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Review article

Global molecular prevalence of *Giardia duodenalis* in pigs (*Sus domesticus*): A systematic review and meta-analysis

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ABSTRACT

Giardia duodenalis is one of the common intestinal parasites causing diarrhea in humans and livestock, including pigs. Thus, a healthy livestock would result in a clean environment, which benefits humans. In the present study, the global molecular prevalence of *G. duodenalis* infection was determined in pig populations, through systematic exploration of 4 international databases (MEDLINE/PubMed, Scopus, Web of Science, and Google Scholar) until March 4th, 2022. A random-effects meta-analysis model was used to estimate the overall and subgroup-based pooled prevalence of *G. duodenalis*, and I^2 index was used for the evaluation of the heterogeneity. Altogether, 42 datasets from 18 papers examined 7272 pigs across 12 nations, showing a 9.1% (95% CI: 5.6–14.3%) pooled molecular prevalence. Sensitivity analysis demonstrated no remarkable variation in the reported total prevalence upon removing individual studies. It was found that 6 Giardia assemblages (A-F) are capable to infect pigs around the world, including assemblage E [16 datasets, 41.1% (95% CI: 24.8–59.6%)], B [8 datasets, 28.2% (95% CI: 12.2–52.6%)], D [3 datasets, 16.2% (95% CI: 10.6–24.1%)], C [3 datasets, 11.6% (95% CI: 7.3–17.9%)], and A [11 datasets, 9.9% (95% CI: 5.6–16.9%)]. Of note, assemblage F was only reported in one study. Meta-regression analysis showed that publication year was not significantly associated with the *Giardia* prevalence in swine population, in contrast to the sample size. Substantially, animals in weaner and fattener stages were more prone to giardiasis. Assemblages A and B are of utmost zoonotic significance for humans, while assemblages C, D and F have, also, been found in dogs and cats. Still, little is known on the prevalence and distribution of Giardia assemblages in pigs and requires more extensive and detailed studies.

1. Introduction

Giardiasis is a gastrointestinal parasitic infection in humans and livestock caused by a flagellated protozoan, *Giardia duodenalis* (syn. *G. intestinalis*, *G. lamblia*) [1]. This diarrheagenic parasite is a significant public health issue, causing chronic malnutrition and

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growth retardation, particularly in affected children [2,3]. Approximately, 28.5 million people suffer from giardiasis worldwide [4]. Direct contact with the infected hosts followed by ingestion of contaminated food and water are the primary transmission routes for *G. duodenalis* cysts. It is mentioned that less than 10 cysts are enough to cause *Giardia* infection in a competent host [5].

Based on molecular evidences, *G. duodenalis* is sorted into eight distinct assemblages (A to H). It is known that human infections are caused by assemblages A, B and, to a lesser extent, by other assemblages, comprising assemblages C and D (dogs), assemblage E (domestic and wild ungulates), assemblage F (cats), assemblage G (mice and rats) and assemblage H (marine mammals) [5,6,7]. In order to accurately gain insight into the genetic diversity of *G. duodenalis*, multiple genes may be used such as small-subunit (SSU) rRNA, glutamate dehydrogenase (gdh), triose phosphate isomerase (tpi) and beta-giardin (bg), using multilocus genotyping (MLG) approach [8,9].

G. duodenalis is believed to be one of the leading causative agents of diarrhea in both children and adults. In developing countries, diarrhea is typical and associated with high rates of mortality among young children, killing a calculated 2.2 million people yearly, 1.9 million being children. Therefore, the microorganisms that can cause diarrhea and clinical symptoms, especially in children, deserve further investigation [10,11]. Animal husbandry may benefit humans in several aspects, but it may, also, endanger the human health through dissemination of zoonotic agents, comprising *Escherichia coli*, *Rotavirus*, *Sapovirus*, *coccidia*, *Cryptosporidium parvum* and *G. duodenalis* [12,13]. Pig raising is an extensive procedure around the world, recent international assessments of the swine population specified that about 677.6 million pigs are globally living up to January 2020, with China containing the largest number of pigs (406 million heads), followed by the European Union (150 million heads) and the United States (77 million heads). With these descriptions pigs may carry and transmit zoonotic pathogens such as *G. duodenalis* to humans [14]. Various molecular-based studies have been conducted worldwide to determine the prevalence and distribution of *Giardia* assemblages in pigs, but there is no comprehensive study that summarizes the information contained in all papers, hence the present systematic review and meta-analysis was designed and implemented in order to investigate the molecular prevalence, assemblage distribution, and zoonotic significance of *G. duodenalis* in swine population globally.

2. Methods

Current review was set to design in 2022 and reported information on the molecular prevalence and assemblage distribution of *G. duodenalis* in pigs (*Sus domesticus*) premised on the "Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA)" checklist [15].

2.1. Search strategy of the systematic review

To retrieve the maximum number of relevant literature, multiple keywords were utilized for systematic search in MEDLINE/PubMed, Scopus, Web of Science, and Google Scholar, including ("Intestinal Parasites" OR "Parasitic infections" OR "*Giardia* spp." OR "*Giardia duodenalis*") AND ("Assemblage" OR "Genotype" OR "Genotyping") AND ("Prevalence" OR "Epidemiology" OR "Frequency" OR "Occurrence") AND ("Pigs" OR "Farm animals" OR "Swine"). The results were imported into the EndNote X7 library and the duplicated records were automatically removed. Finally, the articles were selected by two researchers independently.

2.2. Inclusion and exclusion criteria

The systematic search revealed those studies evaluating the molecular prevalence and assemblage distribution of *Giardia* in pigs until March 4, 2022. Hence, microscopic and serological studies, reviews, case reports, letters, experimental infections, those studies without sample size or less than 10 and those without available full-text were totally excluded. For overlapping studies, the most comprehensive one was included in the meta-analysis.

2.3. Quality assessment

The quality of the methodology and reporting of the included studies was evaluated using Joanna Briggs Institute Checklist [16], in order to address the likely bias in design, conduct and analysis. This checklist includes 9 questions with Yes and No as answers. Articles that scored 4–6 and 7–9 points were considered moderate-quality and high-quality studies, respectively. According to the obtained score, the authors decided to include (4–9 points) or exclude ($\leq$3 points) the articles.

2.4. Data extraction form

A Microsoft Excel spreadsheet was designed and used to collect all available information within the included studies, encompassing the name of the first author, year of publication, the study period, the country of origin, continents, the isolated assemblages, reported prevalence, and sample size.

2.5. Screening of the studies

Four independent authors (M.S, M.E, L.S, and A.S) performed the initial search and article screening, followed by quality assessment and extraction of the required data. Any contradictions encountered during these procedures were obviated by the team

leader (A.A).

2.6. Meta-analysis

Meta-analysis was done using Comprehensive Meta-analysis (CMA) v3 software, with p-values <0.05 as statistically significant [17, 18]. Cochrane's Q and I^2 statistics (with a significance level of 50%) were employed to evaluate the potential heterogeneity in studies. Random- or fixed-effect models were used in case of significant or lack of heterogeneity, respectively [19]. A funnel plot based on Egger's test was drawn to demonstrate the possibility of publication bias during the analysis. The pooled prevalence of giardiasis in pigs was estimated based on publication years, countries, continents, and sample size. Meta-regression analysis was used to investigate the association between the quantitative variables (sample size and publication year) and the prevalence of giardiasis. Moreover, variations in the final weighted prevalence were evaluated by sensitivity analysis using excluding each study method.

3. Results

3.1. Search findings

At first, 8657 articles were found during systematic search in international databases, among which 6359 articles were reviewed in terms of title and abstract, after removing duplicates. Subsequently, 85 articles were selected for the next step, their full text was examined and finally 18 papers [20–37] were qualified to be included in the meta-analysis section. The references of the articles were also reviewed to add relevant studies (Fig. 1). Reasons for removing the papers included animals other than pigs (16 papers), intestinal parasites other than *G. duodenalis* (40 articles), repetitive results (5 studies), and ambiguous findings (6 papers).

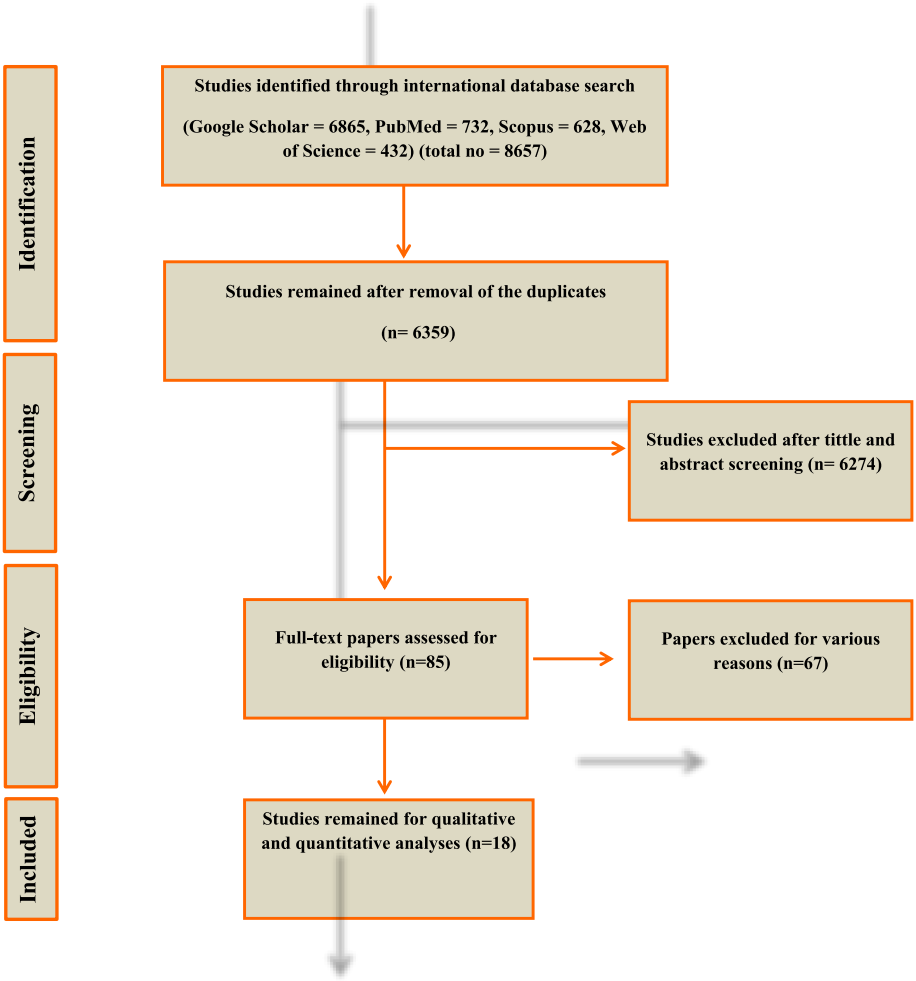

Fig. 1. Flowchart of the included eligible studies in the present study.

3.2. Characteristics of eligible studies

The 18 studies selected in this review were published during 2007–2021 in China (7 studies), Australia, Canada, Denmark, Nigeria, Norway, the Philippines, Poland, South Korea, Spain, Taiwan and the United States (single studies), evaluating 7272 pigs worldwide (Table 1).

3.3. Quality appraisal

Overall, 7 studies had well (≥7 points) and 11 of them had a moderate quality (4–6 points) (Supplementary Table 1).

3.4. Global frequency of giardiasis in pigs

Assessed studies showed a strong heterogeneity ($Q = 586.4$, $I^2 = 97.2\%$, $p \leq 0.001$) and a total prevalence of 9.1% (95% CI: 5.6–14.3%) (Fig. 2).

3.5. Sensitivity analysis

Given the sensitivity analysis, it was discovered that by removing individual papers reporting the molecular frequency of *G. duodenalis* infection in pigs, no considerable variation in the final prevalence was reported (Fig. 3).

3.6. Weighted prevalence of giardiasis in pigs based on evaluated subgroups

The outcomes of the subgroup analysis are demonstrated in Table 2 and Supplementary Figs. 1–4.

3.7. Worldwide prevalence of G. duodenalis assemblages in pigs

Overall, 42 datasets from 18 studies reported various Giardia assemblages in examined pigs. Assemblage E was mostly prevalent [16 datasets, 41.1% (95% CI: 24.8–59.6%)], followed by assemblages B [8 datasets, 28.2% (95% CI: 12.2–52.6%)], D [3 datasets, 16.2% (95% CI: 10.6–24.1%)], C [3 datasets, 11.6% (95% CI: 7.3–17.9%)], and A [11 datasets, 9.9% (95% CI: 5.6–16.9%)] (Fig. 4). Assemblage F has only been isolated from pigs in one study (Table 3).

Table 1
The main characteristics of 18 molecular studies included in the present review.

Author, year	Time tested	Countries	Total samples (no.)	Infected samples (no.)	Prevalence (%)	Diagnostic method	Targeted gene	Ref.
Armson, 2009	2006	Australia	289	90	31.1	PCR-sequencing	18S rRNA	[30]
Lam, 2021	UC	Taiwan	141	6	4.2	PCR-sequencing	bg	[34]
Afable, 2019	2018	Philippines	44	7	15.9	PCR-sequencing	tpi	[20]
Farzan, 2011	2005–2006	Canada	122	81	66.4	PCR-sequencing	18S rRNA, bg	[31]
Akinkuotu, 2019	2015–2016	Nigeria	209	53	25.3	PCR-sequencing	MLG	[21]
Zou, 2019	2017	China	345	2	0.6	PCR-sequencing	gdh	[28]
Lee, 2020	2017–2019	South Korea	745	110	14.8	PCR-sequencing	MLG	[35]
Wang, 2018	2016	China	897	15	1.7	PCR-sequencing	tpi	[26]
Jing, 2019	2017–2018	China	801	21	2.6	PCR-sequencing	MLG	[33]
Zou, 2021	UC	China	396	21	5.3	PCR-sequencing	MLG	[29]
Liu, 2019	2014	China	93	25	26.9	PCR-sequencing	MLG	[36]
Wang, 2017	2016	China	560	45	8	PCR-sequencing	bg	[25]
Rivero-Juarez, 2020	2015–2016	Spain	186	32	17.2	PCR-sequencing	gdh, bg	[22]
Rodriguez-Rivera, 2016	2014–2015	USA	370	16	4.3	PCR-sequencing	MLG	[23]
Zhang, 2019	2017	China	450	28	6.2	PCR-sequencing	MLG	[27]
Stojecki, 2015	2013–2014	Poland	84	8	9.5	PCR-sequencing	bg	[24]
Hamnes, 2007	2004	Norway	684	10	1.5	PCR	18S rRNA	[32]
Petersen, 2015	2011–2012	Denmark	856	120	14	PCR-sequencing	18S rRNA, gdh	[37]

*UC: unclear.
*PCR-sequencing is the nested or conventional single-plex PCR, in which after identifying the positive samples, those sent for sequencing and species identification. However, in one study (Hamnes, 2007), positive samples were detected only by PCR but not sent for sequencing and the parasite species remained unknown.
*MLG: is the multilocus genotyping of giardiasis based on more than one gene (18S, gdh, tpi, and/or bg).

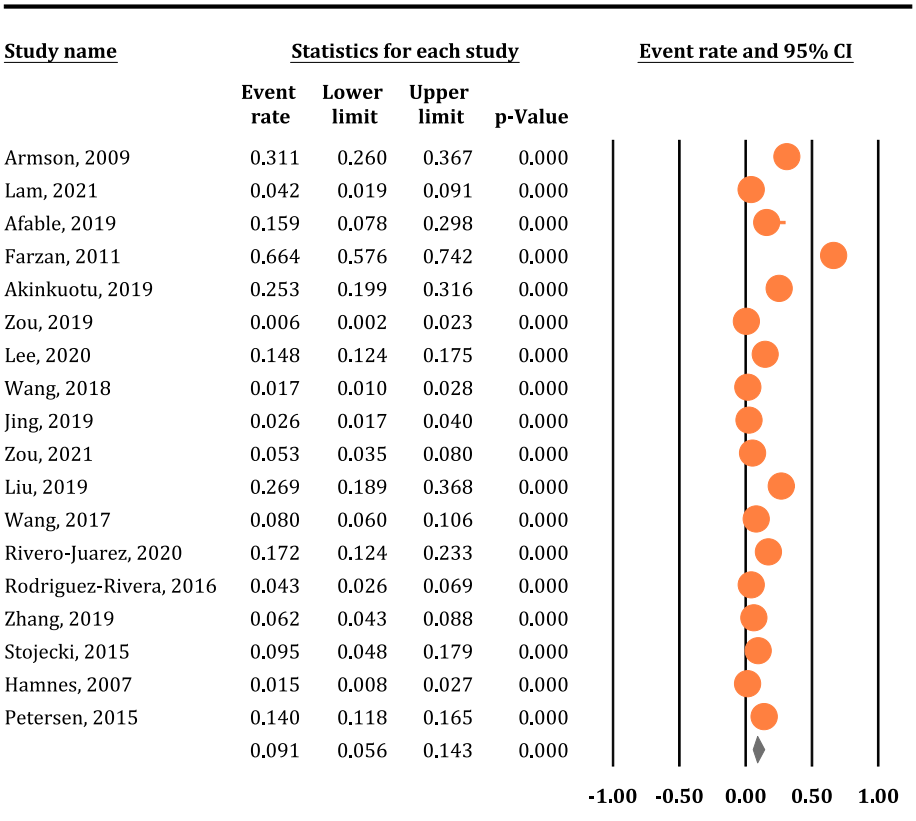

Fig. 2. Molecular epidemiology of *G. duodenalis* in pigs from a global perspective.

3.8. Overall prevalence of unidentified and/or non-genotyped samples

Our findings revealed that based on 9 studies, 66.4% (95% CI: 44.7–82.8%) of the Giardia positive samples reported from pigs were not genotyped (Supplementary Fig. 5).

3.9. Zoonotic importance of giardiasis in pigs

In addition to infecting pigs with their usual assemblage (E), specific assemblages of dogs and cats (C, D, and F) have also been reported from these hosts. Most importantly, A and B zoonotic genotypes also make up a significant percentage of positive swine specimens, highlighting the importance of these hosts in transmitting zoonotic giardiasis to humans (Fig. 4 and Table 3).

3.10. Meta-regression

With respect to meta-regression, publication year was not significantly associated with the *Giardia* prevalence in swine population (Fig. 5A), hence it was not a cause of bias in our findings (Reg Coef = −0.0616, p = 0.344). In contrast, a significant association was reported between sample size and the *Giardia* prevalence in pigs (Reg Coef = −0.0023, p = 0.008) (Fig. 5B).

3.11. Publication bias

There was no significant publication bias within the present systematic review and meta-analysis (Egger's regression: intercept = − 5.509, 95% lower limit = − 11.940, 95% upper limit = 0.921, t-value = 1.816, p = 0.088) (Fig. 6).

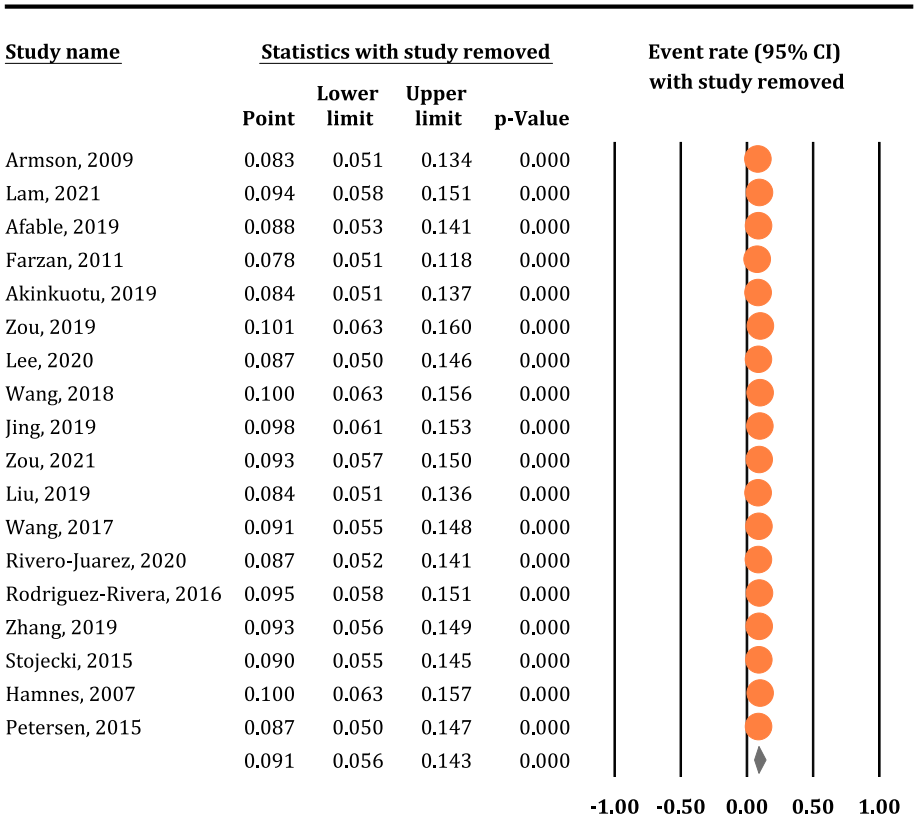

Fig. 3. Sensitivity analysis revealed no considerable variation in the computed final prevalence of *G. duodenalis* infection in pigs.

4. Discussion

Pigs are important livestock consumed as a food source for humans around the world. However, pig farms are a major source of zoonotic infections such as *G. duodenalis*, leading to a self-limited illness with weight loss and malabsorption in both pigs and humans. These animals shed infective cysts into the environment, so investigation of the prevalence and assemblage distribution of *G. duodenalis* in swine population is of utmost medical and veterinary significance [14,27]. Based on our findings, published articles reported prevalence and assemblage data from 7272 pigs in 12 countries, showing a global molecular prevalence of 9.1% (95% CI: 5.6–14.3%). This prevalence was not affected by omitting individual studies, as shown by sensitivity analysis. Comparison of the results with those estimated in previous meta-analyses demonstrated a lower molecular prevalence than in cattle [22% (95% CI, 17–28%)] [38], dogs [15.2% (95% CI 13.8–16.7%)] and cats [12% (95% CI 9.2–15.3%)] [39]. This difference can be related to the type of animal, the number of examined samples, the geographical location and the technique used for the diagnosis.

The diversity of assemblages isolated from pigs worldwide was extremely high, since 6 out of 8 Giardia assemblages were found in swine populations, with the predominance of assemblage E [44.1% (95% CI: 24.8–59.6%)]. In addition, the frequency of assemblages A [9.9% (95% CI: 5.6–16.9%)] and B [28.2% (95% CI: 12.2–52.6%)] was relatively high. Another major finding was that canine- and feline-specific assemblages (C, D and F) were, also, reported in pigs, confirming the circulation of these genotypes among livestock, canids, felids, and humans. Nevertheless, only little is known on the frequency and distribution of assemblage F, since it as only isolated from pigs in a single study [22]. It was estimated that based on the nine papers, 66.4% (95% CI: 44.7–82.8%) of the Giardia positive samples were not molecularly characterized, so a considerable part of the samples was missed and remained unspecified.

Pertinent to the publication year, the highest frequency of the infection in pigs was between 2010 and 2015 [24.6% (95% CI: 5–67%)]; however, a correct analysis could not be reached due to the small number of studies and lack of variability during publication years. Continental and country surveys have demonstrated that the highest prevalence of giardiasis has been reported from Oceania [31.1% (95% CI: 26–36.7%)] and Canada [66.4% (95% CI: 57.6–74.2%), respectively; however, such data are derived from single studies, hence should be interpreted cautiously. The meta-regression results confirmed a direct association between reducing the prevalence of giardiasis and increasing the sample size. Therefore, those articles having below 600 sample sizes showed a lower pooled

Table 2
Prevalence of *G. duodenalis* in pigs based on evaluated subgroups.

Subgroup variable	Prevalence % (95% CI)	Heterogeneity (Q)	df (Q)	I^2 (%)	p-value
Publication year					
<2010	7.7 (0.3–69.9)	99.8	1	99	$p < 0.001$
2010–2015	24.6 (5–67)	140.5	2	98.6	$p < 0.001$
2015–2021	7.2 (4.4–11.6)	252.7	12	95.2	$p < 0.001$
Continent					
Africa	25.3 (19.9–31.6)	–	0	–	N.A
Asia	5.9 (3.3–10.3)	175.1	9	94.8	$p < 0.001$
Europe	8.1 (3.5–17.9)	56.8	3	94.7	$p < 0.001$
North America	23 (0.7–92.4)	139.8	1	99.3	$p < 0.001$
Oceania	31.1 (26–36.7)	–	0	–	N.A
Country					
Australia	31.1 (26–36.7)	–	0	–	N.A
Canada	66.4 (57.6–74.2)	–	0	–	N.A
China	4.6 (2.3–9.3)	112.8	6	94.7	$p < 0.001$
Denmark	14 (11.8–16.5)	–	0	–	N.A
Nigeria	25.3 (19.9–31.6)	–	0	–	N.A
Norway	1.5 (0.8–2.7)	–	0	–	N.A
Philippines	15.9 (7.8–29.8)	–	0	–	N.A
Poland	9.5 (4.8–17.9)	–	0	–	N.A
South Korea	14.8 (12.4–17.5)	–	0	–	N.A
Spain	17.2 (12.4–23.3)	–	0	–	N.A
Taiwan	4.2 (1.9–9.1)	–	0	–	N.A
USA	4.3 (2.6–6.9)	–	0	–	N.A
Sample size					
≤200	18.8 (7.3–40.6)	124.9	5	96	$p < 0.001$
201–400	7.9 (2.8–20.3)	141.5	4	97.2	$p < 0.001$
401–600	7.2 (5.6–9.2)	1.2	1	16.9	N.A
>600	4.5 (1.9–10.5)	166.7	4	97.6	$p < 0.001$

N. A: non-applicable ($p > 0.999$).

prevalence [4.5% (95% CI: 1.9–10.5)] than those with ≤200 sample size [4.5% (95% CI: 1.9–10.5)]. Accordingly, prevalence data obtained from lower sample size studies is closer to the actual occurrence of the parasite. Given meta-regression, although the prevalence of giardiasis has decreased in recently published studies, no statistically significant association was observed between these two variables. In contrast, a statistically remarkable correlation was found between sample size and the prevalence of *G. duodenalis* infection.

Most of the studies did not mentioned data on animal age and the sampling season, hence we could not estimate the total prevalence of the infection based on these subgroups. It is, however, noteworthy that during weaner and fattener stages pigs are highly exposed to the *G. duodenalis* infection [27,33,36]. Also, there are conflicting results on the prevalence of *Giardia* infection by age. Generally said, giardiasis in humans is usually associated with the recreational water activities, particularly during August–September, while it has not a particular seasonal pattern in pigs. However, some studies in weaner and grower pigs found that Giardia infections were more frequent in autumn and winter [27].

Based on the results from most studies, Giardia-positive samples were mostly detected by the amplification of the ssu rRNA gene, rather than protein-coding genes of gdh, tpi or β-giardin. The latter are single-copy genes with low sensitivity for molecular investigation. Hence, the reported findings suggest a low parasitic burden on the examined pig population. Nevertheless, many studies have used multilocus approaches, including gdh, tpi and/or β-giardin for genotyping [23,27,29]. Using one or more of these genes, mixed assemblages have been characterized in human, animal, and environmental samples but were reported mostly as casual findings. In fact, the frequency of mixed infections is believed to be underrated, as studies using assemblage-specific primers have shown that conventional PCR based on Sanger sequencing failed to detect many mixed infections. Next-generation amplicon sequencing (NGS) approaches are nowadays increasingly being employed to accurately determine mixed genetic variants within a sample for protozoan such as *Cryptosporidium* spp. (species/genotypes), *Eimeria* spp. (species) or *Blastocystis* sp. (subtypes) [40]. Lately, a *Giardia* spp. NGS protocol targeting a fragment of the bg gene was evaluated with conventional Sanger sequencing [41]. The findings of this investigation revealed that NGS provided a more acceptable resolution by specifying mixed assemblages in samples that Sanger sequencing ignored. However, this NGS protocol is yet to be used to evaluate the frequency of mixed assemblage infections in any individual host species. In addition, diagnostic methods based on microRNA can also improve the diagnosis of *G. duodenalis* [42].

In the present systematic review and meta-analysis no publication bias was reported among studies ($p = 0.088$). Also, this review met some limitations, including low number of included papers from most countries in different continents and lack of statistical analysis related to some variables such as age and sampling season. A high rate of heterogeneity expressed in the current review can be one of the serious limitations of this meta-analysis, which could substantially influence the outcomes. This may arise from differences in the geographical region, publication year, number of studies in each area, and sample size, as mentioned in Table 2. Some other parameters that didn't mention in the current review may, also, influence the publication bias such as the status of animal health, sampling procedures, sample preservation, raising method of animals, the sensitivity of diagnostic methods, age and sex of the

Group by Assemblage	Study name	Statistics for each study		
		Event rate	Lower limit	Upper limit
A	Armson, 2009a	0.211	0.139	0.307
A	Lam, 2021a	0.167	0.023	0.631
A	Lee, 2020a	0.009	0.001	0.062
A	Wang, 2018a	0.200	0.066	0.470
A	Jing, 2019a	0.095	0.024	0.311
A	Zou, 2021a	0.143	0.047	0.361
A	Liu, 2019a	0.080	0.020	0.269
A	Wang, 2017a	0.200	0.107	0.342
A	Rivero-Juarez, 2020a	0.031	0.004	0.191
A	Rodriguez-Rivera, 2016a	0.125	0.031	0.386
A	Petersen, 2015a	0.017	0.004	0.064
A		0.099	0.056	0.169
B	Afable, 2019a	0.286	0.072	0.673
B	Farzan, 2011a	0.716	0.609	0.803
B	Akinkuotu, 2019a	0.283	0.178	0.418
B	Jing, 2019b	0.762	0.540	0.897
B	Zou, 2021b	0.048	0.007	0.271
B	Liu, 2019b	0.040	0.006	0.235
B	Zhang, 2019a	0.214	0.100	0.402
B	Stojecki, 2015a	0.125	0.017	0.537
B		0.282	0.122	0.526
C	Lee, 2020b	0.109	0.063	0.182
C	Wang, 2018b	0.200	0.066	0.470
C	Liu, 2019c	0.080	0.020	0.269
C		0.116	0.073	0.179
D	Lam, 2021b	0.167	0.023	0.631
D	Zou, 2019c	0.500	0.059	0.941
D	Lee, 2020c	0.155	0.098	0.235
D		0.162	0.106	0.241
E	Armson, 2009b	0.411	0.314	0.515
E	Lam, 2021c	0.667	0.268	0.916
E	Farzan, 2011b	0.062	0.026	0.140
E	Akinkuotu, 2019c	0.717	0.582	0.822
E	Zou, 2019d	0.500	0.059	0.941
E	Lee, 2020d	0.182	0.120	0.265
E	Wang, 2018c	0.600	0.348	0.808
E	Jing, 2019c	0.143	0.047	0.361
E	Zou, 2021c	0.810	0.588	0.927
E	Liu, 2019d	0.800	0.600	0.914
E	Wang, 2017b	0.800	0.658	0.893
E	Rivero?Juarez, 2020b	0.063	0.016	0.218
E	Rodriguez-Rivera, 2016b	0.125	0.031	0.386
E	Zhang, 2019b	0.786	0.598	0.900
E	Stojecki, 2015b	0.500	0.200	0.800
E	Petersen, 2015	0.092	0.051	0.158
E		0.411	0.248	0.596

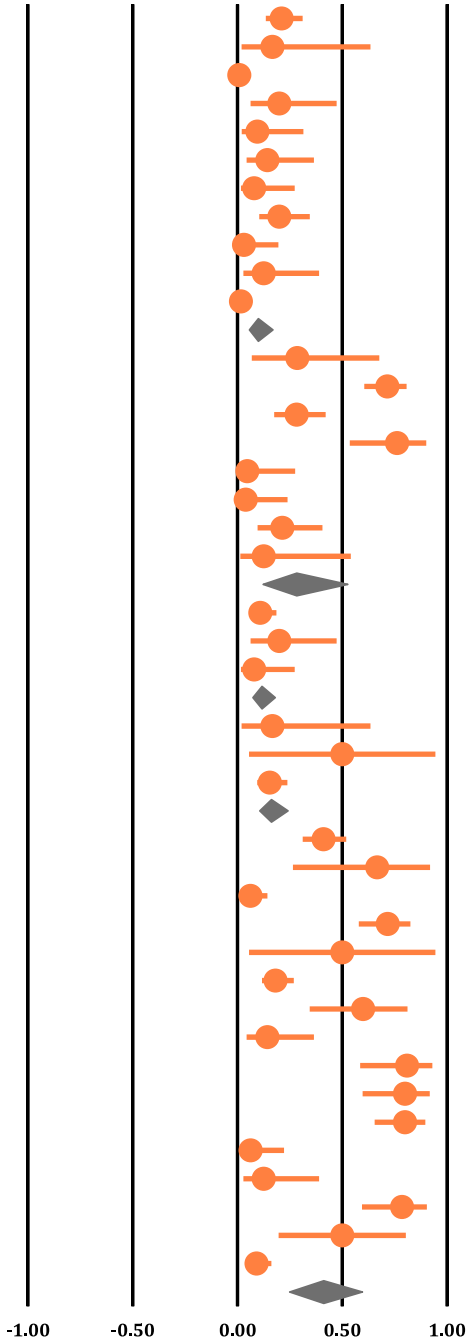

Fig. 4. Global prevalence of *G. duodenalis* assemblages in pigs.

Table 3
The global distribution of *G. duodenalis* genotypes (assemblages) in pigs collected from 17 molecular studies.

Author, year	Total samples (no.)	Infected samples (no.)	Prevalence (%)	Genotyping of infected samples[a]		Zoonotic Assemblage[d] (no/%)
				Genotyped[b] (no/%)	Unidentified[c] (no/%)	
Armson, 2009	289	90	31.1	A (19/21.1), E (37/41.1), F (1/1.1)	33/36.7	19/21.1
Lam, 2021	141	6	4.2	E (4/66.7), A (1/16.6). D (1/16.6)	–	1/16.6
Afable, 2019	44	7	15.9	B (2/28.6)	5/71.4	2/28.6
Farzan, 2011	122	81	66.4	B (58/71.6), E (5/6.2)	18/22.2	58/71.6
Akinkuotu, 2019	209	53	25.3	E (37/69.8), B (14/26.4), Mixed (2/3.8)	–	15/28.3
Zou, 2019	345	2	0.6	E (1/50), D (1/50)	–	–
Lee, 2020	745	110	14.8	E (20/18.2), D (17/15.4), C (12/10.9), A (1/0.9)	60/54.5	1/0.9
Wang, 2018	897	15	1.7	E (9/60), A (3/20), C (3/20)	–	3/20
Jing, 2019	801	21	2.6	B (16/76.2), E (3/14.3), A (2/9.5)	–	18/85.7
Zou, 2021	396	21	5.3	E (17/80.9), A (3/14.3), B (1/4.8)	–	4/19
Liu, 2019	93	25	26.9	E (20/80), A (2/8), C (2/8), B (1/4)	–	3/12
Wang, 2017	560	45	8	E (36/80), A (9/20)	–	9/20
Rivero-Juarez, 2020	186	32	17.2	E (2/6.2), A (1/3.1)	29/90.6	1/3.1
Rodriguez-Rivera, 2016	370	16	4.3	A (2/12.5), E (1/6.2)	13/81.2	2/12.5
Zhang, 2019	450	28	6.2	E (22/78.6), B (6/21.4)	–	6/21.4
Stojecki, 2015	84	8	9.5	E (4/50), B (1/12.5)	3/37.5	1/12.5
Hamnes, 2007	684	10	1.5	–	–	–
Petersen, 2015	856	120	14	E (11/9.2), A (2/1.7)	107/89.1	2/1.7

[a] Out of the positive samples of *Blastocystis*.
[b] Some have been genotyped.
[c] But some have not genotyped or not determined.
[d] The number and percentage of zoonotic genotypes are computed from assemblages A and B.

examined hosts, the quality of studies entered, etc. Hence, the obtained results from the present study must be interpreted with caution. Notwithstanding this, the present systematic review and meta-analysis is the first study to investigate the global molecular prevalence of this parasitic infection along with the distribution of related assemblages in pig populations. Overall, the findings of the existing study highlighted the importance of pigs in animal husbandry, veterinary medicine, zoonotic transmission of giardiasis, and compliance with health protocols in rearing and contact with pigs.

5. Conclusion

Humans are in close proximity to pigs in pig-raising countries; hence, they are highly exposed to the infectious zoonotic agents such as Giardia infection. A remarkably low molecular prevalence (9.1%) of *G. duodenalis* infection was determined among examined pigs worldwide, caused by various assemblages (A-F), among which A and B assemblages are of utmost zoonotic importance. The common pig assemblage, E, was the most prevalent isolated genotype from swine around the world. Still, little is known on the prevalence and distribution of Giardia assemblages in pigs and requires more extensive and detailed studies.

Author contribution statement

All authors listed have significantly contributed to the development and the writing of this article.

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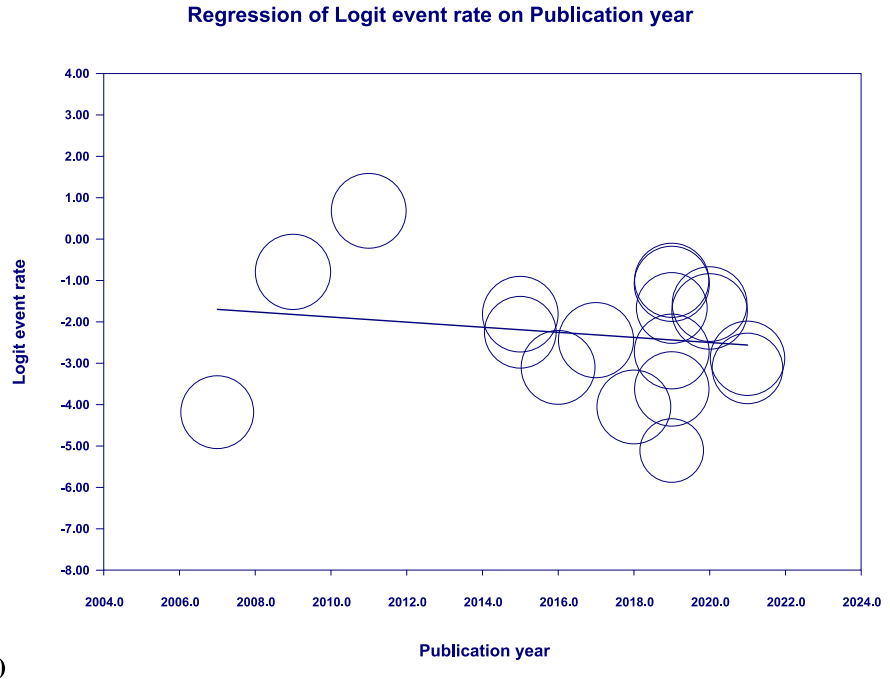
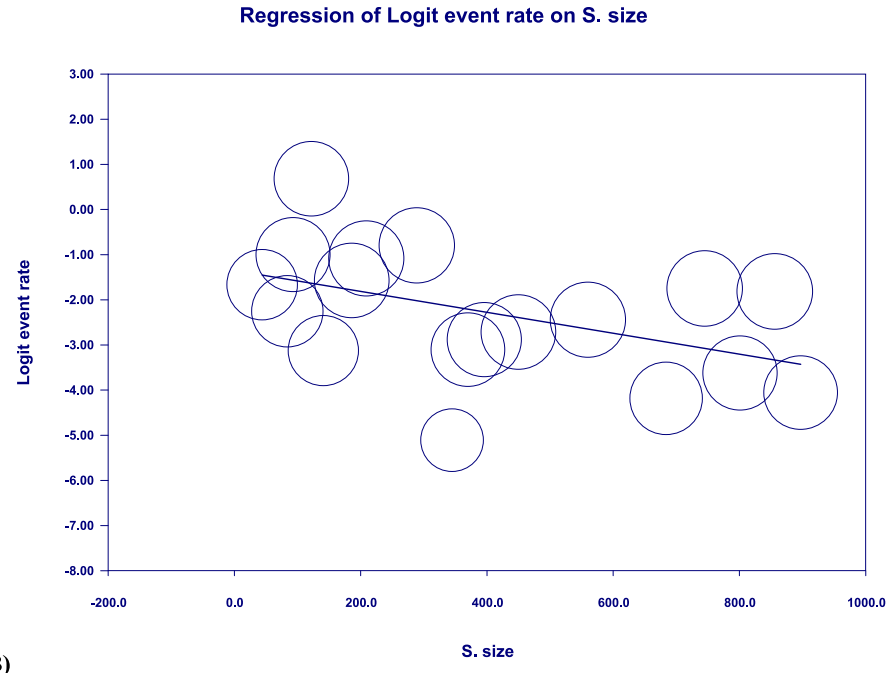
Data availability statement

Data will be made available on request.



(A)



(B)

Fig. 5. Association between the prevalence of giardiasis with publication year (A) and sample size (B) in pigs using meta-regression.

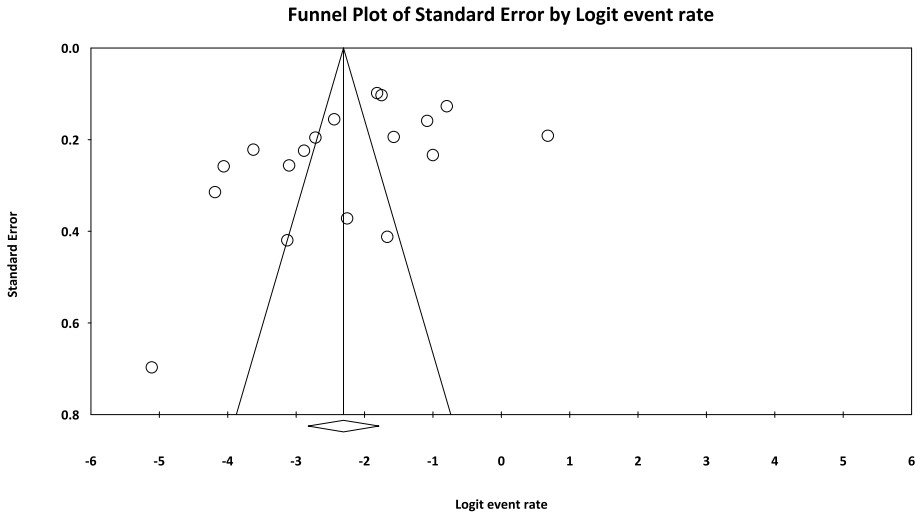


Fig. 6. Funnel plot and publication bias in the present systematic review and meta-analysis (p = 0.088).

Declaration of interest's statement

The authors declare no conflict of interest.

Appendix A. Supplementary data

Supplementary data related to this article can be found at https://doi.org/10.1016/j.heliyon.2023.e13243.

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