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Ovine enzootic abortion disease seroprevalence in small ruminants around the world: a systematic review

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Abstract: Chlamydia abortus is a causative agent of Ovine Chlamydiosis or Ovine Enzootic Abortion (OEA) or Enzootic Abortion of Ewes (EAE) and can be transmitted to humans, especially pregnant women during the lambing or kidding season from sheep, and goats, from infected flocks. The objective of this study was to estimate the pooled prevalence of chlamydial abortus infections in small ruminants. The study followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. Relevant studies were retrieved from PubMed, Scopus, Web of Science, and Google Scholar from 2001 to 2022. The retrieved studies were screened for eligibility and important data were extracted from the included studies. The quality of each included study was evaluated. Of 153 studies, 33 (with a total of 45453 samples) met the inclusion criteria and were included in the meta-analysis. The pooled prevalence of chlamydial infections in small ruminants was 13.4%. Among continents, the average prevalence of chlamydial abortus infections was highest in Asia (48.5%) and lowest in North America (3.0%) This systematic review emphasizes the global paucity of data on the prevalence of Chlamydia infection in sheep and goats. Despite this, studies show a rather high frequency of C. abortus infection in small ruminants. This geographical variance emphasizes the necessity of a regional strategy to chlamydia infection prevention and management in small ruminants, taking into account regional differences and risk factors to avoid its spread and limit the hazards associated with it.
Keywords: Chlamydia abortus; small ruminants (Sheep and Goats); seroprevalence; and World.

1. Introduction

Abortion in small ruminants can be caused by a variety of infectious and non-infectious agents that can be bacterial, viral, or parasitic in origin. It can cause large economic losses (Holler, 2012). These infectious diseases include: by bacteria (i.e., Chlamydia abortus, Campylobacter spp., Listeria spp., Coxiella burnetii, Brucella melitensis), viruses (i.e., Bluetongue virus; a plague of small ruminants virus, border disease virus), and parasites (i.e., Toxoplasma gondii) (Elhaig et al., 2018; Tejedor-Junco et al., 2019). Chlamydiaceae is a family of diverse groups of obligate intracellular Gram-negative bacterial pathogens widely distributed throughout the world, causing a wide range of infections and diseases in both animals and humans (Essig & Longbottom, 2015). Chlamydophila or Chlamydia abortus, formally called C. psittaci serotype 1 is a non-motile, coccoid, obligate intracellular bacterial (Selim, 2016) and the most important agent due to its ability to induce abortion in sheep and goats and the risk of zoonosis. This etiological agent is caused in sheep and goats, the disease known as Ovine Chlamydiosis or Ovine Enzootic Abortion (OEA) or Enzootic Abortion of Ewes (EAE) (Ahmed et al., 2021). The disease can be transmitted to humans especially pregnant women (Borel et al. 2018) during the lambing or kidding season. Sheep and goats from infected flocks represent a potential risk to pregnant women (Essig & Longbottom, 2015).

In animals (i.e., small ruminants), C. abortus can be acquired by inhalation, ingestion, direct inoculation into the eye, and venereal transmission. Sources of these organisms may include birth products, vaginal discharges, feces, urine, semen, and ocular and nasal secretions (CFSPH, 2017). The prominent sign of the disease is the expulsion of dead or weak lambs, peculiarly 2 to 3 weeks before lambing. The lambs usually look mature and normal but, in some cases, there may be 'pot-bellied' lambs due to subcutaneous edema (Ahmed et al., 2021).

Small ruminant farming is a source of income for many households in West Africa. It is sometimes their sole source of income, and other times it is paired with crops to secure their survival (Mensah et al. 2017). Small ruminant farming is integrated into the agricultural operations of rural communities, particularly women. On their farms, though, they encounter infectious diseases. Their contamination and exposure may go overlooked with routine health checks. Because animal abortions (zoonoses) are not properly diagnosed and documented in Benin (DSA, 2021), these infections might be to blame for miscarriage in these women. These infections are a huge issue for these women who want to improve their livelihood and get out of poverty by raising animals (Mensah et al., 2017).

As a result, the overall objective is to conduct a systematic review of the serological prevalence of enzootic ovine abortion disease in small ruminants worldwide, in order to determine and compare the disease's seroprevalence in different geographical regions by identifying regions where the disease is more prevalent and those where it is less prevalent.

2. Material and Methods

2.1. Eligibility criteria

2.1.1. Study inclusion

The inclusion criteria for study eligibility were as follows: (1) the study must be a full-text article published in English and French, (2) the study must be a cross-sectional (survey) study and report the prevalence of *C. abortus* infections in goats and sheep (number of positive and total samples), (3) the article which contained other diseases in combination with *C. abortus* and must be based on prevalence among small ruminants, (4) All studies that were conducted during the time frame of the years (January 2001 to July 2022) were included. We picked papers from 2001 to 2022 because, after 2001, all of the publications reported cases of various disorders in which *C. abortus* was diagnosed. These articles were largely chlamydiaceae information pieces. Other publications focused on the reasons for abortions in small ruminant farms.

2.1.2. Study Exclusion

Exclusion criteria were as follows: (1) Titles and abstracts not relevant to the study or not meeting the inclusion criteria, (2) All studies that were conducted outside the time frame of the years (January 2001 to July 2022), (3) All studies involving animals other than small ruminants, (4) All articles on bacterial or viral diseases that are combined with abortive chlamydia were excluded from this study.

2.2. Information sources and search strategy

A structured electronic search, using PRISMA guidelines, was performed on studies conducted on the serological prevalence of abortive chlamydia in small ruminant (sheep and goat) farms or flocks and published between January 2011 and July 2022. A systematic search was performed in PubMed with full text, Google Scholar, Web of Science, Scopus, and Science Direct. The following search terms were used: (*Seroprevalence* OR *Chlamydia abortus*) AND (*small ruminants OR prevalence* OR world*). Articles published in peer-reviewed journals were considered for review. Bibliographies of selected studies were also considered. Only manuscripts written in English or French (both languages were selected) and related to *C. abortus* seroprevalence in sheep and goats were considered. Articles published on multiple diseases at the same time, including abortive chlamydia, were excluded.

2.3. Study Records

2.3.1. Data Management and Data Collection Process

The mechanism that managed the records and data throughout the exam was software called Rayyan. This is a web-based software that were manage and controls the items that were retrieved through the databases.

2.3.2. Selection Process

Two independent reviewers were evaluating articles for inclusion in the studies based on title and abstract. The full texts were then retrieved and evaluated for inclusion. A third reviewer was making the final decision in case of discrepancies.

2.3.3. Data Items

2.3.3.1. Type of participants

Small ruminants (sheep and goats) from different geographical regions. Any study including both species based on the seroprevalence of *C. abortus* was included.

2.3.3.2. Type of Intervention

Interventions deemed eligible for inclusion in this study must be related to serological testing for *C. abortus* and must have the objective of assessing the prevalence of this disease.

2.3.3.3. Types of Comparison

Geographical comparison: to compare the disease's seroprevalence throughout the continents from which the nations in this study are recruited.

2.3.3.4. Types of Outcomes

Disease prevalence: an estimate of the proportion of diseased animals in a particular population. This is the estimated number of animals that tested positive out of all samples submitted for serological testing in this study.

2.4. Risk of bias

The publications were evaluated for their risk of bias, the performance of the study, the selection, and detection of titles that were related to access, and compare the prevalence obtained to that prevalence contained in the study. This was performed using SYRCLE's risk of bias tool adapted to the CAMARADES checklist.

The following questions for **SYRCLEs** were asked: (1) Was the allocation sequence generated and applied appropriately, (2) Were the groups similar at baseline, or were they adjusted for confounders in the analysis, and (3) Were the allocation to the different groups adequately concealed during the study, (4) Were the animals randomly housed during the experiment, (5) Were caregivers and/or investigators blinded to know which intervention each animal received during the experiment, (6) Were the animals randomly selected for outcome assessment, (7) Were the outcome assessor-blinded?

The **CAMARADES checklist** for study quality was also used and the questions concerning the aspect of (1) peer-reviewed publication; (2) control of sample tested; (3) random allocation for positive sample; (4) blinded induction of *C. abortus*; (5) blinded assessment of outcome; (6) Calculate the prevalence without mention the method used; (7) animal model (aged, infected or healthy); (8) sample size calculation; (9) compliance with animal welfare regulations; and (10) statement of potential conflict of interests, were asked. This is to show the quality of each study the strength of prevalence and the relationship between each study's components.

2.5. Data extraction

2.5.1. Procedure for study selection

The titles and/or abstracts of studies retrieved using the search strategy and those from additional sources were independently reviewed by two review authors to identify studies that potentially meet the inclusion criteria described above. The full text of these potentially eligible studies was retrieved and evaluated independently by two members of the review team. Any disagreement between them about the eligibility of particular studies was resolved by discussion with a third reviewer.

A standardized, pre-piloted form was used to extract data from included studies to assess study quality and evidence synthesis. Information extracted included: country of origin, original sample (number of animals examined), target sample (number of animals positive for the test performed), description of the intervention, study design, animal species involved, specimen, laboratory method used for analysis, results obtained, and information to assess the risk of bias. Missing data were requested from the study authors.

2.5.2. Methods for data selection

Two reviewers independently extracted data from each article. We were first trying to extract numerical data from tables, text, or figures. If these are not reported, we extracted data from graphs using digital software. In case data are not reported or are unclear, we were attempting to contact authors by e-mail (max. 2 attempts). In case an outcome (prevalence) is measured at multiple time points, data from the time point where efficacy is highest were included.

2.6. Data analysis

A narrative synthesis of the findings was provided from the included studies, structured around the type of intervention, target population characteristics, type of outcome, and intervention content. We were providing summaries of intervention effects for each study by calculating risk ratios (for dichotomous outcomes) or standardized mean differences (for continuous outcomes).

We anticipate that there was limited scope for meta-analysis because of the range of different outcomes measured across the small number of existing trials. However, where studies have used the same type of intervention and comparator, with the same outcome measure, we were pool the results using a random-effects meta-analysis, and calculate 95% confidence intervals and P values for the outcome. Heterogeneity between the studies in effect measures was assessed using both the t-test and the I^2 statistic. We were considering an I^2 value greater than 50% indicative of substantial heterogeneity using Review Manager software version 5.4 (RewMan version 5.4). We conduct sensitivity analyses based on study quality. We used stratified meta-analyses to explore heterogeneity in effect estimates according to study quality; study populations; the logistics of intervention provision; and intervention content. We were also assessing evidence of publication bias through the Egger test. The subgroup analysis was assessed by considering the continents, the type of specimens, and the diagnostic techniques used in all 33 studies to assess the seroprevalence of chlamydia abortus.

3. Results (title 4)

3.1. Search results and characteristics of included studies

A total of 153 articles published between 2001 and 2022 were identified from electronic databases such as PubMed (48), Scopus (34), Web of Science (46), and Google Scholar (25). Of these, 111 were excluded (40 duplicate publications and 71 irrelevant titles or abstracts). The full text of the remaining 34 articles was evaluated for eligibility. Of these 42 articles, 09 were review articles or articles not reporting on seroprevalence or prevalence of the disease in sheep and goats. Therefore, 33 studies (Abnaroodheleh et al., 2021; Al-Ahmed & Salman, 2020; Al-Qudah et al., 2004; Benkirane et al., 2015; Chahota et al., 2015; Čisláková n et al., 2007; Clemente et al., 2011; Esmaeili et al., 2021; Esmaeili et al., 2015; Fahad & Saleh, 2017; Fayez et al., 2021; Gokce et al., 2007; Hailat, 2018; Hamedi et al., 2020; Hazlett et al., 2013; Kalender et al., 2013; Simeonov and chilingirova, 2018; Leopoldo et al., 2016; Resplandes[1] et al., 2014; Malal et al., 2020; Malal & Turkyilmaz, 2021; Masala et al., 2005; Paul et al., 2004; Riyadh S. Aljumaah, 2012; Roukbi et al., 2016; Sidibe et al., 2019; Spičic et al., 2015; Sun et al., 2020; Szeredi et al., 2006; Tesfaye et al., 2020; Trávniček et al.,

2002; Yin et al., 2014; Iraninezhad et al, 2020) reporting the prevalence or seroprevalence of chlamydia infections in small ruminants between 2001 and 2022 were included in this systematic review and meta-analysis .

A flow chart of the selection process is presented in Figure 1. The characteristics of the included studies and the data from these studies are presented in Table 1 and Table 2. Across all 33 studies, 6113 samples (of a total of 45453 samples) were positive for chlamydia abortus infections. Most studies were conducted in Asia (n = 16), Europe (n = 11), Africa (n = 3), North America (n = 1), and South America (n = 2). ELISA (n=16) and non-ELISA (n=9) were the most frequently used technical methods for serological analysis. The blood sample (n=27) was reported as the most used specimen in the collection of samples in small ruminants. Most of the included studies (29) were listed in the "moderate" category concerning quality assessment.

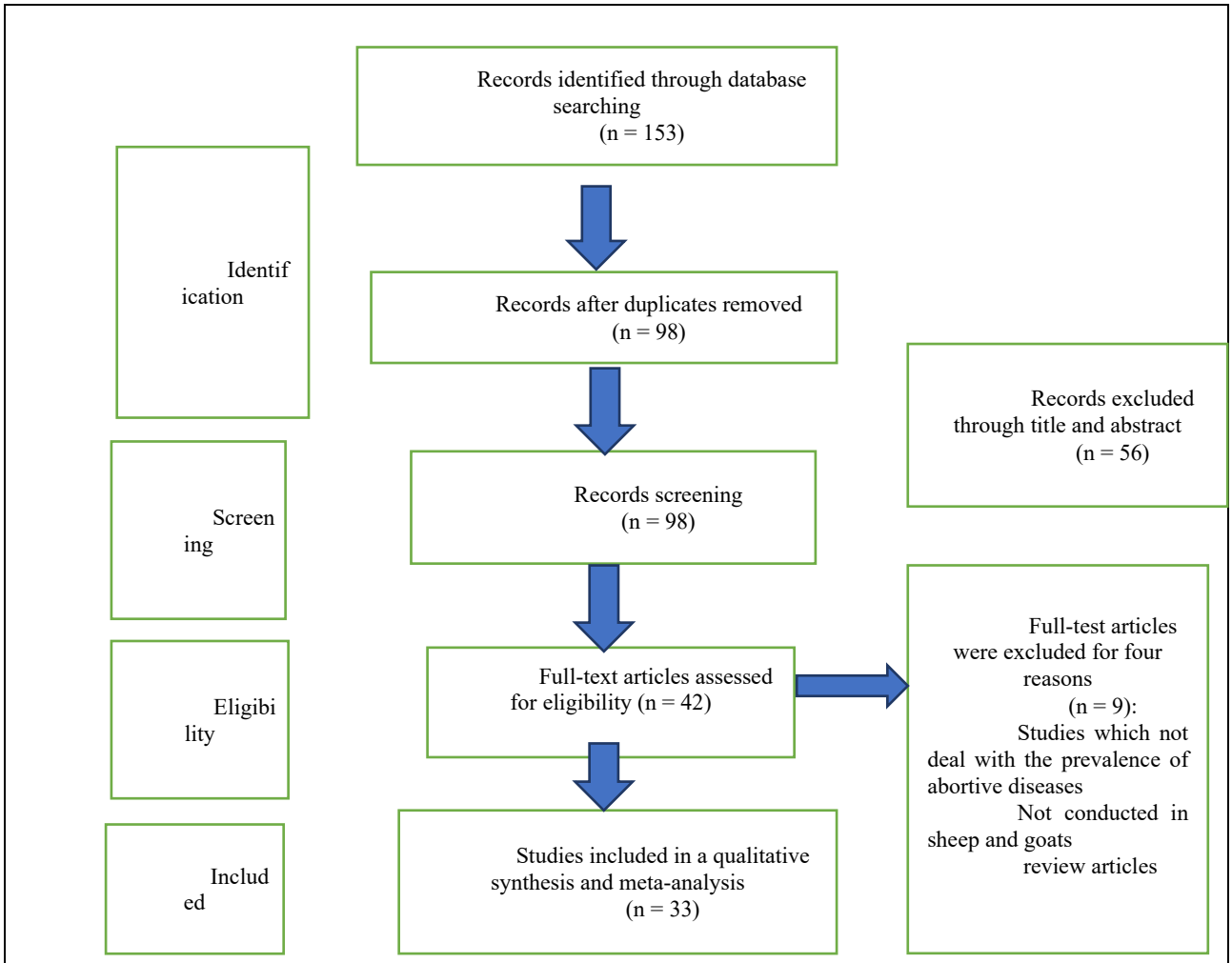

Figure 1 – Flow chart of included studies based on PRISMA guidelines searching C. abortus in English and French

ID	Authors_and_year	Specimen	Method_used	Quality study assessment
1	Abnaroodheleh et al 2021	blood sample	I-ELISA	Moderate
2	Al-Ahmad and Salman 2020	blood sample	I-ELISA	Strong
3	Aljumaah and Hussein 2012	blood sample	ELISA	Moderate
4	Benkirane et al 2015	blood sample	ELISA	Moderate
5	Chahota et al 2015	blood sample	AGP	Moderate
6	Cislakovan et al 2007	blood sample	CFT	Moderate
7	Esmaeili et al 2015	vaginal_ocular swab	ELISA	Moderate
8	Esmaeili et al 2021	blood sample	RT-PCR	Moderate
9	Fahad and Salman 2017	blood sample	ELISA	Moderate
10	Fayez et al 2021	blood sample	ELISA	Moderate
11	Gokce et al 2007	blood sample	CFT	Moderate
12	Hailat et al 2018	Placentas	qPCR and IHC	Moderate
13	Hamedi et al 2020	fœtal sample	PCR	Moderate
14	Hazlett et al 2013	Placentas	RT-PCR	Strong
15	Iraninezhad et al 2020	blood sample	ELISA	Moderate
16	Kalender et al 2013	fœtal sample	Culture and PCR	Moderate
17	Leopoldo et al 2016	blood sample	CFT	Moderate
18	Malal and Turkyilmaz 2021	fœtal tissus_palcenta	RT-PCR	Moderate
19	Malal et al 2020	blood sample	ELISA	Moderate
20	Masala et al 2005	blood sample	ELISA	Moderate
21	Al-Qudah et al 2004	blood sample	I-ELISA	Moderate
22	Rajinder et al 2004	blood sample	ELISA	Moderate
23	Resplandes et al 2014	blood sample	ELISA	Strong
24	Roukbi et al 2016	blood sample	ELISA	Moderate
25	Sidibe et al 2019	blood sample	I-ELISA	Moderate
26	Simeonov & Chilingirova 2018	blood sample	PCR	Moderate
27	Spičic et al 2015	blood sample	ELISA	Moderate
28	Sun et al 2020	blood sample	IHA	Moderate
29	Szeredi et al 2006	blood sample	ELISA	Strong
30	Tavares Clemente et al 2011	blood sample	I-ELISA	Moderate
31	Tesfaye et al 2020	blood sample	ELISA	Moderate
32	Trávniček et al 2002	blood sample	I-ELISA	Moderate
33	Yin et al 2014	blood sample	I-ELISA	Moderate

Table 1 – Characteristics of detection methods for enzootic ovine abortion disease of all included studies.

ID	Authors_and_year	Country	sheep_positive	sheep_samples	goat_positive	goat_samples
1	Abnaroodheleh et al 2021	Iran	22	101	1	23
2	Al-Ahmad and Salman 2020	Iraq	26	100	27	80
3	Aljumaah and Hussein 2012	Saudi Arabia	30	399	59	171
4	Benkirane et al 2015	Morroco	55	202	16	106
5	Chahota et al 2015	India	89	906	70	362
6	Cislakova et al 2007	Slovaquie	2360	20878	85	1162
7	Esmaeili et al 2015	Iran	218	816	150	624
8	Esmaeili et al 2021	Iran	117	504	84	330
9	Fahad and Salman 2017	Iraq	8	30	13	154
10	Fayez et al 2021	Saudi Arabia	187	1717	114	1101
11	Gokce et al 2007	Turkey	236	2302	192	680
12	Hailat et al 2018	Jordan	12	23	2	2
13	Hamedi et al 2020	Iran	36	200	11	200
14	Hazlett et al 2013	Canada	42	162	54	92
15	Iraninezhad et al 2020	Iran	44	271	44	181
16	Kalender et al 2013	Turkey	6	64	1	7
17	Leopoldo et al 2016	Brazil	41	500	38	600
18	Malal and Turkyilmaz 2021	Turkey	63	380	15	70
19	Malal et al 2020	Turkey	183	628	32	205
20	Masala et al 2005	Italy	29	611	6	106
21	Al-Qudah et al 2004	Jordan	433	1984	82	721
22	Rajinder et al 2002	India	80	300	89	271
23	Resplandes et al 2014	Brazil	17	150	21	300
24	Roukbi et al 2016	Syria	65	666	9	142
25	Sidibe et al 2019	Mali	13	368	18	504
26	Simeonov & Chilingirova 2018	Bulgaria	18	43	6	24
27	Spičic et al 2015	Croatia	18	93	8	69
28	Sun et al 2020	China	71	312	29	169
29	Szeredi et al 2006	Hungary	113	246	13	75
30	Clemente et al 2011	Portugal	26	59	28	66
31	Tesfaye et al 2020	Ethiopia	17	213	33	293
32	Trávniček et al 2002	Slovaquie	26	230	24	99
33	Yin et al 2014	Belgium	0	48	38	958

Table 2 – Characteristics of the data from all included studies.

3.2. Pooled prevalence (use dot and one number after = 14.5%, instead of 14,46%)

The pooled prevalence of chlamydial infections was 13.4%. High heterogeneity I^2 was observed among the included studies (Chi2-value = 372.3, df =32, P < 0.00001, I^2 = 91.0%), and the overall effect was 0,25 and was not significant (P = 0.85) (Figure 2).

3.3. Subgroup analysis

Significant differences among subgroups were found for three characteristics (continents, types of specimens, and diagnostic techniques) (Table 2). For continents, the prevalence was highest in Asia (48.5%) and lowest in North America (3%). For specimens, the prevalence was highest for blood samples (81.8%) and lowest for both vaginal samples and fetal tissue samples (3%). For diagnostic techniques, the prevalence was highest for ELISA (48.5%) and lowest for PCR (9.1%).

Characteristics and Subgroups	Effect size			P-value for subgroups
	Study (no)	Point estimate (%)	95% IC	
Overall	33	13,4	13,1 ± 13,8	
Continents				
Africa	3	9,1	2,2 ± 20,4	0,04
Asia	16	48,5	28,9 ± 68,1	
Europe	11	33,3	14,9 ± 51,8	
North America	1	3,0	3,7 ± 9,7	
South America	2	6,1	3,3 ± 15,4	
Specimens				
blood sample	27	81,8	66,7 ± 96,9	0,13
Placenta	2	6,1	3,3 ± 15,4	
Vaginal samples	1	3,0	3,7 ± 9,7	
Fetal sample	2	6,1	3,3 ± 15,4	
Fetal tissue_placenta	1	3,0	3,7 ± 9,7	
Techniques				
ELISA	16	48,5	28,9 ± 68,1	0,03
PCR	3	9,1	2,2 ± 20,4	
Non-PCR	5	15,2	1,1 ±29,2	
Non-ELISA	9	27,3	9,8 ± 44,7	

Table 3 – Pooled seroprevalence and subgroup analysis.

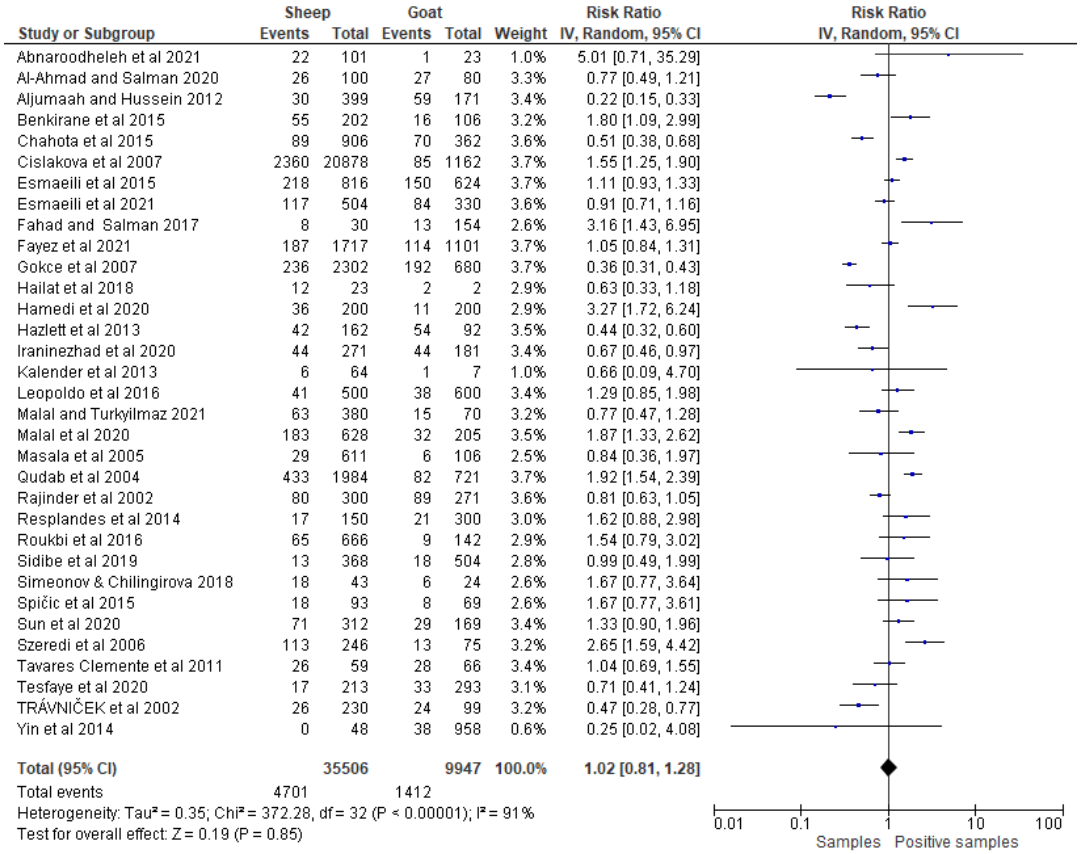

Figure 2 – Forest plot of the pooled prevalence of all included studies.

3.4. Publication of bias

No evidence of publication bias was observed. The funnel plot appeared approximately symmetrical. Egger's test for publication bias was not significant (P = 0.85) (Figure 3).

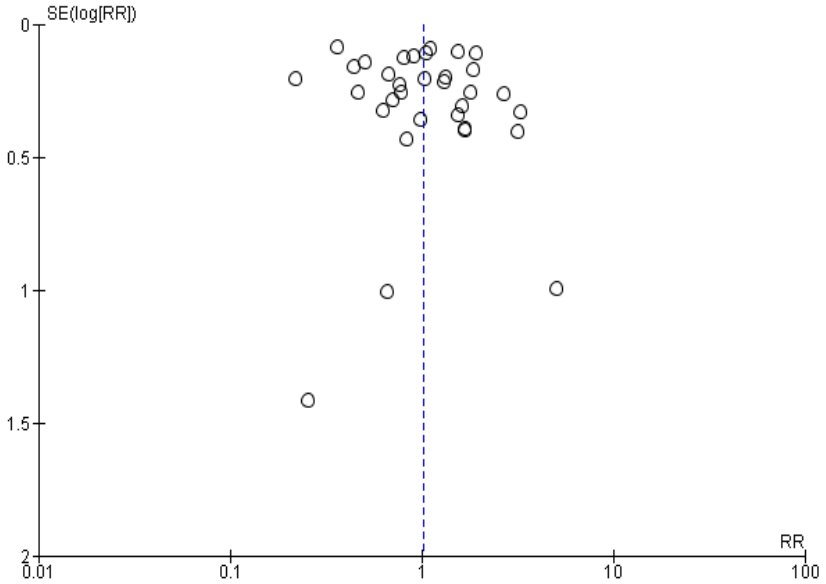

Figure 3 – Funnel plot of the pooled prevalence of all included studies for C. abortus during Meta-analysis

4. Discussion

To our knowledge, this systematic review is the first to provide a comprehensive concept of the incidence of abortive chlamydia in small ruminants by pooling data from seroprevalence studies published from inception from 2001 to 2022. A total of 33 studies were eligible for this review which included 45453 small ruminants of which 6113 were positive (13.4%). The review indicates that there was very little research on this abortive disease in sheep and goats until 2011 when a marked increase in prevalence studies was noted. The findings show that total seroprevalence ranged from 2.0 to 76.1%. However, this seroprevalence is lower than the 32.7% reported by Haif et al. (2021) in their study on abortifacient illnesses and related risk factors in small ruminants in Algeria. Methodological variations and the animal populations considered can explain the observed disparity in seroprevalence between the two studies. Haif et al. (2021) contained only studies done in Algeria, but this systematic review included papers from many nations. Because of environmental variables, differing husbandry techniques, or the existence of certain chlamydia strains, chlamydia infection rates may differ significantly.

When the obtained data was analyzed, it was discovered that the prevalence of chlamydia infections was highest in Asia (48.5%). This suggests that a considerable percentage of small ruminants were infected with Chlamydia in the included research from various Asian nations. Several variables may contribute to Asia's high prevalence. To begin, the study discovered that 16 studies from the Asian continent were included in the analysis, representing a reasonably substantial sample. The existence of a significant number of papers may imply a surge in interest in research on chlamydia infections in small ruminants in Asia, which may explain why the frequency is greater there. Furthermore, these Asian investigations were done across the continent, demonstrating that chlamydia infections in small ruminants are not restricted to a single location, but are ubiquitous across Asia. Environmental circumstances, agricultural techniques, animal eating patterns, and health management approaches might all contribute to this (Hu et al., 2018). Furthermore, compared to other animal groups, the seroprevalence of chlamydia infections in small ruminants is still very low. Previous research has found that birds (20%) (Ebani et al., 2016) and crocodiles (23.5%) (Inchuai et al., 2021) had greater prevalence rates. The number of studies considered and the number of samples analyzed might explain this disparity. The systematic review's avian and crocodile research employed fewer studies (n=20) and fewer samples (n=25) than this small ruminant investigation. However, other continents, including Europe and Africa, were also explored in this systematic study. Based on 11 included research, the average prevalence of chlamydia infections in small ruminants in Europe was 33.3%. This suggests a very high incidence in Europe as well, but significantly lower than in Asia. This review only included three papers from Africa. These revealed a 9.1% frequency of *C. abortus* infections in small ruminants. However, the number of research available for Africa was low in comparison to Asia and Europe, which may compromise the accuracy of the point estimate of prevalence(Inchuai et al., 2021).

It is crucial to highlight that the results found in our systematic review are based on the included studies and may vary depending on study population characteristics, infection detection techniques, and inclusion/exclusion criteria. It is therefore critical to consider these aspects when evaluating the results and the study's limitations. Various types of specimens utilized in chlamydia investigations were discovered in our comprehensive analysis, including blood, placenta, fetal and vaginal specimens, and fetal tissues. According to the included studies, the prevalence of chlamydia infections was greater in blood samples (81.8%) than in other sample types. We might conjecture about the processes underlying these observations to better explain this difference. One possible explanation is that chlamydia is easier to detect in the blood due to its systemic presence (Longbottom & Coulter, 2003). Pathogens can be identified in the bloodstream as the illness travels throughout the body, making them simpler to identify using certain testing procedures. Placenta, fetal and vaginal specimens, and fetal tissues, on the other hand, may have special limits (Selim et al., 2021). For example, the presence of infection may differ based on anatomical location and gestational time. The decreased prevalence in vaginal samples and fetal tissues is likely attributable to the infection's presence in other regions of the reproductive system. Another probable argument is that blood sample procedures are more convenient and less intrusive than other types of samplings. When researchers suspect chlamydia infection, collecting a blood sample may be easier and less harmful for the patient than alternative collection methods, such as placental or fetal tissue sampling (Rodolakis & Laroucau, 2015).

We investigated the various diagnostic procedures used to detect *C. abortus* in this study. The findings of our investigation demonstrated a substantial difference in prevalence between PCR, ELISA, non-PCR, and non-ELISA procedures with the ELISA diagnostic technique having a higher prevalence (48.5%). It is worth mentioning that the ELISA method was used in more investigations than the other techniques. Indeed, the ELISA method was employed in 16 reports, while PCR, non-PCR, and non-ELISA procedures were used in just 3, 5, and 9 studies, respectively. This gap in diagnostic tools emphasizes the necessity of the ELISA approach for detecting *C. abortus*. Based on these findings, we may conclude that the ELISA approach is the best for identifying *C. abortus*. However, it is vital to note that each diagnostic procedure has distinct benefits and limitations, as well as varying sensitivity and specificity. As a result, many criteria such as available resources, logistical restrictions, and the specific aims of the research or clinical environment should be considered when selecting a diagnostic approach (Selim, 2016). It should also be highlighted that our systematic review does not only examine diagnostic procedures, but also other elements of *C. abortus* detection, such as sample

methods, study selection criteria, and sensitivity and specificity assessments (Inchuai et al., 2021). In conclusion, while the ELISA technique was extensively utilized in the included studies and had a high prevalence in our systematic review, it is crucial to consider the individual characteristics of each diagnostic approach and carefully analyze their usefulness in a given situation (Laroucau et al., 2009). To identify the optimal diagnostic procedure for *C. abortus*, a customized, evidence-based strategy is required.

When doing a systematic review, it is critical to acknowledge and discuss the study's shortcomings, as well as suggestions to enhance data quality and decrease potential bias. We acknowledge some limitations in this study that must be addressed for a more accurate interpretation of the data. First, we must emphasize that the meta-analysis approach depends on data from original published research. As a result, the quality and completeness of this data may vary greatly from research to study. A potential enhancement would be to broaden the search to include more data sources, such as unpublished papers, unpublished data, and trials listed in specialist registries. This would result in a more complete dataset, lowering the possibility of bias in research selection.

Furthermore, we observe that the number of papers in our study that describe specific subgroups of certain features is modest. This constraint may have an effect on the statistical strength of our results, leading to a misleading negative interpretation (type 2 error). One solution would be to encourage future research that focuses exclusively on these subgroups of interest. Larger sample sizes in each subgroup would allow for increased statistical power and more solid results. Furthermore, in our study, we must evaluate potential causes of bias. Publication bias, such as researchers' desire to report important and favorable results, may skew the meta-analysis results. Strategies such as searching for unpublished papers, running sensitivity analyses, and applying funnel plot skewness tests can be used to reduce this bias. These methods enable us to detect and quantify the influence of publication bias on our results.

Finally, it should be noted that our systematic evaluation is susceptible to the intrinsic limitations of the studies that were included. These studies may have biases of their own, such as measurement inaccuracy, selection bias, or performance bias. Although we have made attempts to reduce these biases, it is important to understand that they may impact the overall outcomes of the meta-analysis. Despite the limitations discussed, it is crucial to note that this systematic review provides a careful synthesis and assessment of current research on the subject. Additional measures may have been adopted to increase the review's quality, such as broadening the search, increasing the number of papers included in the subgroups of interest, accounting for potential biases, and minimizing their influence. By taking these factors into account, we may improve the validity and dependability of our findings and provide the groundwork for future research and decision-making.

5. Conclusion

This systematic review emphasizes the global paucity of data on the prevalence of *C. abortus* infection in sheep and goats. Despite this, studies show a rather high frequency of the pathogen in small ruminants, reaching 13.4%. The most regularly used diagnostic approach appears to be ELISA, with blood samples being the most usually taken. The prevalence of *C. abortus* infection varies greatly between continents with Asia having the greatest incidence and North America having the lowest. This geographical variance emphasizes the necessity of a regional strategy for chlamydia infection prevention and management in small ruminants. These must take into account regional differences and risk factors to avoid its spread and limit the hazards associated with it.

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