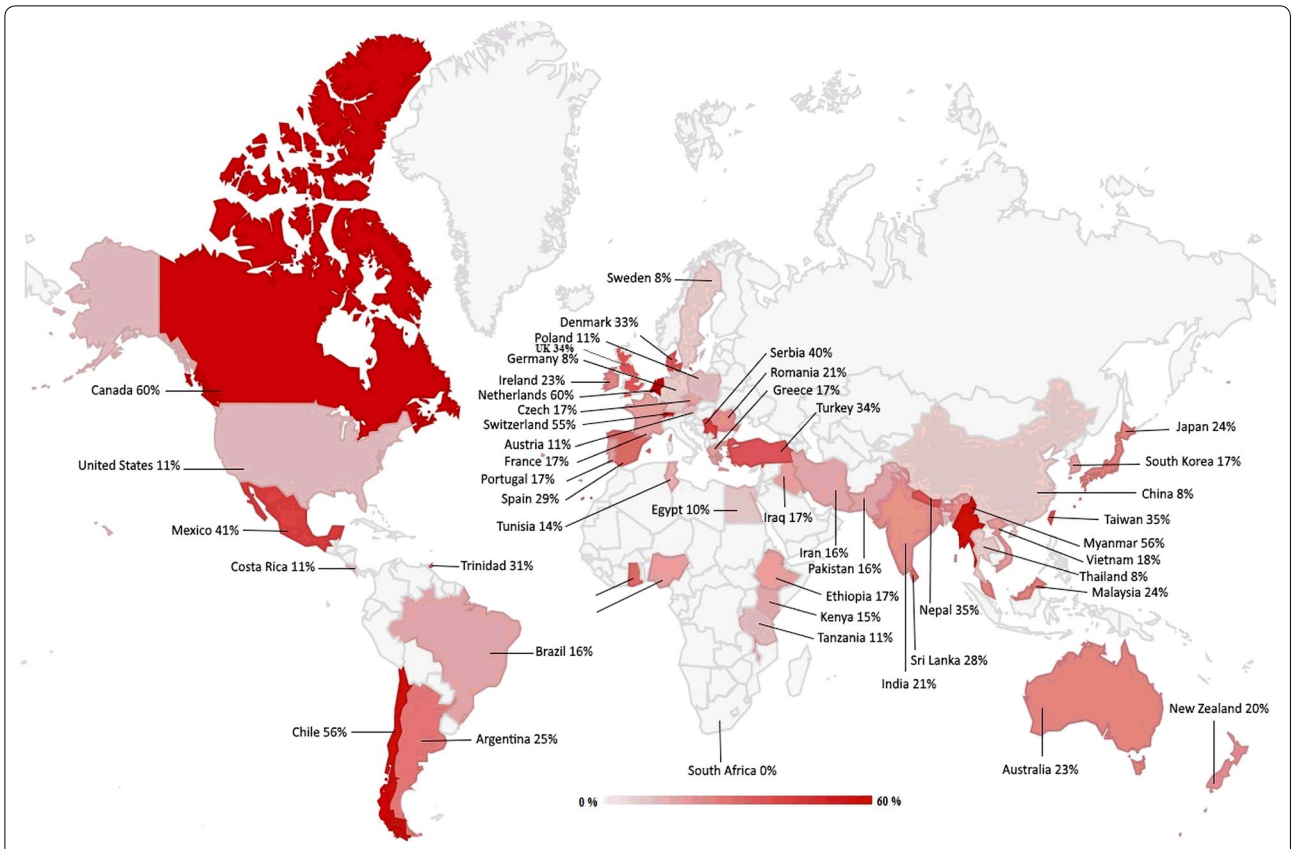

Fig. 8 Overall prevalence of *Cryptosporidium* in different geographical regions in the world. The prevalence in each country was determined from conventional microscopy data in farmed animals (cattle, sheep, goats, pigs, horses and buffaloes)

It has been shown that the median infection dose of *C. parvum* for humans range from below 10 to over 1000 oocysts [22]. Zoonotic transmission of *Cryptosporidium* spp. can easily occur seasonally from young animals such as bovine calves to humans, frequently as an occupational hazard [45, 46].

Nearly 40 *Cryptosporidium* species have been recognized based on molecular, morphological and biological characteristics of the parasites. Previous studies have shown that four major species are responsible for bovine cryptosporidiosis, namely *C. parvum*, *C. andersoni*, *C. bovis* and *C. ryanae* [1]. We showed that the most prevalent *Cryptosporidium* species in ungulates are *C. parvum* and *C. andersoni*, comprising 39.4% and 18.8% of detected parasites, respectively.

The data also suggest that some *Cryptosporidium* species are shared among ungulate hosts (Table 4). This indicates the occurrence of some inter-species transmission of *Cryptosporidium* spp. among ungulate species, making wildlife an important reservoir for infections in domestic animals. Currently, most data on the distribution of *Cryptosporidium* species and genotypes are available on domestic animal populations. Amazingly, there are clear differences in the distribution of *Cryptosporidium* species within the same host species among geographical regions. For example, studies from Ethiopia and Nigeria indicate that *C. andersoni* and *C. bovis* are the most prevalent species in cattle. In contrast, in countries with concentrated animal feeding operations (CAFO) such as Australia, Iran, Japan and New Zealand, as well as many European and North American countries, *C. parvum* is prevalent in cattle (Table 4). Similarly, alpacas in their region of origin are mostly infected with *C. parvum* and *C. ubiquitum*, while alpacas in the UK only tested positive for *C. parvum* (Table 4). Calves, lambs and goat kids in areas with more human activities can even have *C. hominis* infections [19, 41, 47, 48]. Thus, it might be speculated that husbandry systems and contact to other livestock and humans strongly influence the distribution of *Cryptosporidium* species in an ungulate population.

Our meta-analysis had several limitations. We observed a substantial heterogeneity among the included studies. Heterogeneity in the meta-analyses of prevalence is not uncommon, and the random-effect

Table 4 Worldwide occurrence of *Cryptosporidium* species or genotypes in selected domestic and wild populations of ungulate species; where applicable, available data are summarized from different sources per country

Host	Country	No. of isolates	No. of *Cryptosporidium* species/genotypes		Reference
			Monoinfection (*n*)	Mixed infection (*n*)	
Alpaca	Peru	3	*C. parvum* (2); *C. ubiquitum* (1)	–	Gómez-Couso et al. [51]
Alpaca	UK	9	*C. parvum* (9)	–	Twomey et al. [52]; Wessels et al. [53]
Bison	Portugal	1	*C. tyzzeri* (1)	–	Alves et al. [54]
Boar	Czech Republic	32	*C. suis* (13); *C. scrofarum* (7)	*C. suis* + *C. scrofarum* (12)	Němejc et al. [55]
Buffalo	Egypt	70	*C. parvum* (41); *C. ryanae* (17); *C. bovis* (2)	*C. parvum* + *C. ryanae* (7); *C. parvum* + *C. bovis* (3)	Amer et al. [56]; Helmy et al. [57]; Mahfouz et al. [58]; Ibrahim et al. [59]
Buffalo	South Africa	2	*C. ubiquitum* (1); *C. bovis* (1)	–	Abu Samra et al. [60]
Buffalo	Australia	72	*C. parvum* (9); *C. ryanae* (58); *C. scrofarum* (1); *C. bovis* (4)	–	Abeywardena et al. [61]; Zahedi et al. [62]
Buffalo	Italy	6	*C. parvum* (6)	–	Caccio et al. [63]
Buffalo	Brazil	63	*C. parvum* (1); *C. ryanae* (60); unknown genotype (2)	–	Aquino et al. [64]
Camel	China	3	*C. andersoni* (3)	–	Wang et al. [65]; Liu et al. [66]
Cattle	Egypt	238	*C. parvum* (146); *C. andersoni* (7); *C. ryanae* (35); *C. bovis* (15)	*C. parvum* + *C. ryanae* (15); *C. parvum* + *C. bovis* (10); *C. parvum* + *C. andersoni* (3); *C. ryanae* + *C. bovis* (7)	Amer et al. [56]; Helmy et al. [57]; Mahfouz et al. [58]; Ibrahim et al. [59]
Cattle	Ethiopia	71	*C. andersoni* (54); *C. ryanae* (3); *C. bovis* (14)	–	Wegayehu et al. [67]
Cattle	Kenya	27	*C. parvum* (17); *C. andersoni* (3); *C. ryanae* (6); *C. ubiquitum* (1)	–	Szonyi et al. [68]; Kang'ethe et al. [69]
Cattle	Madagascar	17	*C. suis* (17)	–	Bodager et al. [70]
Cattle	Nigeria	65	*C. andersoni* (5); *C. ryanae* (13); *C. bovis* (32)	*C. ryanae* + *C. bovis* (11); *C. bovis* + *C. andersoni* (4)	Ayinmode et al. [71]; Maikai et al. [72]
Cattle	South Africa	6	*C. parvum* (1); *C. andersoni* (2); *C. ubiquitum* (3)	–	Abu Samra et al. [60]; Abu Samra [73]
Cattle	Tunisia	7	*C. parvum* (7)	–	Soltane et al. [74]
Cattle	Zambia	45	*C. parvum* (29); *C. ubiquitum* (1); *C. bovis* (15)	–	Geurden et al. [75]
Cattle	China	299	*C. parvum* (69); *C. andersoni* (100); *C. ryanae* (19); *C. bovis* (89)	*C. parvum* + *C. bovis* (6); *C. parvum* + *C. ryanae* (4); *C. parvum* + *C. andersoni* (3); *C. bovis* + *C. ryanae* (9)	Wang et al. [76, 77]; Huang et al. [78]
Cattle	India	21	*C. parvum* (6); *C. andersoni* (3); *C. ryanae* (3); *C. bovis* (8); *C. occultus* (1)	–	Khan et al. [79]
Cattle	Iran	54	*C. parvum* (50); *C. andersoni* (4)	–	Meamar et al. [80]; Fotouhi et al. [81]; Pirestani et al. [82]
Cattle	Israel	61	*C. parvum* (61)		Tanriverdi et al. [83]
Cattle	Japan	33	*C. parvum* (32); *C. bovis* (1)		Karanis et al. [84]
Cattle	Malaysia	14	*C. parvum* (11); *C. ryanae* (3)		Halim et al. [85]

Table 4 (continued)

Host	Country	No. of isolates	No. of *Cryptosporidium* species/genotypes		Reference
			Monoinfection (*n*)	Mixed infection (*n*)	
Cattle	Australia	439	*C. parvum* (297); *C. andersoni* (20); *C. ryanae* (30); *C. bovis* (72); *C. hominis* (3)	*C. parvum* + *C. bovis* (12); *C. parvum* + *C. ryanae* (4); *C. bovis* + *C. ryanae* (1)	Waldron et al. [86]; Nolan et al. [87]; Ferguson et al. [88]; Ng et al. [89]; McCarthy et al. [90]; O'Brien et al. [91]; Ralston et al. [92]
Cattle	New Zealand	127	*C. parvum* (85); *C. bovis* (42)	–	Learmonth et al. [93]; Grinberg et al. [94]; Al-Mawly et al. [95]
Cattle	Belgium	114	*C. parvum* (105); *C. suis* (1); *C. bovis* (8)		Geurden et al. [96]
Cattle	Czech Republic	2019	*C. parvum* (699); *C. andersoni* (1315); *C. bovis* (5)	–	Kvac et al. [97]; Kvac et al. [98]; Ondrackova et al. [99]
Cattle	Denmark	244	*C. parvum* (100); *C. andersoni* (59); *C. ryanae* (11); *C. bovis* (57); *C. occultus* (3); unknown genotype (4)	*C. parvum* + *C. andersoni* (10)	Langkjaer et al. [100]; Enemark et al. [101]
Cattle	France	91	*C. parvum* (32); *C. ryanae* (14); *C. ubiquitum* (1); *C. bovis* (11)	*C. parvum* + *C. ryanae* (12); *C. parvum* + *C. bovis* (11); *C. ryanae* + *C. bovis* (8); *C. parvum* + *C. ryanae* + *C. parvum* (2)	Follet et al. [102]
Cattle	Hungary	22	*C. parvum* (21); *C. ryanae* (1)	–	Plutzer et al. [103]
Cattle	UK (Northern Ireland)	224	*C. parvum* (213); *C. ryanae* (3); *C. bovis* (8)	–	Thompson et al. [104]
Cattle	Italy	101	*C. parvum* (101)	–	Duranti et al. [105]
Cattle	Poland	113	*C. parvum* (36); *C. andersoni* (17); *C. ryanae* (8); *C. bovis* (52)	–	Rzeżutka & Kaupke [106]
Cattle	Portugal	82	*C. parvum* (82)	–	Mendonca et al. [107]
Cattle	Romania	65	*C. parvum* (65)	–	Imre et al. [108]
Cattle	Scotland	411	*C. parvum* (409); *C. hominis* (2)	–	Smith et al. [109]
Cattle	Serbia	62	*C. parvum* (62)	–	Misic & Abe [110]
Cattle	Spain	267	*C. parvum* (255); *C. andersoni* (1); *C. bovis* (4); *C. felis* (4); unknown genotype (3)	–	Mendonca et al. [107]; Quilez et al. [111]; Cardona et al. [112]
Cattle	Sweden	359	*C. parvum* (33); *C. andersoni* (4); *C. ryanae* (40); *C. bovis* (262); *C. ubiquitum* (1)	*C. parvum* + *C. bovis* (13); *C. parvum* + *C. ryanae* (6)	Silverlas et al. [113]; Silverlas et al. [114]; Silverlas et al. [115]; Bjorkman et al. [116]
Cattle	Switzerland	81	*C. parvum* (81)	–	Uhde et al. [117]
Cattle	Turkey	15	*C. parvum* (15)	–	Tanriverdi et al. [83]
Cattle	UK	306	*C. parvum* (240); *C. andersoni* (20); *C. ryanae* (1); *C. bovis* (31)	*C. parvum* + *C. ryanae* + *C. bovis* (1); *C. ryanae* + *C. bovis* (5); *C. parvum* + *C. bovis* (1); *C. parvum* + *C. ryanae* (1); *C. andersoni* + *C. ryanae* (6)	Thompson et al. [104]; Brook et al. [118]; Featherstone et al. [119]; Moriarty et al. [120]; Smith et al. [121]
Cattle	Canada	134	*C. parvum* (51); *C. andersoni* (38); *C. ryanae* (11); *C. bovis* (34)	–	Coklin et al. [122]; Coklin et al. [123]; Budu-Amoako et al. [124]; Budu-Amoako et al. [125]

Table 4 (continued)

Host	Country	No. of isolates	No. of *Cryptosporidium* species/genotypes		Reference
			Monoinfection (*n*)	Mixed infection (*n*)	
Cattle	USA	698	*C. parvum* (240); *C. andersoni* (203); *C. ryanae* (83); *C. bovis* (171); *C. suis* (1)		Santín et al. [126]; Fayer et al. [127–129]; Szonyi et al. [130]
Cattle	Brazil	57	*C. parvum* (15); *C. andersoni* (33); *C. ryanae* (4); *C. bovis* (5)		Meireles et al. [131]; Sevá et al. [132]; Silva et al. [133]
Giraffe	Czech Republic	1	*C. muris* (1)	–	Kodádková et al. [134]
Goat	Tanzania	5	*C. xiaoi* (5)	–	Parsons et al. [135]
Goat	Zambia	1	*C. parvum* (1)	–	Goma et al. [136]
Goat	China	44	*C. andersoni* (16); *C. ubiquitum* (24); *C. xiaoi* (4)	–	Wang et al. [137]
Goat	Papua New Guinea	10	*C. parvum* (2); *C. hominis* (6); *C. xiaoi* (1); rat genotype II (1)	–	Koinari et al. [138]
Goat	Belgium	11	*C. parvum* (11)		Geurden et al. [139]
Goat	France	31	*C. parvum* (1); *C. ubiquitum* (12); *C. xiaoi* (18)	–	Rieux et al. [140]; Paraud et al. [141]
Goat	Greece	14	*C. parvum* (2); *C. ubiquitum* (5); *C. xiaoi* (7)	–	Tzanidakis [142]
Goat	Spain	68	*C. parvum* (61); *C. xiaoi* (7)	–	Díaz et al. [143]; Díaz et al. [144]
Goat	UK	1	*C. hominis* (1)	–	Giles et al. [46]
Horse	Algeria	4	*C. erinacei* (4)	–	Laatamna et al. [145]
Horse	China	2	*C. andersoni* (2)	–	Liu et al. [146]
Horse	New Zealand	9	*C. parvum* (9)	–	Grinberg et al. [31]
Horse	Czech Republic	12	*C. parvum* (1); *C. muris* (9); *C. ryanae* (1); horse genotype (1)	–	Wagnerová et al. [33]
Horse	Italy	35	*C. parvum* (5); horse genotype (21)	Horse genotype + *C. parvum* (9)	Galuppi et al. [147]
Horse	UK	3	*C. parvum* (3)	–	Smith et al. [121]; Chalmers et al. [148]
Horse	USA	29	*C. parvum* (20); horse genotype (9)	–	Wagnerová et al. [][33]; Burton et al. [149]
Impala	South Africa	2	*C. ubiquitum* (2)	–	Abu Samra et al. [60]
Mouflon sheep	Czech Republic	1	*C. muris* (1)	–	Kotková et al. [150]
Pig	Madagascar	4	*C. parvum* (1); *C. suis* (3)	–	Bodager et al. [70]
Pig	Australia	87	*C. scrofarum* (48); *C. suis* (35); *C, bovis* (4)	–	McCarthy et al. [90]; [Morgan et al. [151]; Johnson et al. [152]; Ryan et al. [153]
Pig	Czech Republic	1031	*C. parvum* (2); *C. muris* (5); *C. scrofarum* (374); *C. suis* (621)	*C. suis* + *C. scrofarum* (29)	Vitovec et al. [154]; Kváč et al. [155, 156]; Němejc et al. [157]
Pig	Denmark	239	*C. scrofarum* (171); *C. suis* (68)		Langkjaer et al. [100]; Petersen et al. [158]
Pig	Ireland	28	*C. parvum* (2); *C. muris* (1); *C. scrofarum* (11); *C. suis* (14)	–	Zintl et al. [32]
Pig	UK	42	*C. parvum* (11); *C. scrofarum* (25); *C. suis* (6)	–	Smith et al. [121]; Featherstone et al. [159]

Table 4 (continued)

Host	Country	No. of isolates	No. of *Cryptosporidium* species/genotypes		Reference
			Monoinfection (*n*)	Mixed infection (*n*)	
Pig	Brazil	2	*C. scrofarum* (2)	–	Fiuza et al. [160]
Red deer	Czech Republic	6	*C. muris* (1); *C. ubiquitum* (5)	–	Kotková et al. [150]
Roe deer	Spain	6	*C. ryanae* (3); *C. bovis* (3)	–	García-Presedo et al. [161]
Sheep	Egypt	3	*C. xiaoi* (3)	–	Mahfouz et al. [58]
Sheep	Tanzania	2	*C. xiaoi* (2)	–	Parsons et al. [135]
Sheep	Tunisia	3	*C. bovis* (3)	–	Soltane et al. [74]
Sheep	Zambia	6	*C. parvum* (5); *C. ubiquitum* (1)	–	Goma et al. [136]
Sheep	China	125	*C. andersoni* (4); *C. ubiquitum* (78); *C. xiaoi* (43)	–	Wang et al. [162]; Li et al. [163]
Sheep	Australia	1005	*C. parvum* (78); *C. andersoni* (6); *Sheep genotype I* (7); *C. scrofarum* (8); *C. suis* (2); *C. ubiquitum* (148); *C. hominis* (1); *C. xiaoi* (641); *C. bovis* (66); *C. macropodum* (4); unknown genotype (1)	*C. parvum* + *C. xiaoi* (42); *C. parvum* + *C. ubiquitum* (1)	Sweeny et al. [43]; Yang et al. [164]; Ryan et al. [165]; Yang et al. [166, 167]
Sheep	Papua New Guinea	6	*C. parvum* (4); *C. andersoni* (1); *C. scrofarum* (1)	–	Koinari et al. [138]
Sheep	Belgium	9	*C. parvum* (9)		Geurden et al. [139]
Sheep	Greece	10	*C. parvum* (7); *C. ubiquitum* (3)	–	Tzanidakis [142]
Sheep	Romania	24	*C. parvum* (20); *C. ubiquitum* (2); *C. xiaoi* (2)	–	Imre et al. [168]
Sheep	Scotland	16	*C. parvum* (16)	–	Galuppi et al. [147]
Sheep	Spain	57	*C. parvum* (46); *C. ubiquitum* (11)	–	Díaz et al. [144, 169]
Sheep	UK	133	*C. parvum* (121); *C. hominis* (2); *C. bovis* (10)	–	Mueller-Doblies et al. [28]; Giles et al. [46]; Smith et al. [121]; Pritchard et al. [170]
Sheep	Brazil	42	*C. parvum* (3); *C. ubiquitum* (24); *C. xiaoi* (15)	–	Fiuza et al. [171]; Paz e Silva et al. [172]; Zucatto et al. [173]
White-tailed deer	Czech Republic	3	*C. muris* (1); *C. ryanae* (2)		Kotková et al. [150]
Yak	China	158	*C. andersoni* (72); *C. ryanae* (37); *C. bovis* (47); *C. occultus* (2)	–	Yang et al. [164]

Notes: C. suis (previously known as pig genotype I); *C. scrofarum* (previously known as pig genotype II); *C. ryanae* (previously deer-like genotype); *C. erinacei* (previously described as hedgehog genotype); *C. bovis* (previously bovine genotype B); *C. macropodum* (previously marsupial genotype II); *C. xiaoi* (previously bovis-like genotype); *C. hominis* (synonym: *C. parvum* genotype 1); *C. parvum* (synonym: *C. parvum* genotype 2); *C. ubiquitum* (previously identified as *Cryptosporidium* cervine genotype)

Abbreviations: *n*, numbers in parentheses are number of positive samples genotypes for each species or genotype

model implicitly incorporates some of the heterogeneity [49]. Nevertheless, we investigated several factors that can contribute to the observed heterogeneity. The diagnostic method used for the detection of *Cryptosporidium* infection was one of the main confounding variables. For example, the pooled prevalence of bovine *Cryptosporidium* infection was estimated 29.1% using PCR compared to 22.5% using conventional microscopy. This seems to indicate that molecular methods such as PCR are highly sensitive and specific for the detection of *Cryptosporidium* infection, but compared with conventional microscopic methods, they are more expensive and require a higher degree of expertise [50].

There are geographical differences in the estimated pooled prevalence of *Cryptosporidium* infection. The prevalence was highest in the continent of America, followed by Europe, Australia, Asia and Africa. Canada had the highest prevalence among countries. Study design, time of sampling, age of animals, and conditions of keeping animals are other factors that can contribute to the observed heterogeneity in cryptosporidiosis prevalence, in addition to the nature of animal management.

The outcome of our study is probably affected by the publication bias. Publication bias occurs when the results of studies affect the likelihood of their inclusion in the systematic review and meta-analysis [49]. Our systematic review was limited to studies published after 1984 in English. Moreover, many studies did not provide enough information to be included in the meta-analysis.

Conclusions

Results of the meta-analysis suggest that *Cryptosporidium* infection is highly prevalent in ungulates, especially ruminants. Geographical differences in *Cryptosporidium* prevalence and distribution of *Cryptosporidium* species are seen for most domestic ungulate hosts. These within-host-species differences could be partially attributed to differences in animal management among geographical regions. The highest prevalence in farmed ungulates occurs in America and Europe where CAFO is widely practiced. The major farm animal hosts of *Cryptosporidium* spp. appear to be cattle, buffalo, sheep and pigs. These farm animals are potent reservoirs for a variety of *Cryptosporidium* species. *Cryptosporidium* prevalence is also clearly higher in farmed animals than in wild ungulate populations. Inter-species transmission of *Cryptosporidium* spp. appears to be affected by contact with other host species (humans or other animals) and infection pressure (intensive farming), rendering the investigated ungulate hosts capable of propagating both zoonotic and non-zoonotic *Cryptosporidium* species.

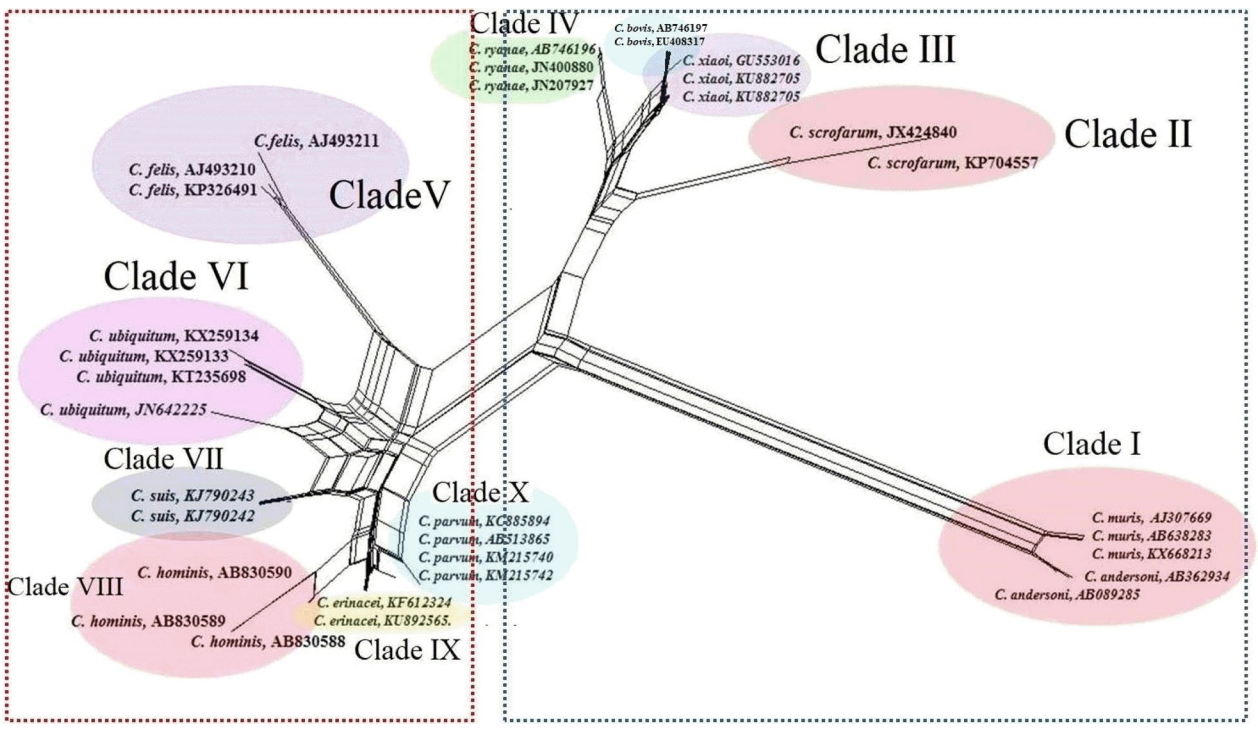

Fig. 9 The phylogeny of *Cryptosporidium* spp

Supplementary information

Supplementary information accompanies this paper at https://doi.org/10.1186/s13071-019-3704-4.

Additional file 1: Table S1. PRISMA checklist.

Additional file 2: Table S2. Worldwide prevalence of *Cryptosporidium* spp. in herbivorous animals.

Abbreviations

CM: conventional microscopy; ELISA: enzyme-linked immunosorbent assay; ICT: immunochromatographic test; PCR: polymerase chain reaction; PRISMA: Preferred Reporting Items for Systematic Reviews and Meta-Analyses; QLAT: quantitative latex agglutination test.

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Authors' contributions

KHN, EH, DC and LX contributed to the design of the study. KHN, EA and AS conducted the systematic review of the literature and extracted data. EA, AS, DC and LX analyzed data and drafted the first version of the manuscript. EA, DC, BB and LX contributed to the interpretation of data and writing of the first draft. All authors read and approved the final manuscript.

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Availability of data and materials

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Competing interests

The authors declare that they have no competing interests.

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