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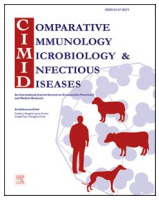

Review article

Prevalence, genetic diversity, and zoonotic potential of *Giardia duodenalis* in New and Old World Camelids: A comparative systematic review and meta-analysis

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ABSTRACT

This study aimed to review and analyze the prevalence, genetic diversity, and zoonotic potential of *Giardia duodenalis* in New World Camelids (NWCs) and Old World Camelids (OWCs), highlighting geographic and host-related variations. The statistical analyses were conducted using CMA software to estimate pooled prevalence rates. Heterogeneity was evaluated with the I^2 statistic, and sensitivity analysis tested pooled prevalence after removing certain studies. Meta-regression examined the association between *G. duodenalis* prevalence in camelids and factors like publication year and sample size. Subgroup analyses investigated prevalence variations based on countries, continents, WHO regions, publication years, diagnostic methods, and sample sizes. A total of 22 studies/23 datasets were included, with eight on NWCs and 15 on OWCs, covering 5008 camelids across nine countries. The weighted *G. duodenalis* prevalence in camelids was 8.7 % (95 % CI: 5.6–13.3), with NWCs at 10.3 % (95 % CI: 3–29.7) and OWCs at 9.1 % (95 % CI: 6.7–12.2). Geographical analyses revealed the highest prevalence of *G. duodenalis* in South America (40.4 %) and the AMR WHO region (10.8 %), with notable rates in Peru (40.4 %) and Iraq (11.9 %). Sensitivity analysis showed that prevalence rates remain robust, unaffected by study exclusions. Neither the year of study nor sample size influenced infection rates in camelids. The identification of zoonotic assemblages A and E, and zoonotic sub-assemblage AI in camelids, is of public health significance. These insights enhance our understanding of *G. duodenalis* epidemiology in camelids, underscoring the need for ongoing surveillance and research regarding their effects on human and animal health.

1. Introduction

Giardia duodenalis, also known as *G. intestinalis* or *G. lamblia*, is a flagellated protozoan parasite that infects the small intestine of numerous hosts, including humans and animals [1]. It is a common intestinal pathogen worldwide, causing giardiasis, which is characterized by diarrhea and malabsorption [2]. The parasite has two morphological forms: trophozoite, the active, motile form in the small intestine, which is pear-shaped with eight flagella and a ventral adhesive disc for attachment to the intestinal mucosa; and cyst, the dormant, environmentally resistant form that aids in transmission [3,4]. Cysts are oval-shaped and can survive for extended periods outside the host, promoting fecal-oral transmission [5,6]. *G. duodenalis* primarily spreads through the fecal-oral route, notably by ingesting water containing infectious cysts, consuming food prepared with contaminated water/-individuals, person-to-person contact, especially in areas with poor

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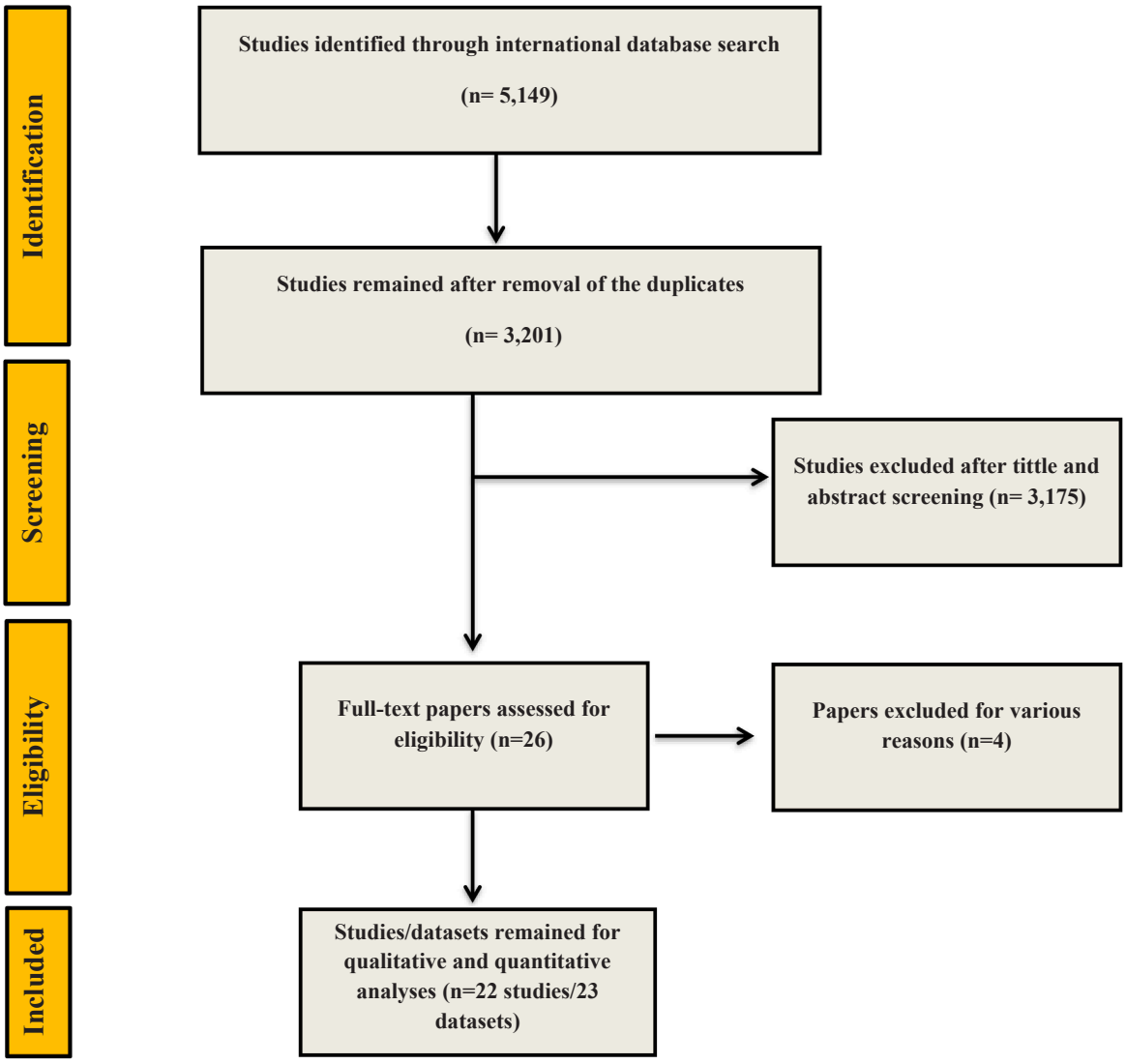

Fig. 1. Flowchart illustrating the process of included studies in this review.

sanitation, and contact with infected animals, emphasizing the zoonotic potential of the parasite [7,8].

The zoonotic nature of *G. duodenalis* complicates control efforts, as various animals can harbor the pathogen [9–11]. In humans, giardiasis can be asymptomatic or severe, presenting symptoms like diarrhea, abdominal pain, bloating, nausea, and vomiting, which typically last 1–3 weeks and may recur, leading to malabsorption and debilitation [12–14]. Children are especially vulnerable, with infections potentially causing growth stunting and cognitive impairments [15,16]. Giardiasis in animals can cause dehydration, weight loss, and stunted growth, especially in young animals. Infected animals can shed cysts, which contaminate the environment and pose a risk of zoonotic transmission [17–20].

G. duodenalis has significant genetic diversity, categorized into eight assemblages (A–H) [21]. Assemblage A includes sub-assemblages AI (humans and animals), AII (humans), AIII and AIV (animals) [11,22,23]. Assemblage B consists of sub-assemblages BIII and BIV, primarily affecting humans but also found in animals [24]. Assemblages C and D infect canines, assemblage E targets hoofed livestock, assemblage F affects cats, assemblage G infects rodents, and assemblage H is found in marine mammals [23,25]. There have been sporadic reports of human infections with uncommon assemblages (C, E, and F) [25–29].

Molecular techniques are vital for accurately identifying *G. duodenalis* assemblages and sub-assemblages [30]. Key genetic loci used in diagnostics include the small subunit ribosomal RNA (*SSU rRNA*) gene for genus and species identification, along with glutamate dehydrogenase (*gdh*), beta-giardin *(bg*), and triosephosphate isomerase (*tpi*) genes, which assist in assessing genetic diversity and differentiating assemblages and sub-assemblages through multilocus genotyping (MLG) [31–33]. These molecular tools are essential for epidemiological studies, enabling the tracking of transmission patterns and infection sources.

Camelids, which include both New World Camelids (NWCs) like llamas and alpacas, and Old World Camelids (OWCs) such as dromedaries and Bactrian camels, are vital to many communities by providing meat, milk, and transportation [34,35]. Given the absence of a comprehensive systematic review and meta-analysis of *G. duodenalis* infections in camelids, this global study aimed to assess the prevalence, genetic diversity, and zoonotic transmission potential of *G. duodenalis* in both NWCs and OWCs.

2. Methods

2.1. Ethics and study design

The current study was approved by the Ethics Committee of Qazvin University of Medical Sciences, Qazvin, Iran (approval no. IR.QUMS.

Table 1
Key characteristics of 22 articles/23 datasets on the prevalence and assemblage/sub-assemblage distribution of *G. duodenalis* in camelids.

Author, year	Host's common name	Host category	Time tested	Country	Total no.	Infected no.	Prevalence (%)	Method	Assemblages	Sub-assemblages
Rulofson, 2001 [45]	Llama	NWCs[b]	1996–1997	USA	354	12	3.4	MIC[e]	-	-
Cebra, 2003 [54]	Llama and Alpaca	NWCs	1999–2002	USA	45	8	18	MIC	-	-
Trout, 2008 [48]	Alpaca	NWCs	UC[d]	USA	61	3	4.9	MOL[f]	A	-
Gomez-Couso, 2012 [56]	Alpaca	NWCs	2009–2010	Peru	274	137	50	MOL	A, E	-
Maesano, 2014 [43]	Llama	NWCs	2011	Poland	11	0	0	MIC	-	-
Hussin, 2015 [58]	Camel spp.[a]	OWCs[c]	2014–2015	Iraq	100	24	24	MIC	-	-
Khedr, 2015 [40]	Camel spp.	OWCs	2014–2015	Egypt	120	6	5	MIC	-	-
Jawad, 2016 [59]	Dromedary camel	OWCs	2015–2016	Iraq	200	40	20	MOL	-	-
Koehler, 2018 [41]	Alpaca	NWCs	2016–2017	Australia	81	6	7.4	MOL	A, E	AI
Zhang, 2019 [51]	Bactrian camel	OWCs	2018	China	40	3	7.5	MOL	A, E	-
Bouragba, 2020 [53]	Dromedary camel	OWCs	2015–2018	Algeria	717	0	0	MIC	-	-
Zhao, 2020 [52]	Bactrian camel	OWCs	2016–2019	China	852	84	9.85	MOL	A, E	-
Alfatah, 2021 [39]	Dromedary camel	OWCs	2020–2021	Saudi Arabia	1377	137	9.9	MIC	-	-
Hasan, 2021 [57]	Camel spp.	OWCs	UC	Iraq	120	5	4.2	MIC	-	-
Locklear, 2021 [42]	Camel spp.	OWCs	1980–2020	USA	77	1	1.3	MIC	-	-
Wang, 2021 [49]	Bactrian camel	OWCs	UC	China	40	3	7.5	MOL	-	-
Elmahallawy, 2023 [55]	Dromedary camel	OWCs	2021	Egypt	102	4	3.9	MOL	-	-
Maxamhud, 2023 [44]	Dromedary camel	OWCs	2017–2021	Algeria	63	10	15.9	MOL	-	-
Salama, 2023 [46]	Dromedary camel	OWCs	2020–2021	Egypt	121	16	13	MOL	-	-
Sanchez, 2024 [47]	Alpaca	NWCs	UC	Peru	19	5	26.3	MOL	-	-
An, 2024a [50]	Bactrian camel	OWCs	2020–2021	China	10	0	0	MOL	-	-
An, 2024b [50]	Alpaca	NWCs	2020–2021	China	24	0	0	MOL	-	-
Albayati, 2024 [38]	Dromedary camel	OWCs	2021–2022	Iraq	200	14	7	MIC	-	-

[a] Old World Camelids without a specific classification
[b] New World Camelids
[c] Old World Camelids
[d] Unclear
[e] Microscopic detection
[f] Molecular detection

REC.1403.426). This systematic review and meta-analysis followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines to ensure methodological rigor and transparency [36].

2.2. Study design and search strategy

This systematic review and meta-analysis was conducted to evaluate the prevalence, genetic diversity, and zoonotic potential of *G. duodenalis* in New World Camelids (NWCs) and Old World Camelids (OWCs). A comprehensive literature search was performed using PubMed, Web of Science, Scopus, and ScienceDirect databases to identify relevant studies published up to December 2, 2024. The search terms included combinations of keywords such as "*Giardia duodenalis*," "camelids," "New World Camelids," "Old World Camelids," "prevalence," and "zoonotic potential." Google scholar was searched for gray literature, and additional articles were identified by cross-referencing the bibliographies of relevant studies.

2.3. Eligibility criteria

Studies were included if they reported the prevalence of *G. duodenalis* in NWCs or OWCs, provided sufficient data for prevalence calculations, employed established diagnostic methods (e.g., microscopy, PCR), and were published without time or language restrictions. Studies/datasets were excluded if they did not provide clear data on *G. duodenalis* in camelids, focused exclusively on other hosts, were reviews or opinion articles, or had sample sizes under 10.

2.4. Data extraction and quality assessment

Data extraction was performed using a predesigned checklist to gather study characteristics (author name, publication year, country, continent, and WHO region), host details (species, sample size), diagnostic methods, and reported prevalence of *G. duodenalis* in camelids. Two independent reviewers screened titles, abstracts, and full texts, resolving discrepancies through discussion or consultation with a third reviewer. The quality of included studies was evaluated using the Joanna Briggs Institute (JBI) critical appraisal checklist for prevalence studies, which assessed sample size, population, objectives, confounding factors, outcomes, methodology, statistical analysis, and reporting clarity [37]. Studies scoring >6 were considered high quality, 4–6 as moderate quality, and those with a score of ≤ 3 were excluded from the review.

2.5. Statistical analysis

Pooled prevalence rates and 95 % confidence intervals (CIs) were

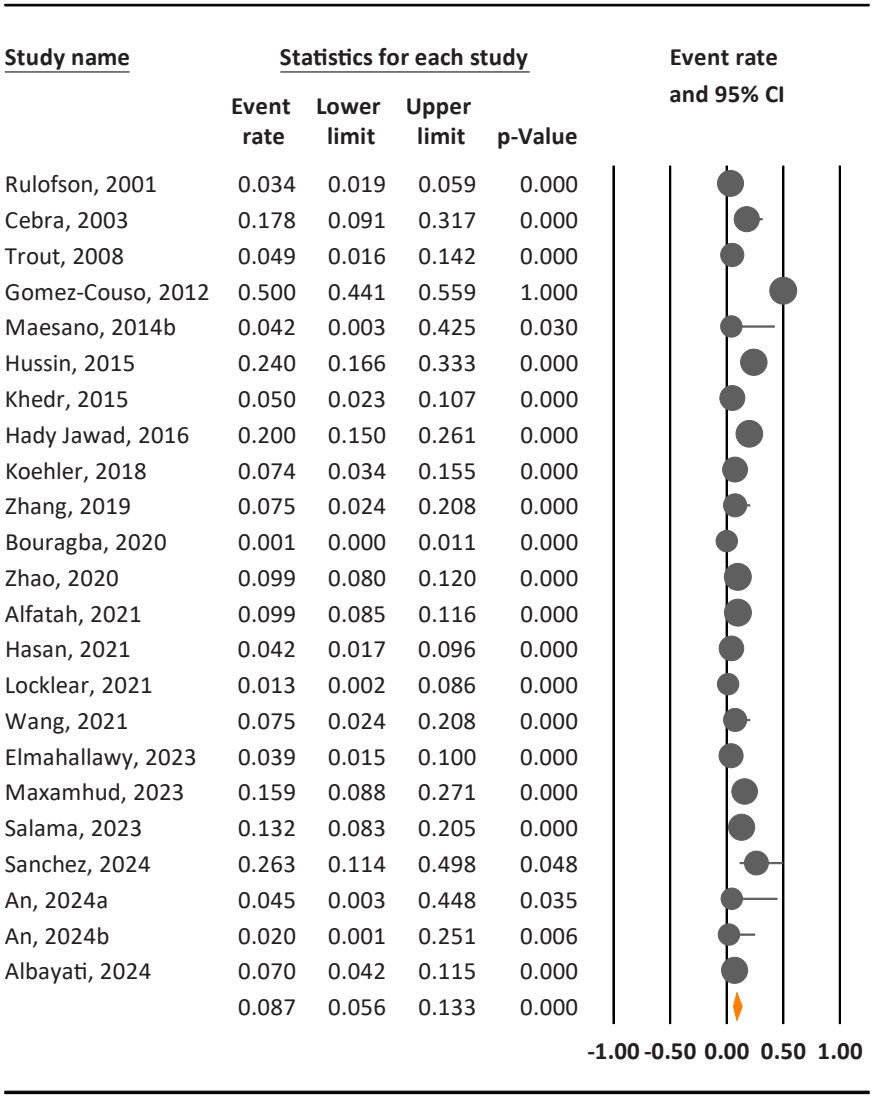

Fig. 2. The pooled prevalence of *G. duodenalis* in camelids using a random-effects model and 95 % CIs. Gray colors indicate the event rate/prevalence reported in each study, while orange represents the final weighted prevalence.

calculated using a random-effects model in Comprehensive Meta-Analysis (CMA) software to address study heterogeneity, assessed with the I^2 statistic (values above 50 % indicating high heterogeneity). Subgroup analyses explored prevalence differences by publication year, geographical regions (countries, continents, and WHO regions), camel types (NWCs vs. OWCs), diagnostic methods, and sample size. Meta-regression analyzed the impact of quantitative variables such as publication year and sample size on prevalence estimates. Sensitivity analysis excluded individual studies to test the robustness of the pooled rates. Publication bias was assessed with a funnel plot and Egger's test for studies reporting prevalence rates. A p-value of < 0.05 was deemed statistically significant for all analyses, with all statistical tests being two-tailed. The genetic diversity of *G. duodenalis* was analyzed descriptively, summarizing different assemblages/sub-assemblages and their potential implications for zoonotic transmission.

3. Results

3.1. Study selection

The systematic search identified 22 studies with 23 datasets that met the inclusion criteria, encompassing data from 5008 camelids across nine countries on six continents [38–59]. Among these, eight datasets focused on NWCs and 15 on OWCs. The screening process is illustrated in the PRISMA flow diagram in Fig. 1.

3.2. Characteristics of included studies

The studies took place in various geographical locations, with NWCs represented in five countries across five continents and OWCs in seven countries across three continents. Sample sizes ranged from 10 to 1377, totaling 869 NWCs and 4139 OWCs analyzed. Diagnostic methods included microscopy and molecular techniques (PCR). Publications ranged from 2001 to 2024, indicating a growing focus on this research over time (Table 1). According to the JBI checklist, 12 studies were rated as high quality and 10 studies as moderate quality (Supplementary Table 1).

3.3. Pooled prevalence of G. duodenalis in camelids

The pooled prevalence of *G. duodenalis* in camelids was 8.7 % (95 % CI: 5.6–13.3) under a random-effects model (Fig. 2). Heterogeneity among studies was high ($I^2 = 94$ %, $p < 0.001$), indicating substantial variability in prevalence estimates. Fig. 3 illustrates the prevalence and

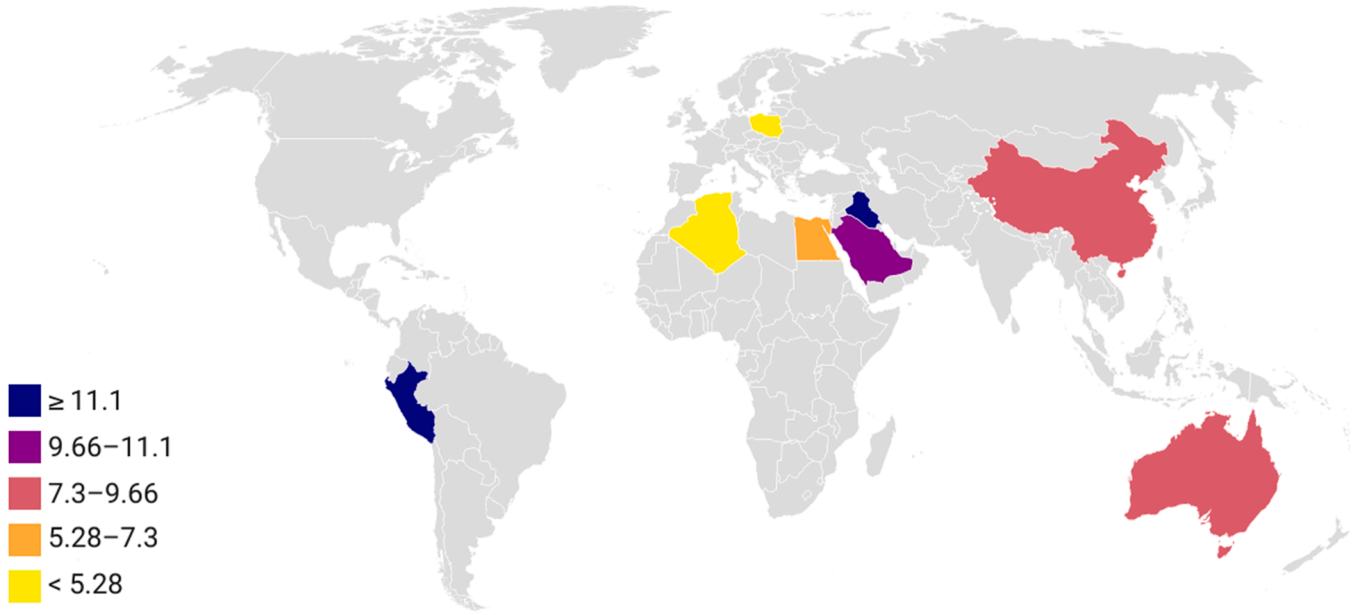

Fig. 3. The prevalence and geographical distribution of *G. duodenalis* in camelids across the surveyed countries.

geographical distribution of *G. duodenalis* in camelids across the surveyed countries.

3.4. Comparative pooled prevalence of G. duodenalis in NWCs and OWCs

The weighted prevalence of *G. duodenalis* was slightly higher in NWCs (10.3 %, 95 % CI: 3–29.7) compared to OWCs (9.1 %, 95 % CI: 6.7–12.2) (Fig. 4).

3.5. Assemblage and sub-assemblage distribution of G. duodenalis in camelids

Limited genotyping data revealed two zoonotic assemblages A and E, and one zoonotic sub-assemblage AI in camelids, underscoring their potential role in infecting humans and other domestic animals (Table 1).

3.6. Subgroup analyses

Table 2 presents the prevalence of *G. duodenalis* infections by publication year, country, continent, WHO region, diagnostic methods, and sample size (Supplementary Figs. 1–6).

3.7. Sensitivity analysis

Sensitivity analysis confirmed the robustness of the pooled prevalence. Excluding individual studies had minimal impact on the pooled estimates, with the pooled prevalence remaining within the confidence intervals reported in the primary analysis (Supplementary Figs. 7).

3.8. Meta-regression

Meta-regression analyses showed no significant association between *G. duodenalis* prevalence and either publication year ($p = 0.64$) or sample size ($p = 0.72$) (Fig. 5).

3.9. Publication bias

No evidence of publication bias was detected, as indicated by visual inspection of the funnel plot and Egger's regression test ($p = 0.13$) (Fig. 6).

4. Discussion

Raising both New World (like llamas and alpacas) and Old World camelids (such as dromedaries and Bactrian camels) presents various benefits and risks [60]. Camels are strong animals that can carry heavy loads and facilitate transportation in arid regions [61]. Certain types, such as alpacas, provide valuable wool for textiles [62]. Additionally, camels offer nutritious meat and milk, which are especially important in areas where other livestock may not thrive [63]. They can graze on vegetation unsuitable for other animals, aiding land management and benefiting the ecosystem [34,64]. In many cultures, camels are vital to traditions, economies, and livelihoods [35,65]. However, they can also carry zoonotic parasites like *G. duodenalis*, which can infect humans via contaminated food or water, causing gastrointestinal issues such as diarrhea, abdominal pain, and nausea [55,66].

It is estimated that 65 % of fatalities in OWCs and 50 % in NWCs are caused by infectious diseases [67]. The risk of zoonotic diseases in addition to threatening the health of the animals themselves challenges public health, emphasizing the need for proper hygiene and veterinary care. Exposure to domestic animals should be considered a risk factor for human diarrheal illness [68]. Therefore, while domesticated camels provide significant economic, ecological, and cultural advantages, effective management and awareness of zoonotic risks are crucial [60].

In the present study, the overall pooled prevalence of 8.7 % (95 % CI: 5.6–13.3) reflected moderate infection rates of *G. duodenalis* in camelids globally. High heterogeneity ($I^2 = 94$ %) across studies likely stems from geographic, diagnostic, and methodological variations. Existing literature supports such variability, with prevalence rates ranging widely in other host species, including livestock and wild mammals [69,70]. The slightly elevated prevalence in NWCs (10.3 %, 95 % CI: 3–29.7) compared to OWCs (9.1 %, 95 % CI: 6.7–12.2) corroborates findings in some livestock studies, where close interactions of NWCs with humans and diverse ecosystems facilitated zoonotic transmission [71–73]. However, the overlapping confidence intervals signal no statistically significant difference, suggesting that other factors such as climate, husbandry, or sampling biases may drive observed disparities. The sensitivity analysis confirmed the robustness of the pooled prevalence estimate, further validating the reliability of the results despite high heterogeneity. Moreover, the meta-regression findings suggested that neither temporal trends nor study size accounted for the observed heterogeneity and variability in *G. duodenalis* prevalence rates.

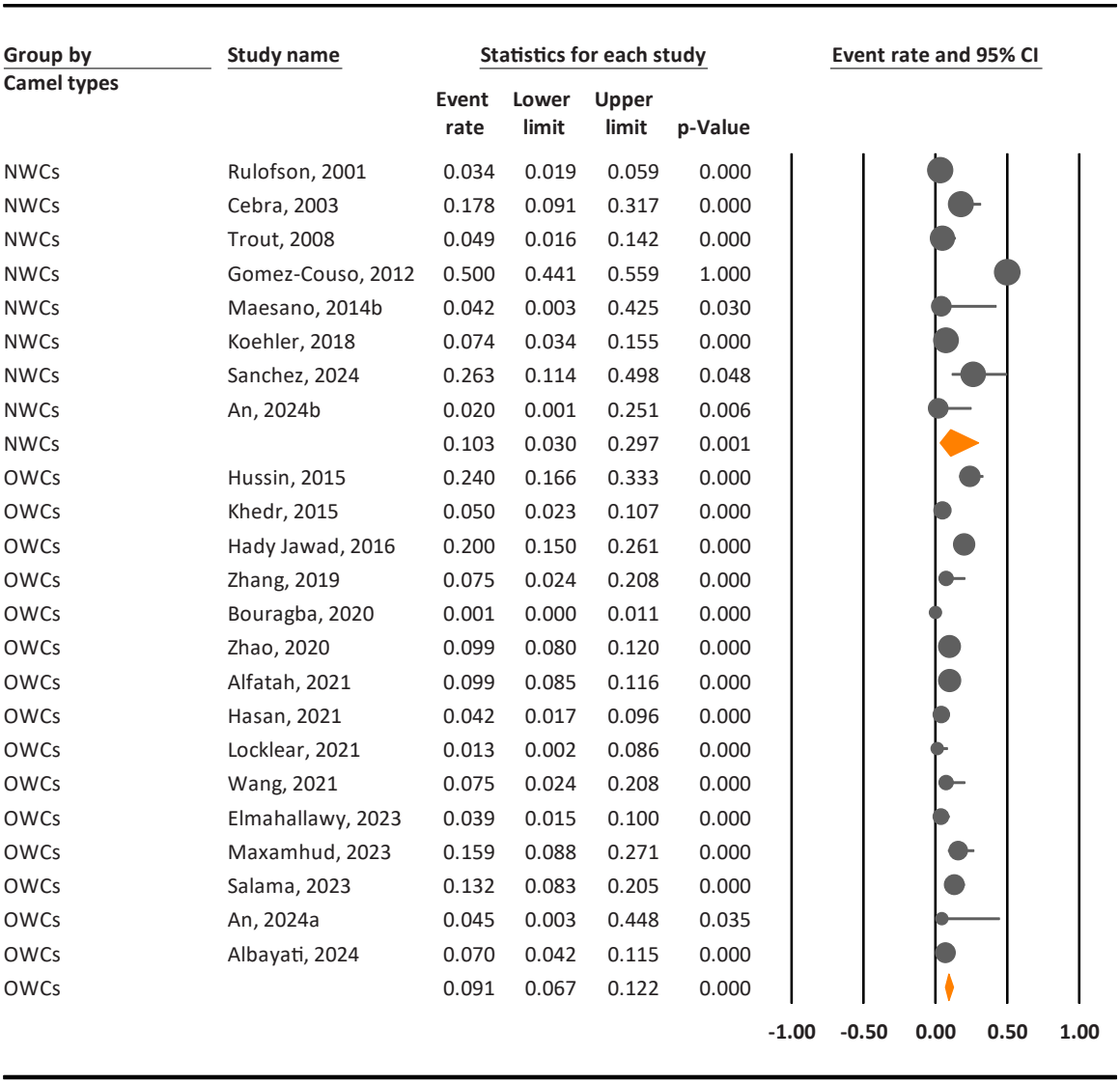

Fig. 4. The comparative pooled prevalence of *G. duodenalis* in NWCs and OWCs using a random-effects model and 95 % CIs. Gray colors indicate the event rate/ prevalence reported in each study, while orange represents the final weighted prevalence.

Table 2
Subgroup analysis of *G. duodenalis* prevalence in camelids by publication years, continents, WHO regions, countries, sample sizes, and diagnostic methods.

Subgroup variable	Prevalence % (95 % CI)	Heterogeneity (Q)	df (Q)	I^2 (%)	p-value
Publication year					
≤ 2019	11.3 (5.2–23)	193.2	9	95.3	$p < 0.05$
> 2019	8.5 (6.2–11.3)	37.9	12	68.3	$p < 0.05$
Continent					
Africa	5.8 (2.4–13.8)	23.5	4	83	$p < 0.05$
Asia	10.5 (7.6–14.5)	46.1	9	80.4	$p < 0.05$
Europe	4.2 (0.3–42.5)	0	0	0	$p < 0.05$
North America	5.2 (1.8–14.6)	16.5	3	81.8	$p < 0.05$
Oceania	7.4 (3.4–15.5)	0	0	0	$p < 0.05$
South America	40.4 (20.3–64.3)	3.7	1	73	$p < 0.05$
WHO region					
AFR	1.3 (0–76.5)	14.8	1	93.2	$p < 0.05$
AMR	10.8 (2.5–35.8)	147.5	5	96.6	$p < 0.05$
EMR	9.9 (6.6–14.7)	51.1	7	86.3	$p < 0.05$
EUR	4.2 (0.3–42.5)	0	0	0	$p > 0.05$
WPR	9.4 (7.8–11.3)	2.5	5	0	$p > 0.05$
Country					
Algeria	1.3 (0–76.5)	14.8	1	93.2	$p < 0.05$
Australia	7.4 (3.4–15.5)	0	0	0	$p > 0.05$
China	9.6 (7.8–11.6)	2.1	4	0	$p > 0.05$
Egypt	6.9 (3–15.1)	7.8	2	74.4	$p < 0.05$
Iraq	11.9 (5.8–23)	28.7	3	89.5	$p < 0.05$
Peru	40.4 (20.3–64.3)	3.7	1	73	$p > 0.05$
Poland	4.2 (0.3–42.5)	0	0	0	$p > 0.05$
Saudi Arabia	9.9 (8.5–11.6)	0	0	0	$p > 0.05$
USA	5.2 (1.8–14.6)	16.5	3	81.8	$p < 0.05$
Sample size					
≤ 100	10.5 (6.5–16.4)	30	11	63.4	$p < 0.05$
> 100	8 (4.2–14.7)	334.7	10	97	$p < 0.05$
Detection methods					
MIC	6.5 (3.8–10.8)	64.8	9	86.1	$p < 0.05$
MOL	11.4 (6.1–20.3)	226.2	12	94.7	$p < 0.05$

The identification of zoonotic assemblages A and E, and zoonotic sub-assemblage AI in camelids, is of public health significance. The wide host range and zoonotic potential of assemblage A are well-documented, posing risks to humans and other animals in shared environments [74,75]. Assemblage E, traditionally associated with livestock, is increasingly reported in wildlife and humans, indicating cross-species transmission dynamics [28,76]. The limited genotyping data, however, restricts a comprehensive understanding of assemblage/sub-assemblage distribution across camel populations. Future studies should prioritize genotyping to better assess zoonotic risks and interspecies transmission dynamics.

Analysis of publication years revealed that the pooled prevalence of *G. duodenalis* in camelids was higher before 2019 (11.3 %) than after (8.5 %). However, the timing of some studies did not align with their publication dates, and the number of studies in the two periods was unequal. Geographical analyses revealed the highest prevalence of *G. duodenalis* in South America (40.4 %) and the AMR WHO region (10.8 %), with notable rates in Peru (40.4 %) and Iraq (11.9 %). The data suggests a concerning trend in the spread of *G. duodenalis*, particularly in regions where water quality and sanitation infrastructure may be suboptimal. A direct association was reported between increasing sample size and decreasing pooled prevalence of *G. duodenalis* in camelids. This suggests that larger sample sizes may provide a more accurate representation of the true prevalence rates within camel populations. Molecular studies revealed a higher pooled prevalence of *G. duodenalis* in camelids than microscopy-based studies. This discrepancy highlights the limitations of traditional microscopy techniques, which may fail to detect low parasite loads or atypical forms of *G. duodenalis*. Molecular techniques, such as PCR, offer increased sensitivity and specificity, allowing for the identification of different assemblages/sub-assemblages and potentially uncovering asymptomatic carriers.

Despite its robust design, this study has limitations. The considerable heterogeneity underscores the need for standardized methodologies, including consistent diagnostic criteria and sampling techniques. The lack of different studies from diverse geographical regions, low sample sizes in some studies, lack of identical studies in the camels studied, unavailability of information such as age and sex of the camels studied, and reliance on single studies/datasets in some analyses were among the important limitations. Additionally, the scarcity of genotyping data limits insights into the full diversity and transmission dynamics of *G. duodenalis* assemblages/sub-assemblages in camelids. Future research should prioritize longitudinal studies, expanded molecular analyses, and investigations into environmental factors shaping infection risk. Of note, the analyses and conclusions of this study are based on limited information, necessitating cautious interpretation of the results.

5. Conclusion

This systematic review and meta-analysis underscores the role of camelids as potential reservoirs for *G. duodenalis* infections and its zoonotic assemblages/sub-assemblages, particularly in regions with high human-animal interaction. While overall prevalence is moderate, considerable heterogeneity highlights the need for targeted interventions and further research. Standardized diagnostic approaches, enhanced genotyping efforts, and a focus on zoonotic transmission pathways will be critical for mitigating the public health risks posed by *G. duodenalis*.

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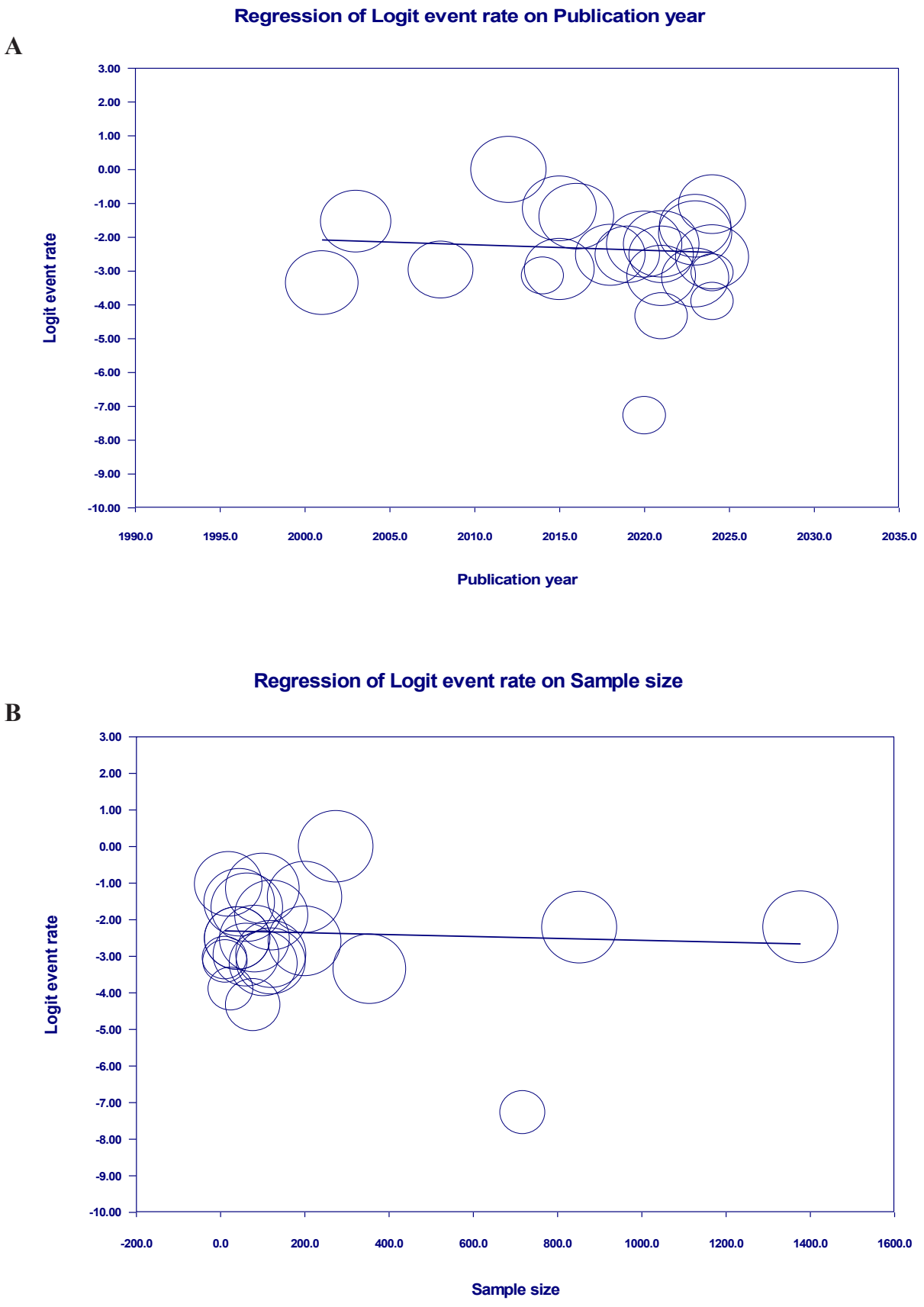

Fig. 5. The meta-regression indicated no statistically significant association between *G. duodenalis* infection prevalence in camelids and the quantitative variables of (A) publication year and (B) sample size.

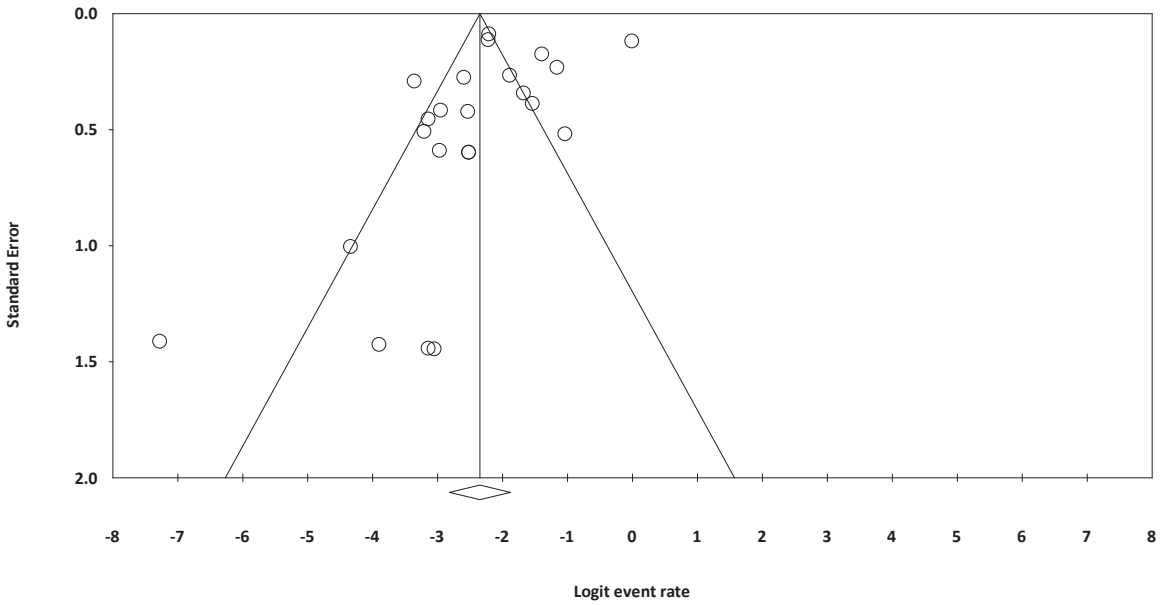

Fig. 6. Publication bias in the present study.

CRediT authorship contribution statement

Mohammadi Mohammad Reza: Investigation, Methodology, Writing – review & editing. **Ahmadi Mohammadreza Hafezi:** Writing – review & editing, Methodology, Investigation. **Pouryousef Ali:** Methodology, Investigation. **Mamizadeh Mina:** Writing – original draft, Methodology, Investigation. **Asghari Ali:** Writing – review & editing, Writing – original draft, Supervision, Software, Methodology, Investigation. **Nourmohammadi Hassan:** Writing – review & editing, Methodology, Investigation.

Declaration of Competing Interest

The authors declare no potential conflicts of interest regarding this research, authorship, or publication.

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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.2025.102316.

Data availability

The datasets used and/or analysed during the current study are available in the online version.

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