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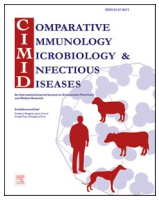

Global prevalence and genetic diversity of *Cryptosporidium* spp. in pigeons: A systematic review and meta-analysis

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ABSTRACT

Cryptosporidium spp. are globally important protozoan pathogens infecting many vertebrates, including birds. Pigeons, which live in close contact with humans, may contribute to environmental contamination and zoonotic transmission, yet their infection patterns have not been comprehensively reviewed. We conducted a systematic search of international databases from inception to November 25, 2025, identifying 52 eligible studies. A random-effects meta-analysis was performed using Comprehensive Meta-Analysis (CMA) software, with subgroup analyses by continent, country, publication year, sample size, age, sex, and diagnostic method. Heterogeneity was assessed using the I^2 statistic, publication bias using funnel plots and Egger's test, and robustness through sensitivity analysis. Univariable random-effects meta-regression examined potential sources of heterogeneity. The pooled global prevalence of *Cryptosporidium* spp. in pigeons was 10 % (95 % CI: 6.9–14.4 %), with substantial heterogeneity (I^2 = 95.2 %). Prevalence differed significantly by continent, publication year, and sample size. Higher infection rates were reported in younger pigeons, whereas sex and diagnostic method showed minimal impact. Sequential study exclusion did not materially alter the pooled estimate. Funnel-plot asymmetry and Egger's test (p = 0.01) indicated significant publication bias. Meta-regression identified publication year and sample size as significant predictors of variability, though considerable residual heterogeneity persisted. Winter exhibited the highest detection rate. Eight species and seven gp60 subtypes were reported, including five zoonotic species (*C. meleagridis*, *C. parvum*, *C. hominis*, *C. andersoni*, and *C. muris*). These findings highlight the potential zoonotic relevance of *Cryptosporidium* spp. detected in pigeons and reinforce the need for improved surveillance and molecular characterization within a One Health framework.

1. Introduction

Cryptosporidium is a genus of apicomplexan protozoa responsible for cryptosporidiosis, an enteric disease affecting a wide range of vertebrate hosts, including humans [1]. Infection is mainly acquired through the fecal-oral route, either by ingestion of contaminated water or food or through direct contact with infected animals or their feces [2]. The disease is characterized by watery diarrhea, abdominal cramps,

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dehydration, and fever. While immunocompetent individuals typically experience self-limiting illness, *Cryptosporidium* spp. can cause severe, persistent, and potentially life-threatening disease in immunocompromised persons, including young children, the elderly, and individuals with HIV/AIDS or other causes of impaired immunity [3–5]. Oocysts are environmentally robust, highly infectious, and resistant to many disinfectants, allowing them to persist in water sources and contribute to large outbreaks [6]. Consequently, *Cryptosporidium* spp. is now recognized as one of the leading parasitic causes of diarrhea globally and is listed among high-priority organisms by international public-health agencies [7].

Advances in molecular diagnostics during the past two decades have revealed extensive genetic diversity within the genus. Around 47 species and more than 120 genotypes have been identified. Among these, *C. hominis* and *C. parvum* are the predominant causes of human cryptosporidiosis worldwide. Other species, such as *C. meleagridis*, *C. felis*, *C. canis* and *C. ubiquitum*, also possess zoonotic potential and have been increasingly reported in human infections [8,9]. This growing recognition of the zoonotic and multi-host nature of *Cryptosporidium* spp. supports a One Health perspective, emphasizing interconnectedness among human, animal, and environmental health. The detection of genetically identical subtypes across animal and human populations further reinforces the epidemiological relevance of animal reservoirs in sustaining transmission cycles [10].

Although mammals, particularly ruminants [11–13], dogs [14], cats [15], pigs [16], camels [17], and rodents [18], have been widely studied as reservoirs of *Cryptosporidium* spp., birds represent an understudied yet important host group. Avian species can harbor both bird-adapted and zoonotic *Cryptosporidium* species. For example, *C. meleagridis*, currently the third most common cause of human cryptosporidiosis, was originally considered primarily a bird parasite before its widespread recognition in human infections [9]. Similarly, avian populations may carry *C. parvum* and *C. hominis*, both of which are important human pathogens. Birds can contaminate water bodies, agricultural environments, animal housing, and public spaces through shedding of oocysts, thereby contributing to indirect exposure pathways. The ecological plasticity and high mobility of birds may further facilitate the wider dissemination of *Cryptosporidium* spp. in the environment [19].

Within avian hosts, pigeons hold particular epidemiological interest. These birds inhabit virtually all major cities worldwide and thrive in rural and peri-urban areas, often living in close proximity to human populations, livestock, domestic animals, and shared water resources. Their feeding and roosting behaviors, high population density in urban settings, and constant interaction with human infrastructure, buildings, markets, parks, and food-production areas create potential opportunities for cross-species transmission [20]. Pigeons may therefore act as carriers or amplifiers of *Cryptosporidium* spp., shedding infectious oocysts that contaminate the surrounding environment [19]. Despite this, the global epidemiology of *Cryptosporidium* spp. in pigeons remains poorly characterized. Existing studies are scattered geographically, vary widely in their diagnostic methods, and differ substantially in sample sizes, age groups, and reporting quality. Moreover, only a subset of studies conducts molecular typing, limiting understanding of species distribution and zoonotic relevance.

The present systematic review and meta-analysis aim to address these gaps by providing the first global synthesis of *Cryptosporidium* spp. infection in pigeons. By aggregating prevalence estimates, examining host- and study-level factors, and summarizing available molecular evidence, this study seeks to clarify the epidemiological role of pigeons in the transmission ecology of *Cryptosporidium* spp. and to inform future research, surveillance strategies, and public-health interventions.

2. Methods

2.1. Study design and reporting framework

This study was conducted as a systematic review and meta-analysis to estimate the global prevalence and species/subtype distribution of *Cryptosporidium* spp. infection in pigeons. The review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [21]. All steps, including search strategy, study selection, data extraction, risk-of-bias assessment, and quantitative synthesis, were performed independently by two reviewers, with discrepancies resolved through discussion.

2.2. Search strategy

A comprehensive search of five international databases, PubMed, Web of Science, Scopus, ScienceDirect, and Google Scholar, was performed from database inception to November 25, 2025. The search terms combined controlled vocabulary and free-text keywords related to *Cryptosporidium* spp. and *pigeons* (e.g., "*Cryptosporidium* spp.," "cryptosporidiosis," "*Cryptosporidium* infection," "prevalence," "pigeon," "bird," "avian"). Boolean operators ("AND," "OR"), phrase matching, and MeSH terms (when available) were applied. No restrictions were placed on language, study design, or geographic location at the search stage. Reference lists of all eligible studies were screened to identify additional relevant publications.

2.3. Eligibility criteria

Studies were eligible for inclusion if they met all the following criteria: 1) Original research reporting the presence or prevalence of *Cryptosporidium* spp. in pigeons or mixed avian samples with extractable pigeon-specific data, 2) cross-sectional, observational, or surveillance studies reporting primary data, 3) clear reporting of total sample size and number of positive pigeon cases, 4) use of microscopic, molecular, or combined diagnostic methods, and 5) full-text availability. Studies were excluded for any of the following reasons: a) duplicate publication of the same dataset in more than one language, b) absence of pigeon-specific denominators/total number examined or number positive, c) ambiguous, conflicting, or uninterpretable results, d) experimental infection studies, e) reviews, f) case reports, g) outbreak descriptions without prevalence data, h) conference abstracts, i) non-original research, and j) studies lacking full-text access after exhaustive retrieval attempts.

2.4. Quality assessment

Study quality was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies, consisting of eight items [22]. Each item was scored as: Yes = 1 point, No = 0 points, and Unclear = 0.5 points. Total scores were categorized as follows: low quality: ≤ 3.5, moderate quality: 4–6.5, and high quality: 7–8.

2.5. Statistical analysis

All statistical analyses were conducted using Comprehensive Meta-Analysis (CMA) software, version 3 [23]. Pooled prevalence estimates were calculated using the random-effects model with 95 % confidence intervals (CIs), based on the assumption of substantial expected heterogeneity across countries and diagnostic approaches [24]. Heterogeneity was quantified using the I^2 statistic, with values ≥ 75 % considered indicative of high heterogeneity. To explore sources of heterogeneity, prespecified subgroup analyses were conducted by continent, country, publication year, sample size, diagnostic method, age group, and sex. To further assess the contribution of study-level variables to heterogeneity, univariable random-effects meta-regression was performed for

publication year and sample size. The R^2 analog was used to estimate the proportion of between-study variance explained. Publication bias was assessed visually using funnel plots and statistically using Egger's regression test, with $p < 0.05$ considered evidence of significant bias. A sensitivity analysis was conducted by removing one study at a time to evaluate the stability of the pooled estimates. Because seasonal data lacked complete denominators, and species/subtype data were incomplete in many studies, seasonality and genetic diversity were summarized descriptively rather than meta-analytically. All statistical tests were two-tailed, and $p < 0.05$ was interpreted as statistically significant.

3. Results

3.1. Study selection

The systematic search retrieved a total of 7451 records across the five international databases using predefined keywords related to *Cryptosporidium* spp. and pigeons. The distribution of records by database was as follows: PubMed (1184 records), Web of Science (1362 records), Scopus (2145 records), ScienceDirect (1068 records), and Google Scholar (1692 records). After merging all records, 2947 duplicates were identified and removed, leaving 4504 unique records for title and abstract screening. Following this stage, 4434 records were excluded because they were unrelated to *Cryptosporidium* spp., did not involve pigeons, were non-original reports (reviews, conference abstracts), or clearly failed to meet inclusion criteria. A total of 65 articles were retrieved for full-text assessment. During the full-text review, 13 studies were excluded for the following reasons: duplicate publication of the same study in two languages (n = 3), lack of pigeon-specific sample size or number of positive cases (n = 7), or unclear, contradictory, or uninterpretable results (n = 3). Ultimately, 52 studies met all eligibility criteria and were included in the present meta-analysis [25–76] (Fig. 1).

3.2. Characteristics of included studies

The 52 included studies were published between 2008 and 2025 and together represent the complete body of published evidence on *Cryptosporidium* spp. in pigeons identified by our searches. Individual study

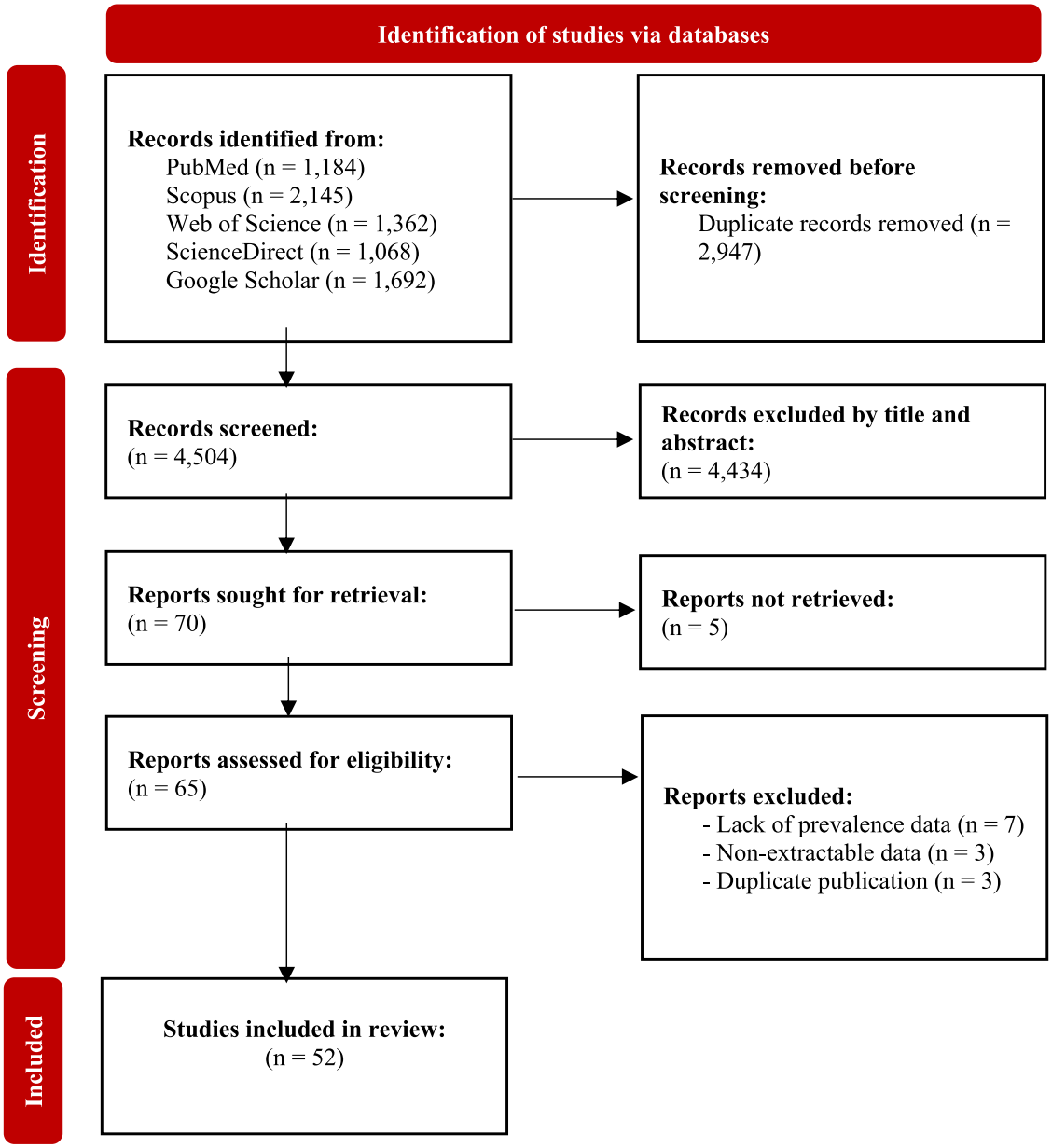

Fig. 1. The PRISMA 2020 flow diagram depicting the process of included studies in the present systematic review.

sample sizes ranged from 2 to 1625 pigeons, and the total number of pigeon samples included across studies was 8760. Studies originated from 16 countries across four continents (Africa, Asia, Europe and South America). The largest contributors were Iraq (10 studies), Iran (9 studies), China (7 studies), Egypt (5 studies), Brazil (4 studies) and Turkey (3 studies); all remaining countries contributed one or two studies each. Regarding diagnostic approach, 27 studies used microscopy-based methods while 25 studies employed molecular techniques for detection and/or characterization of *Cryptosporidium* spp. Four studies reported prevalence stratified by sex, eight reported age-group stratified prevalence, and seven provided descriptive information on seasonality (Table 1 and Table 2).

3.3. Quality assessment

Study quality was appraised using the JBI checklist for prevalence studies (eight items), which is appropriate for cross-sectional designs reporting infection prevalence. Based on this instrument, all included studies were judged to be of moderate quality (score range 4–6.5 out of 8). The primary, recurring methodological shortcoming was inadequate handling or reporting of potential confounding factors and of strategies for their identification and control in the statistical analysis; this deficiency limited the internal validity of many prevalence estimates (Supplementary Table 1).

3.4. Weighted prevalence of Cryptosporidium spp. in pigeons

The pooled prevalence of *Cryptosporidium* spp. infection in pigeons was 10 % (95 % CI: 6.9–14.4 %), and substantial between-study heterogeneity was observed (I^2 = 95.2 %, P < 0.001) (Fig. 2). Given the substantial between-study heterogeneity, the pooled prevalence should be interpreted as an overall average across highly diverse epidemiological settings rather than a precise global estimate.

3.5. Genetic diversity of Cryptosporidium spp. in pigeons

In this review, a total of eight *Cryptosporidium* species and seven gp60 subtypes were identified in pigeons across the included studies. The detected species comprised *C. baileyi*, *C. meleagridis*, *C. parvum*, *C. hominis*, *C. muris*, *C. galli*, *C. andersoni*, and *C. ornithophilus*. Reported gp60 subtypes included IIIaA20G4R1, IIIlA8G2R1, and IIIbA21G1R1 for *C. meleagridis*, and IIaA16G1R1, IIaA15G2R1, IIdA20G1, and IIdA19G1 for *C. parvum*. Because the majority of studies did not perform species-level or subtype characterization and instead reported infections broadly as *Cryptosporidium* spp., and because several species lacked complete information on total samples and positive cases, a quantitative meta-analysis of genetic diversity was not feasible. Consequently, species and subtype findings were summarized descriptively. It should be noted that in studies relying solely on microscopy, avian-adapted *Cryptosporidium* species may have been under- or overestimated due to morphological similarities between species. Based on the available data, the most frequently reported species in pigeons were *C. baileyi*, *C. meleagridis*, and *C. parvum* (Table 1).

3.6. Subgroup-based prevalence of Cryptosporidium spp. in pigeons

Overall pooled prevalence estimates of *Cryptosporidium* spp. in pigeons varied substantially by subgroup (Table 2). Pooled prevalence increased from 6.2 % (95 % CI: 3.3–11.4 %) in studies published 2008–2017–14.1 % (95 % CI: 8.9–21.7 %) in 2018–2025 (Supplementary Fig. 1). By continent, Africa showed the highest pooled prevalence (19.9 %, 95 % CI: 10.2–35.1 %) while Europe showed the lowest (3.1 %, 95 % CI: 2.2–4.4 %) (Supplementary Fig. 2). Studies with sample size ≤ 100 reported higher pooled prevalence (14.7 %, 95 % CI: 10–21 %) than studies with > 100 samples (6.5 %, 95 % CI: 3.5–12 %) (Supplementary Fig. 3). The diagnostic method had little influence on the estimated prevalence, with microscopy (10.3 %, 95 % CI: 6.2–16.9 %) and molecular techniques (9.6 %, 95 % CI: 5.4–16.6 %) yielding comparable pooled estimates (Supplementary Fig. 4). Age and sex subgrouping suggested a higher pooled prevalence in young birds (29 %, 95 % CI: 15–48.5 %) compared with adults (15 %, 95 % CI: 5.5–35.1 %) (Supplementary Fig. 5), and a similar prevalence between males and females (≈30 %) (Supplementary Fig. 6). At the country level, notable extremes included very low pooled prevalence in Italy (0 %, 95 % CI: 0–21.5 %), and high point estimates in single-study countries such as India (50.0 %, 95 % CI: 22.5–77.5 %) and Venezuela (38.5 %, 95 % CI: 34.4–42.8) (Supplementary Fig. 7). Heterogeneity was frequently high (many I^2 values >75 %), indicating substantial between-study variation across most subgroup analyses. Finally, seasonal data were reported in only eight of the 52 included studies: seven reported winter as the season with the highest *Cryptosporidium* spp. detection and one reported summer as the peak. Seasonal findings, including the higher detection rate observed in winter, are reported descriptively and were not meta-analyzed due to incomplete seasonal sample data across studies; therefore, these observations should be considered hypothesis-generating rather than indicative of a causal association. (Table 1).

3.7. Sensitivity analysis

Sequential exclusion of individual studies did not materially alter the overall prevalence estimate, indicating the robustness of the findings (Supplementary Fig. 8).

3.8. Meta-regression analysis

Two univariable random-effects meta-regression models were conducted to explore sources of heterogeneity (Fig. 3). Publication year was significantly associated with the logit prevalence of *Cryptosporidium* spp. infection (coefficient = 0.1031, SE = 0.0409, p = 0.0118), indicating an increasing trend in reported prevalence over time. However, the model explained only a small proportion (4 %) of between-study variance (R^2 = 0.04), and residual heterogeneity remained high (I^2 = 94.91 %). Sample size was also a significant predictor of prevalence (coefficient = –0.0019, SE = 0.0007, p = 0.0038), suggesting that studies with smaller sample sizes tended to report higher prevalence. This model accounted for 17 % of between-study variance (R^2 = 0.17), yet substantial heterogeneity persisted (I^2 = 94.10 %). Together, these findings indicate that although publication year and sample size contribute to variability in reported prevalence, they do not fully explain the substantial heterogeneity observed across studies.

3.9. Publication bias

Visual inspection of the funnel plot suggested noticeable asymmetry. This was confirmed statistically by Egger's regression test, which demonstrated significant publication bias (p = 0.01). These findings indicate that smaller studies with higher prevalence estimates may have been more likely to be published or included, potentially influencing the pooled effect size (Fig. 4).

4. Discussion

Although numerous systematic reviews and meta-analyses have evaluated *Cryptosporidium* spp. prevalence in a variety of domestic and wild animals, our analysis on pigeons fills a clear gap in the literature, especially given the close proximity of pigeons to human populations in urban and rural settings. For instance, a global meta-analysis on pigs estimated a pooled prevalence of 16.3 % (95 % CI 15.0–17.6 %) across 131 datasets from 36 countries [16]. A systematic review in camels yielded a pooled prevalence of 13.8 % (95 % CI 10.3–18.4 %) in 7372 individuals from multiple countries [17]. In cats, the global pooled prevalence was lower, around 6 % (95 % CI 4–8 %) [15]. In dairy cattle,

Table 1
Main characteristics of the 52 studies included in the present study on the prevalence and genetic diversity of *Cryptosporidium* spp. in pigeons.

Author, year	Time tested	Country	Total no.	Infected no.	Prevalence (%)	Species (n)/subtypes	Detection method	Highest frequency by season
Mirzaei, 2008	2005–2006	Iran	400	10	2.5	*Cryptosporidium* spp. (10)	MIC	Winter
QunShan, 2008	UC	China	1625	16	1	*C. baileyi*, *Cryptosporidium* spp.	MIC	-
Gul, 2009	UC	Turkey	145	0	0		MIC	-
Abreu-Acosta, 2009	2005	Spain	34	2	5.9	*C. hominis* (2)	MOL	-
Al-Mahmood, 2011	2007–2008	Iraq	50	15	30	*C. baileyi* (8), *Cryptosporidium* spp. (7)	MIC	-
Qi, 2011	2008–2009	China	21	1	4.8	*C. meleagridis* (1)	MOL	-
Radfar, 2012	2008–2009	Iran	102	3	2.9	*Cryptosporidium* spp. (3)	MIC	-
Bahrami, 2012	2011	Iran	250	3	1.2	*Cryptosporidium* spp. (3)	MIC	-
Bamaiyi, 2013	UC	Nigeria	41	1	2.4	*Cryptosporidium* spp. (1)	MIC	-
Faraj, 2014	2013	Iraq	120	48	40	*C. meleagridis*, *C. baileyi*, *C. galli*	MIC	Winter
Koompapong, 2014	2012	Thailand	70	1	1.4	*C. meleagridis* (1)	MOL	-
Badparva, 2015	2011–2012	Iran	37	1	2.7	*Cryptosporidium* spp. (1)	MIC	-
Reboredo-Fernandez, 2015	2007–2009	Spain	10	1	10	*Cryptosporidium* spp. (1)	MOL	-
Li, 2015	2012–2013	China	244	2	0.8	*C. baileyi* (1), *C. meleagridis* (1)	MOL	-
Jasim and Marhoon, 2015	2013–2014	Iraq	30	8	26.7	*C. parvum* (2), *C. baileyi* (2), *Cryptosporidium* spp. (4)	MOL	-
Mustapha, 2016	UC	Nigeria	8	0	0	-	MIC	-
Marenzoni, 2016	UC	Italy	100	0	0	-	MIC, SER	-
Mirzaghavami, 2016	2012–2013	Iran	40	1	2.5	*Cryptosporidium* spp. (1)	MIC	-
Li, 2016	UC	China	4	1	25	*C. baileyi* (1)	MOL	-
Kılınc, 2016	2015	Turkey	32	5	15.6	*Cryptosporidium* spp. (5)	MIC	-
De Pina Costa and Bomfim, 2016	UC	Brazil	387	53	13.7	*Cryptosporidium* spp. (53)	MOL	-
Khalil, 2017	2015–2016	Iraq	50	34	29.5	*Cryptosporidium* spp. (34)	MIC	-
Roy and Rahman, 2017	2016	Bangladesh	65	9	13.8	*C. baileyi* (9)	MIC	-
Da Cunha, 2017	2013–2014	Brazil	2	0	0	-	MOL	-
Oliveira, 2017	UC	Brazil	100	7	7	*C. parvum* (6), *Cryptosporidium* spp. (1)	MOL	-
Cazorla Perfetti, 2019	2017–2018	Venezuela	516	199	38.5	*Cryptosporidium* spp. (199)	MIC	-
Mehmood, 2019	2015–2016	India	10	5	50	*Cryptosporidium* spp. (5)	MIC	-
Kabir, 2020	UC	Bangladesh	4	2	50	*C. baileyi* (1), *C. meleagridis* (1)/IIIbA21G1R1	MOL	-
Altamimi and Al-Zubaidi, 2020a	2019	Iraq	100	11	11	*C. baileyi* (9), *C. parvum* (2)	MOL	-
Altamimi and Al-Zubaidi, 2020b	2019	Iraq	100	21	21	*C. meleagridis* (13), *C. baileyi* (7), *C. hominis* (1)	MOL	-
Dos Santos, 2020	2018	Brazil	50	9	18	*Cryptosporidium* spp. (18)	MIC	-
Khalifa, 2020	2018	Egypt	50	10	20	*Cryptosporidium* spp. (10)	MIC	-
Liao, 2021	2018	China	28	1	3.6	*C. muris* (1)	MOL	-
Dong, 2021	2018–2019	China	428	1	0.2	*C. parvum* (1)	MOL	-
Ebani, 2021	2016	Italy	22	0	0	-	MOL	-
Gholami-Ahangaran, 2022	2018	Iran	100	6	6	*Cryptosporidium* spp. (6)	MOL	Winter
Alhasnawi, 2022	2020–2021	Iraq	250	30	12	*Cryptosporidium* spp. (12)	MIC	-
Adhikari, 2022	2020	Nepal	155	5	3.2	*Cryptosporidium* spp. (5)	MIC	-
Gokpınar, 2023	UC	Turkey	105	9	8.6	*Cryptosporidium* spp. (9)	MIC	-
Albogami, 2023	2022	Saudi Arabia	212	17	8	*Cryptosporidium* spp. (17)	MIC	-
Abou Elez, 2023	2021–2022	Egypt	150	29	19.3	*C. parvum* (7), *Cryptosporidium* spp. (22)	MOL	-
Mirzaghavami, 2023	2012–2019	Iran	100	2	2	*C. parvum* (2)/IIdA20G1, IIdA19G1	MOL	-
Khamar, 2024	UC	Iran	135	4	0.3	*Cryptosporidium* spp. (4)	MIC	Winter
Hashim and Al Zubaidi, 2024	2022–2023	Iraq	120	85	70.8	*Cryptosporidium* spp. (85)	MOL	Winter
Essam, 2024	2022–2023	Egypt	57	15	26.3	*Cryptosporidium* spp. (15)	MIC	Summer
Khordadmehr, 2024	2021	Iran	100	62	62	*C. parvum* (4), *C. meleagridis* (1), *Cryptosporidium* spp. (57)	MOL	-
Holubova, 2024	UC	Czech Republic	940	27	2.9	*C. meleagridis* (10)/IIIaA20G4R1, IIIlA8G2R1, *C. baileyi* (5), *C. parvum* (4)/IIaA16G1R1, IIaA15G2R1, *C. andersoni* (2), *C. muris* (2), *C. galli* (2), *C. ornithophilus* (2)	MOL	-
Abdullah, 2024	2021–2022	Iraq	45	16	35.5	*Cryptosporidium* spp. (16)	MIC	-
Li, 2025	2023	China	376	7	1.9	*C. meleagridis* (7)	MOL	-
El-Salama, 2025	2023–2024	Egypt	140	68	48.6	*Cryptosporidium* spp. (68)	MIC	Winter
Al Qasimi and Alshaebani, 2025	2024–2025	Iraq	50	12	24	*Cryptosporidium* spp. (12)	MOL	-
Gamal, 2025	UC	Egypt	450	56	12.4	*C. meleagridis*, *C. baileyi*	MOL	Winter

UC: unclear, MIC: microscopic detection, MOL: molecular detection, SER: serological detection

Table 2
Subgroup analysis of *Cryptosporidium* spp. prevalence in pigeons according to publication year, continent, sample size, country, sex, age group, and diagnostic method.

Subgroup variable	Prevalence % (95 % CI)	Heterogeneity (Q)	No. studies	df (Q)	I^2 (%)	P-value
Publication year						
2008–2017	6.2 (3.3–11.4)	306.3	25	24	92.2	$P < 0.05$
2018–2025	14.1 (8.9–21.7)	665.4	27	26	96.1	$P < 0.05$
Continent						
Africa	19.9 (10.2–35.1)	81.6	7	6	92.6	$P < 0.05$
Asia	8.6 (5–14.3)	716.2	35	34	95.3	$P < 0.05$
Europe	3.1 (2.2–4.4)	3.8	5	4	0	$P > 0.05$
South America	17.2 (7.3–35.5)	84.4	5	4	95.3	$P > 0.05$
Sample size						
≤ 100	14.7 (10−21)	176.1	31	30	82.9	$P < 0.05$
> 100	6.5 (3.5–12)	874.8	21	20	97.7	$P < 0.05$
Country						
Bangladesh	24 (5.3–64.1)	3	2	1	66.4	$P > 0.05$
Brazil	12.7 (8.8–18.1)	4.3	4	3	31.1	$P > 0.05$
China	1.7 (0.8–3.7)	16.3	7	6	63.1	$P > 0.05$
Czech Republic	2.9 (2–4.2)	0	1	0	0	$P > 0.05$
Egypt	23.7 (12.2–40.9)	75.4	5	4	94.7	$P < 0.05$
India	50 (22.5–77.5)	0	1	0	0	$P > 0.05$
Iran	3.5 (0.7–16)	211.1	9	8	96.2	$P < 0.05$
Iraq	28.2 (17.3–42.5)	135.2	10	9	93.3	$P < 0.05$
Italy	0 (0–21.5)	0	2	1	0	$P > 0.05$
Nepal	3.2 (1.3–7.5)	0	1	0	0	$P > 0.05$
Nigeria	2.3 (0.3–14.9)	0.1	2	1	0	$P > 0.05$
Saudi Arabia	8 (5–12.5)	0	1	0	0	$P > 0.05$
Spain	7 (2.3–19.6)	0.2	2	1	0	$P > 0.05$
Thailand	1.4 (0.2–9.4)	0	1	0	0	$P > 0.05$
Turkey	9.5 (3.5–23.3)	4.5	3	2	55.9	$P > 0.05$
Venezuela	38.5 (34.4–42.8)	0	1	0	0	$P > 0.05$
Sex						
Female	30.6 (8.1–68.9)	64.1	4	3	95.3	$P < 0.05$
Male	31.1 (14–55.4)	31.9	4	3	90.6	$P < 0.05$
Age group						
Adult	15 (5.5–35.1)	123.4	8	7	94.3	$P < 0.05$
Young	29 (15–48.5)	46.9	8	7	85.1	$P < 0.05$
Diagnostic method						
MIC	10.3 (6.2–16.9)	544.5	27	26	95.2	$P < 0.05$
MOL	9.6 (5.4–16.6)	488.2	25	24	95.1	$P < 0.05$

a more targeted meta-analysis estimated infection by *C. andersoni* at 4.7 % (95 % CI 4.5–4.9 %) [11]. Although the host species, husbandry conditions, age distributions, and diagnostic methods differ widely across these studies, the overall 10 % (95 % CI: 6.9–14.4 %) pooled prevalence found in pigeons lies within, or not far from, the range reported for other animals. This suggests that pigeons might harbour levels of *Cryptosporidium* spp. infection comparable to many domesticated mammals and companion animals. Given that pigeons are often free-ranging, inhabit public spaces, and often live in close contact with humans (especially in urban or peri-urban areas), a 10 % prevalence is epidemiologically meaningful, even if lower or similar to some livestock species, the risk for environmental contamination and zoonotic spillover remains nontrivial.

In the present review, eight *Cryptosporidium* species were identified in pigeons: *C. baileyi*, *C. meleagridis*, *C. parvum*, *C. hominis*, *C. muris*, *C. galli*, *C. andersoni*, and *C. ornithophilus*, along with seven gp60 subtypes belonging to *C. meleagridis* (IIIaA20G4R1, IIIlA8G2R1, IIIbA21G1R1) and *C. parvum* (IIaA16G1R1, IIaA15G2R1, IIdA20G1, IIdA19G1). When these findings are compared with the broader global diversity of *Cryptosporidium* spp. known to infect humans [8,9], currently comprising 20 species and three genotypes, including major zoonotic pathogens such as *C. hominis, C. parvum, C. meleagridis, C. canis, C. felis, C. ubiquitum, C. cuniculus, C. viatorum, C. muris, C. andersoni, C. erinacei, C. tyzzeri, C. bovis, C. suis, C. scrofarum, C. occultus, C. xiaoi, C. fayeri, C. ditrichi, C. mortiferum,* and several host-adapted genotypes (e.g., mink genotype, skunk genotype, and horse genotype), it becomes evident that at least five of the species detected in pigeons in this study (*C. meleagridis*, *C. parvum*, *C. hominis*, *C. muris*, and *C. andersoni*) are recognized human pathogens. Moreover, the presence of zoonotic gp60 subtype families (IIa, IId, and IIIa/IIIb/IIIl) further underscores the potential for pigeons to harbour and disseminate subtypes that are epidemiologically relevant to human cryptosporidiosis [9]. Although this does not confirm direct transmission from pigeons to humans, the overlap between pigeon-derived species/subtypes and those regularly reported in human infections supports the biological plausibility of pigeons acting as environmental reservoirs or indirect contributors to zoonotic exposure pathways.

Interpretation of species and subtype patterns should consider several limitations. A large proportion of included studies did not perform molecular characterization and reported infections only as *Cryptosporidium* spp., which restricts the ability to assess the full spectrum of genetic diversity present in pigeon populations. In addition, some species identifications in microscopy-based studies relied solely on morphological features, which can lead to misclassification or overestimation of certain species due to the limited discriminatory capacity of microscopic examination. The incomplete reporting of total samples and positive cases for specific species further constrained the ability to conduct quantitative analyses. These limitations suggest that the species distribution reported here likely underrepresents the true diversity of *Cryptosporidium* spp. circulating in pigeons and that additional, yet-undetected species or subtypes may be present. From a public-health perspective, the detection of zoonotic species and subtypes in pigeons, particularly in urban environments or areas of close human-bird interaction, points to a potential role for pigeons in environmental contamination and transmission pathways. Although direct transmission from pigeons to humans has not been conclusively demonstrated, their widespread distribution, free-ranging behaviour, and frequent presence in public spaces create opportunities for indirect exposure through contaminated water, soil, feed, or fomites. Preventive measures such as improved sanitation in areas with high pigeon density, proper

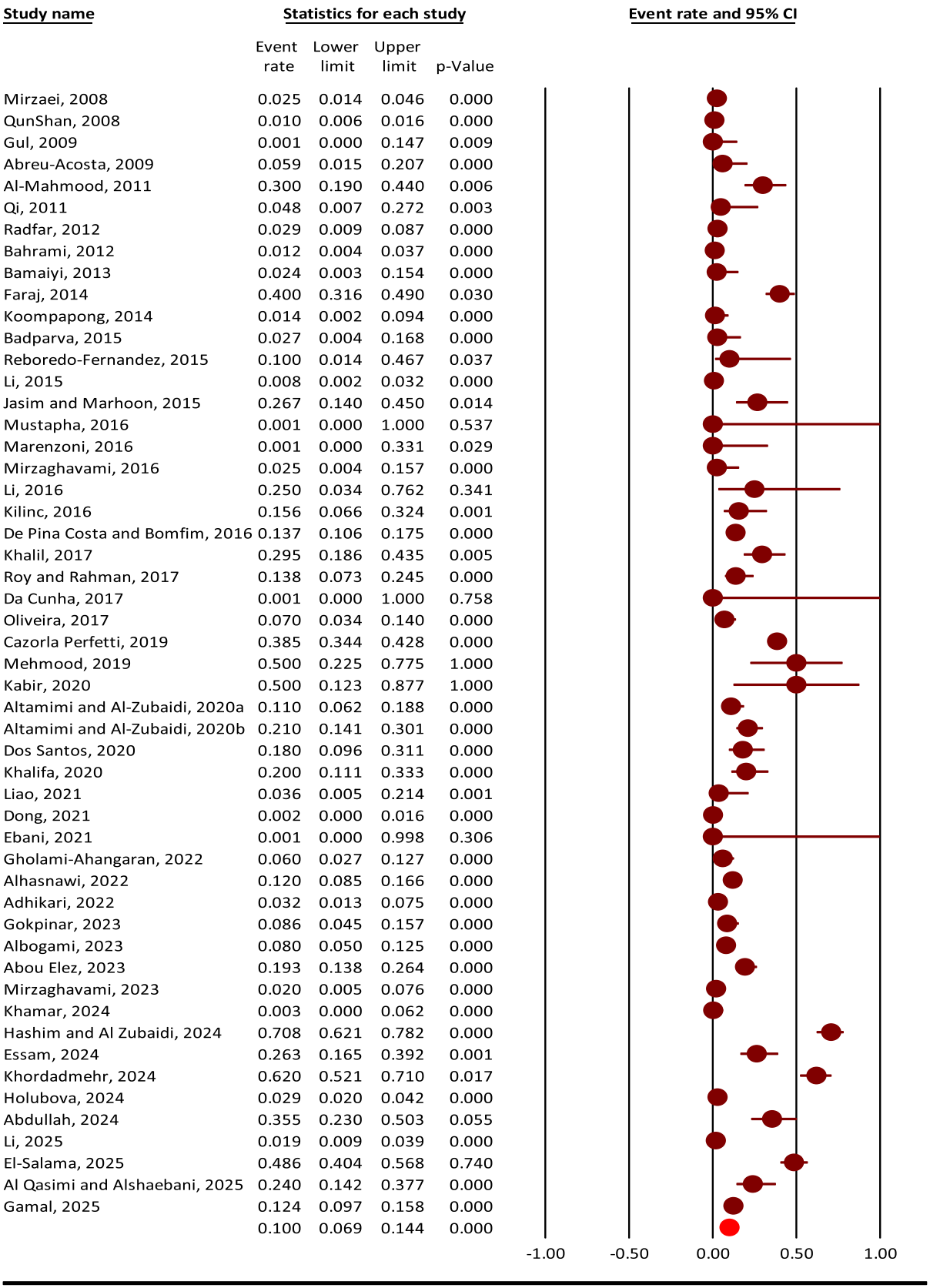

Fig. 2. Forest plot showing the prevalence of *Cryptosporidium* spp. in pigeons. Each horizontal brown line represents the 95 % confidence interval (CI) for the prevalence reported in an individual study. The brown circles indicate the point estimate (event rate) for each study. The red circle at the bottom summarizes the pooled prevalence and its 95 % CI.

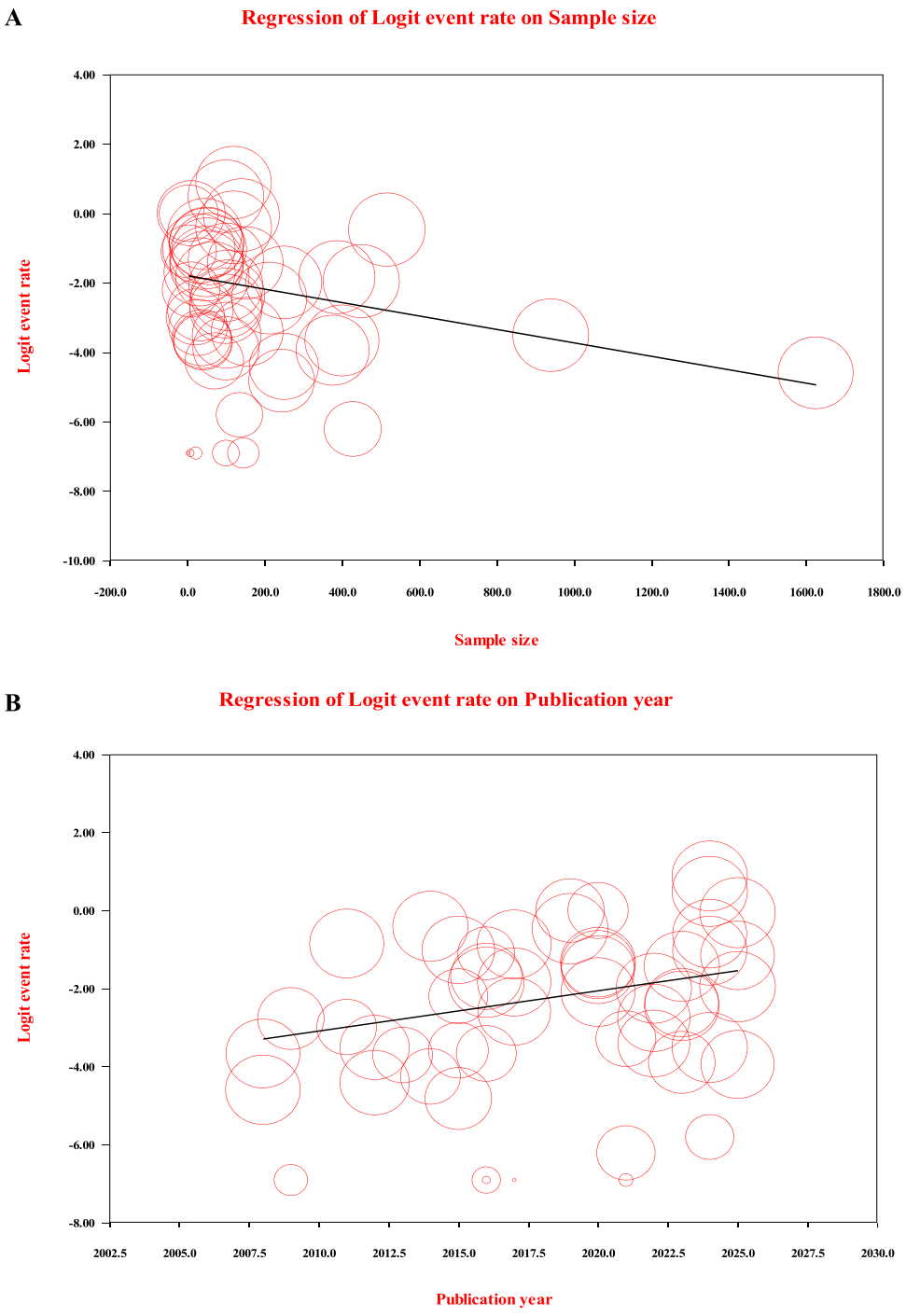

Fig. 3. Meta-regression analyses evaluating the effect of sample size (A) and publication year (B) on the prevalence of *Cryptosporidium* spp. in pigeons. Both variables showed statistically significant associations with prevalence ($P < 0.05$).

management of pigeon housing facilities, regular cleaning of droppings, and routine molecular surveillance of avian populations can help reduce environmental contamination and support early detection of zoonotic strains. Expanding molecular typing in future studies will be essential to clarify transmission pathways, assess zoonotic risk more accurately, and understand the broader One Health implications of *Cryptosporidium* spp. infection in pigeons.

When comparing the spectrum of *Cryptosporidium* species reported in pigeons with those documented in other animals, several interesting patterns emerge. In pigs [16], for example, seven species have been reported globally, including *C. scrofarum*, *C. suis*, *C. parvum*, *C. muris*, *C. tyzzeri*, *C. andersoni* and *C. struthioni*. In camels [17], a recent global review identified eight species: *C. parvum*, *C. andersoni*, *C. bovis*, *C. muris*, *C. ratti*, *C. occultus*, *C. ubiquitum*, and *C. hominis*. In cats [15], *C. felis* predominates, followed by *C. parvum* and rodent-associated genotypes. By contrast, in pigeons our review identified a distinct combination: eight species including *C. meleagridis*, *C. parvum*, *C. baileyi*, *C. hominis*, *C. muris*, *C. galli*, *C. andersoni*, and *C. ornithophilus*, and seven gp60 subtypes (among *C. meleagridis* and *C. parvum*) that are recognized in zoonotic infections. This overlap with species found in livestock and other mammals (notably *C. parvum*, *C. andersoni*, and *C. muris*) indicates that pigeons could share or exchange *Cryptosporidium* species with mammals, directly or indirectly, via environmental contamination. On the other hand, avian-adapted species like *C. baileyi*, *C. galli* and

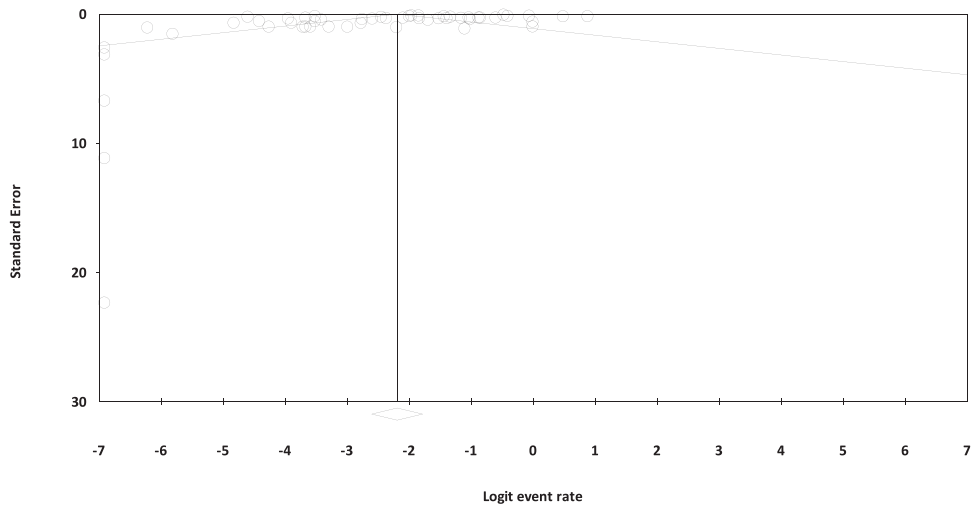

Fig. 4. Funnel plot assessing publication bias in studies reporting *Cryptosporidium* spp. prevalence in pigeons. Visual asymmetry, supported by Egger's regression test ($p < 0.05$), indicates the presence of significant publication bias.

C. ornithophilus appear characteristic of avian hosts and are not commonly reported in mammals; their presence underscores that avian hosts maintain a partly distinct *Cryptosporidium* spp. reservoir [77–79]. Thus, the species/subtype profile of pigeons reflects a dual role: partly as a "mammal-like" reservoir (for zoonotic species/subtypes) and partly as an avian-specific reservoir. This duality enhances the epidemiological importance of pigeons, especially in mixed human-animal-environment settings, and supports the view that pigeon populations might contribute to cross-species transmission cycles, or at least environmental persistence of *Cryptosporidium* spp. in urban ecosystems.

Findings from this systematic review and meta-analysis demonstrate that *Cryptosporidium* spp. infection in pigeons is globally widespread but highly variable across geographic regions, host-related factors, and methodological characteristics of the included studies. Considerable differences were evident among continents, with the highest pooled prevalence observed in African studies and the lowest in European reports, and country-level values ranged from very low estimates, such as those reported in Italy, Thailand, and China, to markedly high values that originated predominantly from single, small-sample investigations. The infection appeared more common in younger pigeons, a biologically plausible finding given their less-developed immunity, while sex and diagnostic method did not markedly influence prevalence. Prevalence estimates were also higher in studies with smaller sample sizes and in those published more recently, patterns that were, at least in part, consistent with findings from the meta-regression models. Although winter emerged descriptively as the season with the highest frequency of infection in most studies that reported seasonal data, the limited availability of seasonal denominators precluded quantitative analysis and rendered these findings hypothesis-generating rather than conclusive. Across all subgroup analyses, heterogeneity remained strikingly high, demonstrating that the observed variability reflects not only genuine regional and ecological differences but also substantial methodological diversity within the literature.

The presence of publication bias, confirmed by Egger's regression test, suggests that smaller studies reporting higher prevalence were more likely to be published or captured in the evidence base, which may have inflated the overall pooled estimates. This interpretation is further supported by the meta-regression analysis, where sample size showed a significant negative association with prevalence, indicating that smaller studies tended to report higher infection rates. Publication year was also significantly associated with prevalence, corroborating the subgroup finding of increasing prevalence in more recent publications; however, because this variable explained only a very small proportion of the total between-study variance, the temporal trend should be interpreted cautiously. Importantly, despite both variables reaching statistical significance, residual heterogeneity remained extremely high in all meta-regression models, indicating that these factors alone do not adequately explain the variability in findings. Moreover, all included studies were rated as having moderate methodological quality based on the JBI checklist. Because of the limited variability in quality scores across studies, quality score was not included as a covariate in meta-regression analyses, as it was unlikely to explain between-study heterogeneity. Taken together, the interplay between genuine epidemiological variation, differences in sampling frames, potential reporting and publication biases, ecological and climatic influences, and inconsistent study designs likely underlies the complex pattern of heterogeneity observed in this review. These findings highlight the need for standardized, adequately powered, and methodologically transparent studies, especially those reporting season-specific denominators and incorporating molecular typing, to better elucidate the epidemiology of *Cryptosporidium* spp. in pigeon populations.

This study provides the first comprehensive systematic review and meta-analysis focused exclusively on *Cryptosporidium* spp. infection in pigeons, integrating global data from diverse geographic regions, host populations, and diagnostic approaches. A major strength of the study is the broad scope of included literature and the application of rigorous statistical methods, including random-effects modelling, subgroup analysis, publication bias assessment, sensitivity analysis, and univariable meta-regression to explore sources of heterogeneity. The review also synthesizes, for the first time, the global range of *Cryptosporidium* species and subtypes reported in pigeons, offering valuable insights into their zoonotic and ecological significance. However, several limitations warrant consideration. High heterogeneity persisted across most analyses, and although publication year and sample size accounted for part of this variability, a large proportion of the between-study variance remained unexplained. Species-level and subtype data were incomplete for many studies, and reliance on microscopy in some investigations may have introduced misclassification bias. Furthermore, limited reporting of sample denominators, age structure, management systems, and seasonal patterns restricted the ability to conduct more detailed quantitative assessments. Together, these limitations highlight the need for well-designed epidemiological studies employing standardized sampling, diagnostic, and reporting protocols.

5. Conclusion

In conclusion, this review demonstrates that pigeons harbour a notable prevalence of *Cryptosporidium* spp. infection and a diverse set of

species and subtypes, including several with established zoonotic potential. Given the close ecological association of pigeons with human populations, particularly in urban and peri-urban environments, the presence of both avian-adapted and zoonotic *Cryptosporidium* species underscores their relevance within One Health frameworks. While substantial heterogeneity and gaps in species-level reporting limit definitive inferences, the findings highlight the importance of ongoing surveillance, molecular characterization, and improved reporting practices to better understand transmission dynamics and public-health risks. Future studies adopting a One Health approach should incorporate parallel sampling of pigeons, humans, and environmental matrices such as water and soil to more accurately elucidate potential transmission pathways of *Cryptosporidium* spp.

CRediT authorship contribution statement

Mina Mamizadeh: Writing – original draft, Methodology, Investigation. **Farzad Mahdavi:** Writing – review & editing, Writing – original draft, Methodology, Investigation. **Fariba Shadfar:** Writing – review & editing, Writing – original draft, Investigation, Data curation. **Ali Asghari:** Writing – review & editing, Writing – original draft, Supervision, Software, Project administration, Methodology, Investigation, Data curation. **Giovanni Sgroi:** Methodology, Investigation. **Ali Pouryousef:** Software, Methodology, Investigation. **Mohammad Reza Mohammadi:** Methodology, Investigation.

Ethics approval

Not applicable.

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Author contributions

A.A and F.M conceived and designed the study. F.M, M.M, M.R.M, A. P, G.S, and F.S had a role in data extraction and methodology. A.A and F. M performed the data analysis. A.A, F.M, M.M, and F.S wrote the manuscript. A.A, G.S, and F.S critically revised the manuscript. All the authors have read and approved the final manuscript.

Avail ability of data and materials

Data are available in the article's supplementary materials.

Declaration of Competing Interest

The authors declare no competing interests.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.cimid.2025.102437.

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