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Review

A One Health systematic review and meta-analysis of Coxiella burnetii prevalence in humans, animals, and vectors in Algeria

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Abstract

Coxiella burnetii, the causative agent of Q fever, is a globally distributed zoonotic pathogen affecting humans, domestic animals, and arthropod vectors. In Algeria, fragmented data suggest widespread circulation, yet no comprehensive quantitative assessment exists. This study aimed to systematically review and meta-analyse the prevalence of *C. burnetii* in humans, animals, and vectors in Algeria, using a One Health perspective. A systematic search of PubMed, Scopus, Web of Science, and Google Scholar was conducted up to January 2026. Studies reporting serological or molecular detection of *C. burnetii* in Algeria were included. Random-effects meta-analysis was performed to estimate pooled prevalence, with subgroup analyses by host species, region, and diagnostic method. A total of 35 studies were included, encompassing 8,372 samples and 80 prevalence observations. Pooled prevalence was highest in camels (73.7%; 95% CI: 66.5–79.8%), followed by small ruminants (15.8%; 95% CI: 10.6–22.9%) and cattle (11.8%; 95% CI: 7.2–18.8%). Ticks showed a pooled prevalence of 10.0% (95% CI: 3.2–27.1%), while human infection had a pooled prevalence of 3.7% (95% CI: 0.9–13.9%). The south-eastern region exhibited the highest prevalence, and serological methods generally reported higher rates than molecular methods. High heterogeneity (I^2 > 75%) was observed across studies. *Coxiella burnetii* is widely circulating among humans, domestic animals, camels, and ticks in Algeria, with notable variation between hosts and regions. Camels and small ruminants act as major reservoirs, while humans remain at risk, particularly those in close contact with livestock. Integrated One Health surveillance and targeted control strategies are urgently needed to reduce the burden of Q fever.

Keywords

Coxiella burnetii, One Health, Algeria, Q fever, meta-analysis, Zoonosis, Prevalence

Introduction

Q fever is a worldwide zoonosis caused by *Coxiella burnetii*, an obligate intracellular Gram-variable bacterium characterised by high infectivity and environmental persistence (Maurin & Raoult, 1999). Domestic ruminants—particularly cattle, sheep, and goats—constitute the main reservoirs (Cutler et al., 2007). Although infection in livestock is often asymptomatic, it may lead to reproductive disorders such as abortion, stillbirth, infertility, metritis, and mastitis, resulting in significant economic losses (Rodolakis, 2009). Massive bacterial shedding occurs during parturition, especially through placentas and birth fluids, representing the primary source of environmental

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contamination (Arricau-Bouvery & Rodolakis, 2005; Schimmer et al., 2011). In goats, abortion rates of up to 90% have been reported during outbreaks (Rodolakis et al., 2007).

In humans, infection is mainly acquired through inhalation of contaminated aerosols generated during animal parturition or handling of infected materials. The environmental resistance of *C. burnetii* facilitates airborne spread over considerable distances (Angelakis & Raoult, 2010). Clinically, acute Q fever commonly manifests as a febrile illness, pneumonia, or hepatitis, while a minority of cases progress to chronic forms such as endocarditis (Tissot-Dupont & Raoult, 2008; Million et al., 2010). Due to its multi-host ecology and impact on both veterinary and human health, Q fever represents a significant One Health challenge.

In Algeria, livestock production—including sheep, goats, cattle, and camels—plays a major socio-economic role. Despite frequent reports of reproductive disorders, Q fever remains underdiagnosed. Over the past decade, several serological and molecular investigations have demonstrated the circulation of *C. burnetii* in multiple animal species and regions of the country (Yahiaoui et al., 2013; Agag et al., 2016; Benaissa et al., 2017; Menadi et al., 2020). However, prevalence estimates vary considerably according to host species, geographic area, and diagnostic methods.

Recent global systematic reviews have highlighted substantial heterogeneity in Q fever epidemiology worldwide and emphasised the need for region-specific quantitative syntheses (Rahal et al., 2025). To date, no systematic review and meta-analysis have comprehensively integrated available serological and molecular data to estimate the pooled prevalence of *C. burnetii* infection in Algeria.

Therefore, the objective of the present study is to conduct a systematic review and meta-analysis to (i) estimate the pooled prevalence of Q fever in Algeria, (ii) evaluate heterogeneity according to host species, geographic region, and diagnostic approach, and (iii) identify epidemiological gaps relevant to veterinary and public health interventions.

Materials and methods

Study design

This study was designed as a systematic review and meta-analysis to synthesise available evidence on the prevalence of *Coxiella burnetii* in humans, animals, and vectors in Algeria. The methodology followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines to ensure transparency, reproducibility, and methodological rigour. The PRISMA checklist and flow diagram were used to guide study identification, screening, eligibility assessment, and inclusion.

Search strategy

A comprehensive literature search was conducted in PubMed, Scopus, Web of Science, and Google Scholar from database inception to January 31, 2026. The search strategy combined Medical Subject Headings (MeSH) terms and free-text keywords related to the pathogen, the disease, and the geographic location. Boolean operators (“AND”, “OR”) were applied to maximize search sensitivity. The core search string used across all databases was:

("*Coxiella burnetii*" OR "*Coxiella*" AND "*burnetii*" OR "Q fever" OR "Query fever") AND (Algeria OR Algerian) AND (human* OR patient* OR cattle OR sheep OR goat* OR camel* OR horse* OR dog* OR cat* OR tick* OR vector*)

Search strings were adapted to each database syntax. No restriction on publication year was applied. Studies published in English or French were eligible.

Full-text restriction

Only studies for which full texts were accessible were included to allow accurate extraction of methodological details and raw prevalence data (sample size and number of positive cases). When full texts were not directly available, attempts were made to retrieve them via institutional access and direct author contact. Studies for which sufficient quantitative data could not be obtained were excluded to ensure analytical validity.

Reference lists of included articles and relevant reviews were manually screened to identify additional eligible studies. All records were exported into reference management software, and duplicates were removed prior to screening.

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Eligibility criteria

Inclusion criteria

Studies were included in the systematic review and meta-analysis if they met all of the following criteria:

(i) Original research articles reporting epidemiological data on *C. burnetii* infection or exposure;(ii) Studies conducted in Algeria;

(iii) Investigations involving human populations, domestic or wild animals, and/or arthropod vectors;

(iv) Use of validated serological and/or molecular diagnostic methods for the detection of *C. burnetii*;

(v) Provision of sufficient data to calculate prevalence estimates, including sample size and number of positive cases (Figure 1).

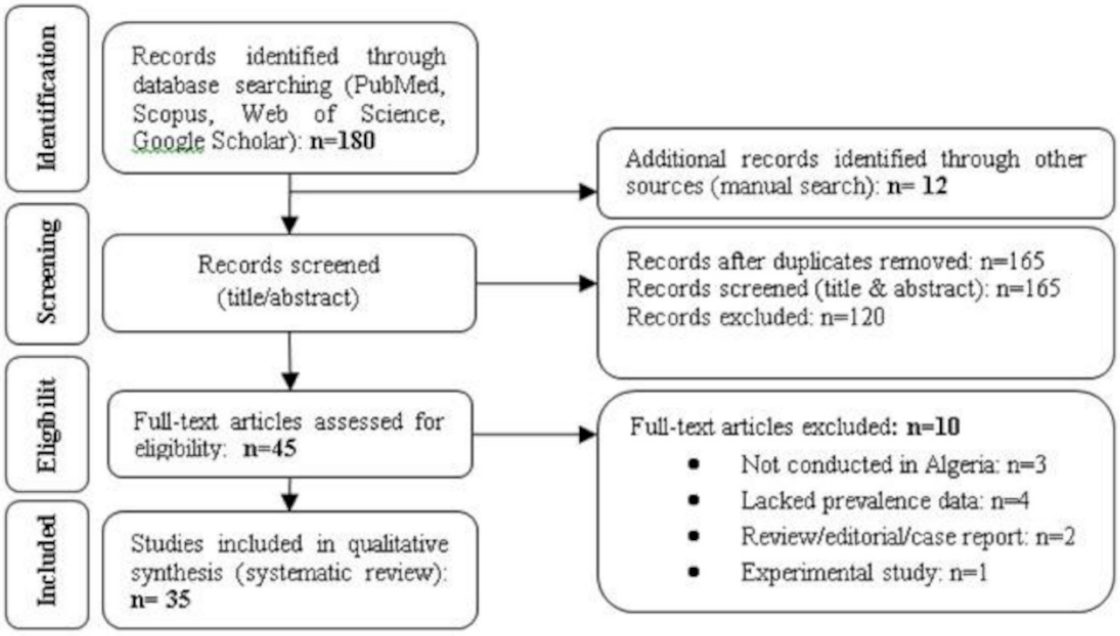

Figure 1. PRISMA flow diagram illustrating the selection process of studies reporting the prevalence of C. burnetii infection in Algeria.

Exclusion criteria

Studies were excluded if they met any of the following criteria:

(i) Review articles, meta-analyses, editorials, letters to the editor, conference abstracts, or case reports;

(ii) Experimental infection studies or laboratory-based studies without field prevalence data;

(iii) Studies conducted outside Algeria;

(iv) Articles lacking essential epidemiological information or clear prevalence data;

(v) Duplicate publications or overlapping datasets, in which case the most comprehensive or most recent study was retained (Figure 1).

Data extraction

Data extraction was conducted independently for each eligible study using a standardised data extraction form. The following variables were extracted: year of publication, geographical region of the study, host type (humans, domestic animals, wild animals, or arthropod vectors), sample size, diagnostic method used (serological and/or molecular techniques), number of positive cases, and reported or calculated prevalence.

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When prevalence was not explicitly reported, it was calculated as the proportion of positive cases relative to the total sample size. Any discrepancies identified during the data extraction process were resolved through discussion to ensure the accuracy and consistency of the extracted data (Figure 1).

Several studies reported multiple prevalence estimates according to host species, diagnostic method, or sampling period; therefore, each independent estimate was treated as a separate prevalence dataset in the meta-analysis.

Statistical analysis

Statistical analyses were performed using Python (v3.10) with the pandas, NumPy, SciPy, and statsmodels libraries.

Meta-analysis model

The primary outcome of this meta-analysis was the prevalence of *C. burnetii*. To address the mathematical constraints inherent to proportion data, which are bounded between 0 and 1, and to stabilise variance, a logit transformation ($\ln[p/(1-p)]$) was applied to the raw prevalence estimates prior to pooling. For studies reporting zero events, a continuity correction of 0.5 was added to both the number of positive cases and non-cases to enable statistical computation.

Pooled prevalence estimates and corresponding 95% confidence intervals (CI) were calculated using a random-effects model. Between-study variance (τ^2) was estimated using the restricted maximum likelihood (REML) method, which is recognised for providing robust and relatively unbiased variance estimates, particularly in the presence of substantial heterogeneity. For ease of interpretation, pooled estimates were back-transformed to the original proportion scale for presentation.

Assessment of heterogeneity

Statistical heterogeneity among studies was assessed using Cochran's Q test and quantified using the I^2 statistic. I^2 values of approximately 25%, 50%, and 75% were interpreted as indicating low, moderate, and high levels of heterogeneity, respectively.

Subgroup analysis

To explore potential sources of heterogeneity, subgroup analyses were conducted according to host category (humans, animals, and vectors) and by specific host species. Separate pooled prevalence estimates were calculated for each subgroup using random-effects models. Forest plots were generated to visually display individual study estimates and corresponding pooled estimates within each subgroup.

Publication bias

Potential publication bias was assessed both visually and statistically. Funnel plots were constructed by plotting the logit-transformed prevalence estimates against their standard errors. Funnel plot asymmetry was evaluated using Egger's linear regression test, with a *p-value* < 0.05 considered indicative of statistically significant publication bias.

Results

Study selection

Figure 1 illustrates the PRISMA flow diagram describing the selection process of studies reporting the prevalence of *C. burnetii* infection in Algeria.

A total of 180 records were initially identified through database searches (PubMed, Scopus, Web of Science, and Google Scholar), and 12 additional records were identified through manual searches. After removal of duplicates, 165 records remained and were screened based on titles and abstracts. Of these, 120 records were excluded because they were not relevant to the research question.

Subsequently, 45 full-text articles were assessed for eligibility. Following full-text evaluation, 10 articles were excluded for predefined reasons: studies not conducted in Algeria (n = 3), lack of extractable prevalence data (n = 4), review

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articles or case reports (n = 2), and experimental studies (n = 1).

Ultimately, 35 studies met the inclusion criteria and were included in the qualitative synthesis (systematic review), forming the evidence base for the assessment of *C. burnetii* prevalence in Algeria.

Characteristics of included studies

A total of 35 studies met the inclusion criteria and were included in the quantitative synthesis (Figure 1), yielding 80 independent prevalence datasets. The included studies covered a broad geographical range across Algeria, spanning from the northern coastal regions to the Saharan areas. Publication years ranged from 2005 to 2026, with a marked increase in research output observed after 2015. Overall, the dataset comprised a cumulative sample size of 8,372 individuals, including humans, animals, and arthropod vectors. Diagnostic approaches varied among studies. Of the 80 independent prevalence datasets, 38 employed serological methods, including enzyme-linked immunosorbent assay (ELISA), indirect immunofluorescence assay (IFA), complement fixation test (CFT), and micro-immunofluorescence (MIF), while 42 datasets relied on molecular techniques, primarily polymerase chain reaction (PCR) and quantitative PCR (qPCR).

Animal reservoirs accounted for the largest proportion of the data, contributing 50 datasets. Among animal hosts, dromedary camels exhibited the highest infection burden. Analysis of seven datasets (n = 368) revealed a pooled prevalence of 73.71% (95% CI: 66.49–79.84%), identifying camels as a hyper-endemic reservoir of *C. burnetii*. Small ruminants, including sheep and goats, which represent the most common livestock species in Algeria, showed a pooled prevalence of 15.84% (95% CI: 10.66–22.91%) across 22 datasets (n = 2,383). In cattle, analysis of 14 datasets (n = 2,477) yielded a pooled prevalence of 11.82% (95% CI: 7.20–18.81%). Lower prevalence estimates were observed in horses (10.31%), dogs (4.21%), and cats (3.22%); however, data for these species were limited and should be interpreted with caution (Table I, Table II, Figure 2, 3).

Arthropod vectors were investigated in 16 datasets. Ticks constituted the primary vector studied, with 11 datasets (n = 805) showing a pooled prevalence of 10.02% (95% CI: 3.23–27.08%). A lower pooled prevalence of 2.24% (95% CI: 0.59–8.12%) was reported in lice across five datasets (n = 616) (Table III).

Human infection with *C. burnetii* was investigated in four studies, contributing four datasets to the final analysis (n = 1,177). The pooled prevalence in humans was estimated at 3.69% (95% CI: 0.90–13.89%), which was markedly lower than that observed in animal reservoirs, consistent with the role of humans as incidental hosts in the transmission cycle (Figure 2).

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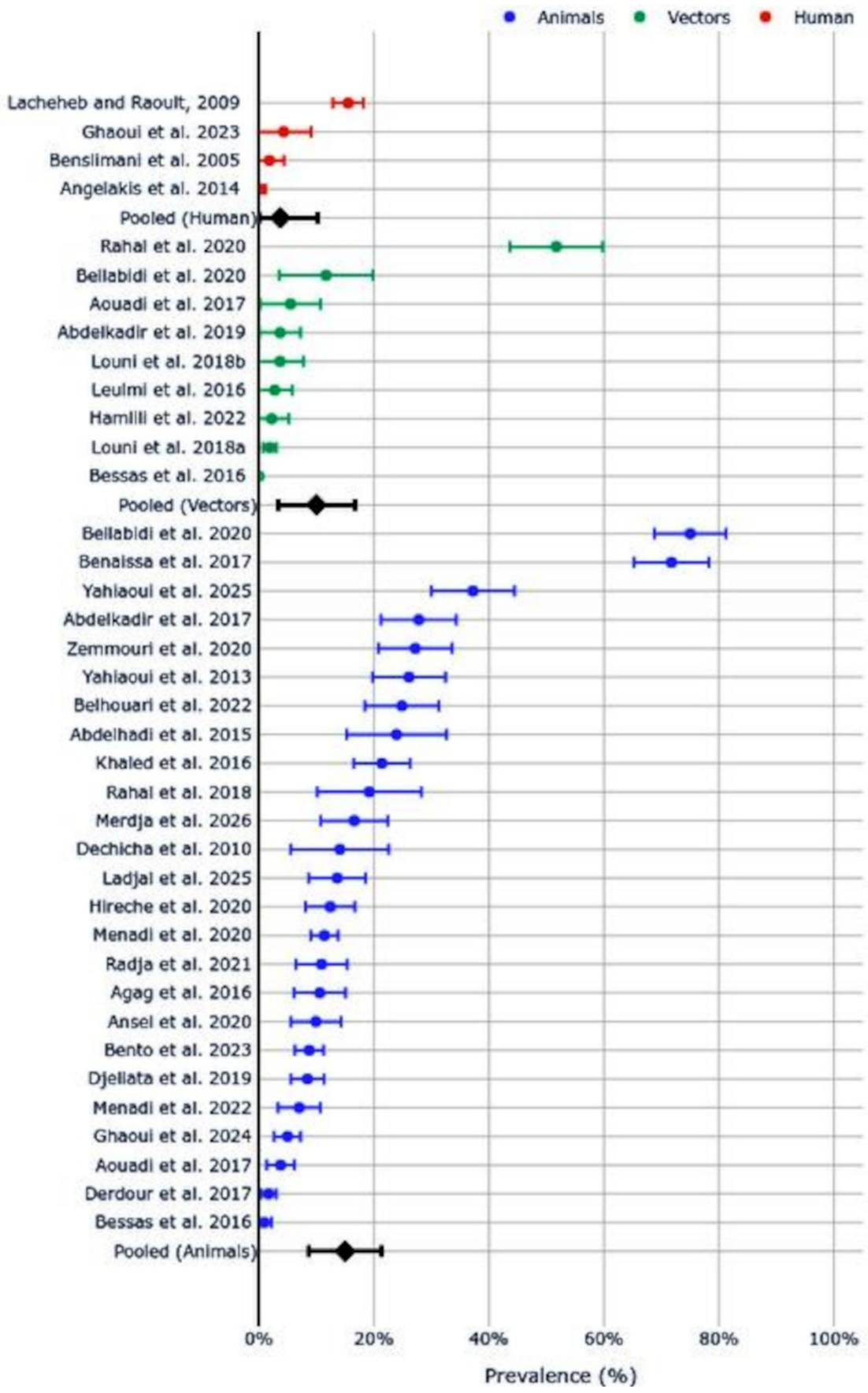

Figure 2. Forest Plot by Subgroup Analysis using REML model. Subgroups: Humans, Vectors, and Animals. Pooled Estimates: Humans: ~3.7%, Vectors: ~10%, Animals: ~15%.

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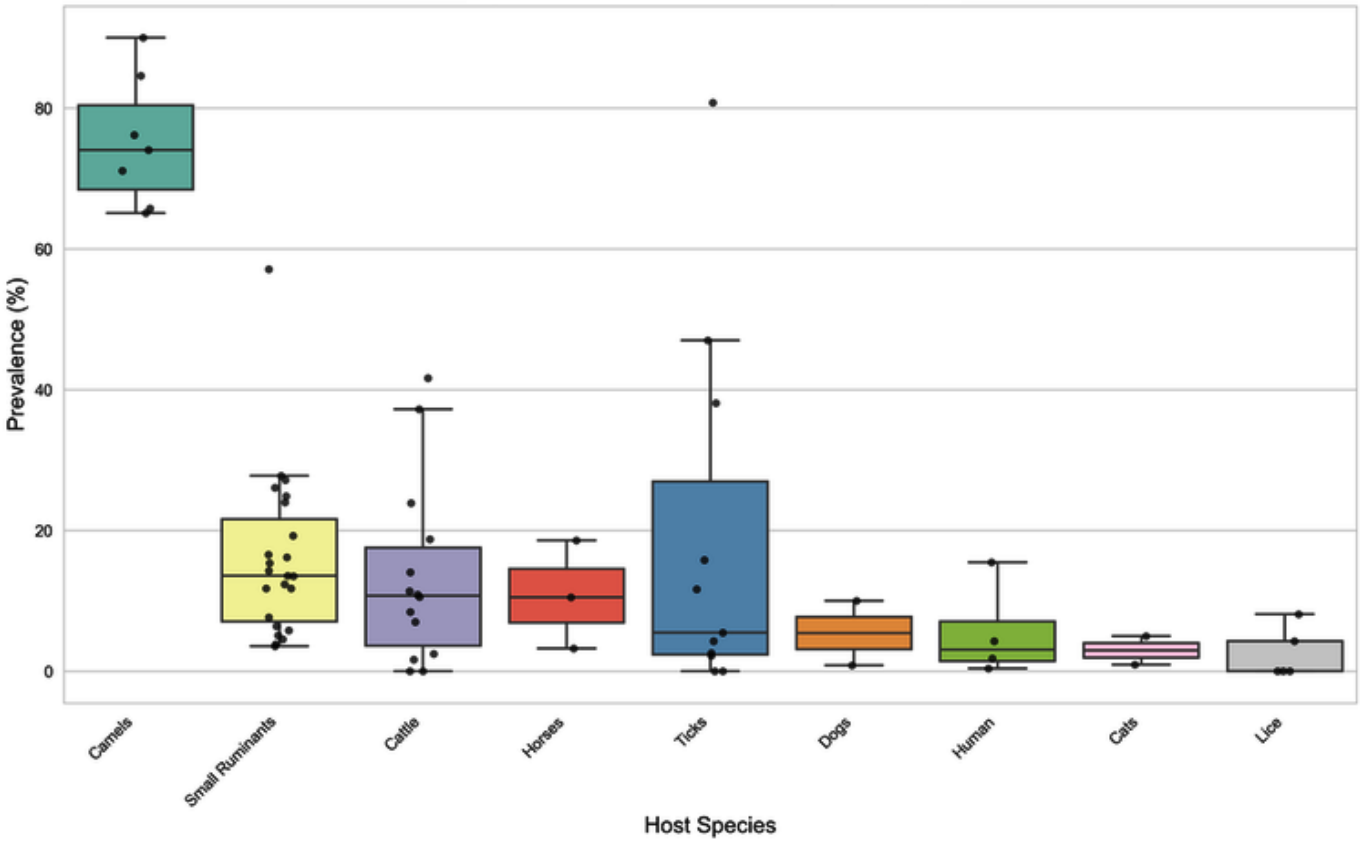

Figure 3. Boxplot : Prevalence of C. burnetii by host species.

Study	Host species	Regions	Sample size	Positive cases	Seroprevalence (%)
Dechicha *et al.* 2010	Cattle	Tipaza	64	9	14.06
Yahiaoui *et al.* 2013	Sheep	Medea	184	48	26.09
Abdelhadi *et al.* 2015	Cattle	Tiaret	92	22	23.91
Agag *et al.* 2016	Cattle	Bejaia	180	19	10.56
Khaled *et al.* 2016	Sheep and goats	Medea, Constantine, Ain Defla, Djelfa, Biskra, BordjBouArreridj, Skikda and El Bayadh	227	32	14.1
Abdelkadir *et al.* 2017	Sheep	Sidi Bel Abbes	180	50	27.78
Benaissa *et al.* 2017	Camels	Ouargla, Biskra, ElOued and Ghardaia	184	132	71.74
Derdour *et al.* 2017	Cattle	Algiers	360	6	1.67
Djellata *et al.* 2019	Cattle	Blida, Tipaza and Algiers	368	31	8.42
Ansel *et al.* 2020	Horses	Tiaret, El Bayadh and Ghardaia	182	18	9.9
Bellabidi *et al.* 2020	Camels	Ouargla, El Oued and Biskra	184	138	75
Hireche *et al.* 2020	Sheep	Constantine	226	28	12.39
Menadi *et al.* 2020	Cattle	Setif	678	77	11.36
Zemmouri *et al.* 2020	Sheep	Msila	184	50	27.20
Radja *et al.* 2022	Cattle	Jijel	184	20	10.87
Belhouari *et al.* 2022	Sheep	Ain Defla	173	43	24.86
Bento *et al.* 2023	Goats	Mila, Constantine, Guelma and El Tarf	504	44	8.73
Ladjal *et al.* 2025	Sheep	El Bayadh	184	25	13.59
Yahiaoui *et al.* 2025	Cattle	Northern	172	64	37.21
Merdja *et al.* 2026	Sheep and goats	Medea	157	26	16.56
Benslimani *et al.* 2005	Human	Algiers	110	2	1.82
Lacheheb and Raoult, 2009	Human	Setif	729	113	15.5
Ghaoui *et al.* 2023	Human	Northern	70	3	4.29

Table I. Seroprevalence of C. burnetii in animals and humans in Algeria (n=35). C. burnetii = Coxiella burnetii, causative agent of Q fever; Seroprevalence (%) = (Positive cases / Sample size) × 100; Regions correspond to the geographic locations reported in each study.

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Study	Host species	Regions	Sample size	Positive cases	Infection rate (%)
Bessas *et al.* 2016	Dogs	Algiers	117	1	0.85
Bessas *et al.* 2016	Cats	Algiers	107	1	0.93
Khaled *et al.* 2016	Sheep, goats	Medea, Constantine, Ain Defla, Djelfa, Biskra, BordjBouArreridj, Skikda and El Bayadh	267	57	21.35
Aouadi *et al.* 2017	Sheep	Souk Ahras	120	7	5.83
Aouadi *et al.* 2017	Goats	Souk Ahras	120	2	1.67
Rahal *et al.* 2018	Cattle	Blida, Medea, Bouira and BordjBouArreridj	73	14	19.18
Bellabidi *et al.* 2020	Camels	Ouargla, El Oued and Biskra	138*	0	0
Menadi *et al.* 2022	Cattle	Setif	186	13	6.99
Ghaoui *et al.* 2024	Cattle	Algiers	120	3	2.50
Ghaoui *et al.* 2024	Sheep	Algiers	84	3	3.57
Ghaoui *et al.* 2024	Dogs	Algiers	80	8	10.00
Ghaoui *et al.* 2024	Cats	Algiers	60	3	5.00
Angelakis *et al.* 2014	Human	Oran	268	1	0.37
Ghaoui *et al.* 2023	Human	Northern	70	1	1.43

Table II. Molecular detection of C. burnetii infection in animals and humans. *: Seropositive by ELISA

Vectors	Species	Host species	Sample size	Positive cases	Infection rate (%)	Study
Ticks	*I. vespertilionis*	Bats	19	3	15.8	Leulmi *et al.* 2016
	R. sanguineus, R. bursa, H. lusitanicum, H. scupense, H. anatolicum excavatum, H. marginatum, I. ricinus and *I. hexagonus*	Cattle, Sheep, Goats and Dogs	191	0	0	Leulmi *et al.* 2016
	R. sanguineus	Dogs and Cats	115	0	0	Bessas *et al.* 2016
	R. bursa	Sheep	73	4	5.48	Aouadi *et al.* 2017
	H. excavatum and *R. bursa*	Cattle and Sheep	109	4	3.67	Abdelkadir *et al.* 2019
	H. excavatum, H. dromedarii and *H. impeltatum*	Camels	60	7	11.67	Bellabidi *et al.* 2020
	D. marginatus, H. sulcata, H. excavatum, H. detritum, H. lusitanicumn, H. marginatum, Hyalomma spp., R. bursa, R. sanguineus SL-A, Rhipicephalus spp., and *I. ricinus*	Cattle	147	76	51.7	Rahal *et al.* 2020
	H. dromedarii and *H. impeltatum*	Camels	91	2	2.2	Hamlili *et al.* 2022
Lice	*Pediculus h. humanus*	Humans	524	10	1.9	Louni *et al.* 2018a
	Pediculus humanus capitis	Humans	82	3	3.65	Louni *et al.* 2018b

Table III. Molecular detection of C. burnetii infection in vectors. I. = Ixodes; R. = Rhipicephalus; H. = Hyalomma; D. = Dermacentor; Infection rate (%) = (Positive cases / Sample size) × 100; Molecular detection methods as reported in the cited studies.

Overall pooled prevalence and heterogeneity

The results of this systematic review and meta-analysis provide compelling evidence that *C. burnetii* is endemic throughout Algeria, with an overall pooled prevalence of 13.11% (95% CI: 9.41–17.97%). This substantial prevalence highlights the widespread circulation of the pathogen across both animal and human populations in the country. Considerable heterogeneity was observed among the included studies, with a Cochran's Q statistic of 1,050.6 ($p < 0.001$) and an I^2 value of 92.9%, indicating a very high level of variability. Such extremely high heterogeneity indicates that pooled estimates should be interpreted with caution, as prevalence varies substantially according to ecological, methodological, and host-related factors. The between-study variance (τ^2) was estimated at 2.28 using the restricted maximum likelihood (REML) method. Given this pronounced heterogeneity, the application of a random-effects model was appropriate, and further subgroup analyses were performed to explore potential sources of variability.

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Subgroup analysis

Subgroup analyses were performed to investigate potential sources of heterogeneity (Table IV). Geographically, the south-eastern region exhibited the highest prevalence at 61.22% (95% CI: 37.7–80.47%), markedly higher than the north-centre (11.90%) and north-eastern (12.72%) regions. Regarding diagnostic methods, notable differences were observed: serological assays, which detect past exposure, yielded a pooled prevalence of 20.47% (95% CI: 14.09–28.76%), whereas molecular methods, which detect active infection, produced a lower pooled prevalence of 7.47% (95% CI: 4.53–12.09%). Temporal analysis indicated an apparent increase in prevalence over time, rising from 7.23% in studies published before 2015 to 17.27% in studies published in 2020 and later.

Subgroup	Category	N. observations (*k*)	Total samples	Positive cases	Pooled prevalence	95% CI	I^2
Host	Camels	7	368	270	73.71	66.49-79.84	50.3
	Small ruminants	22	2383	387	15.84	10.66-22.91	86.2
	Cattle	14	2477	278	11.82	7.20-18.81	91.2
	Horses	3	182	18	10.31	3.67-25.73	76.2
	Ticks	11	805	96	10.02	3.23-27.08	91.9
	Dogs	2	197	9	4.21	0.51-27.42	83.5
	Human	4	1177	119	3.69	0.90-13.89	90.6
	Cats	2	167	4	3.22	0.80-12.02	54.3
	Lice	5	616	13	2.24	0.59-8.12	59.0
Diagnostic method	Serological	38	5576	1000	20.47	14.09-28.76	94.5
	Molecular	42	3231	223	7.47	4.53-12.09	88.5
Region	South-eastern	8	400	242	61.22	37.7-80.47	91
	South-western	3	267	39	15.16	11.34-19.99	0
	South-centre	4	186	46	15.15	3.44-47.2	93.6
	North-eastern	17	2245	253	12.72	8.47-18.65	76.4
	North-centre	31	4462	531	11.90	5.84-15.22	92.3
	North-western	6	742	80	6.57	1.97-19.69	90.8
	Northern	1	70	3	4.93	1.74-13.18	NA
Year of publication	2020 and later	29	3726	651	17.27	10.82-26.43	94.3
	2015-2019	36	3291	370	11.24	6.94-18.51	91.9
	Before 2015	5	1355	173	7.23	1.83-24.54	90.7

Table IV. Pooled prevalence of C. burnetii by host, diagnostic method, region, and year of publication. k = Number of studies included in the subgroup analysis; Pooled prevalence (%) calculated using a random-effects meta-analysis; 95% CI = 95% confidence interval for the pooled prevalence; I^2 = Measure of heterogeneity among studies; values >75% indicate high heterogeneity; NA = Not applicable (heterogeneity could not be calculated for a single study).

Meta-regression analysis

A multivariable random-effects meta-regression model was fitted to evaluate the independent effects of region, diagnostic method, and host species on the prevalence of *C. burnetii* (Table V). The model explained 38.5% of the between-study variance (R^2 = 38.5%), indicating that these covariates account for a substantial portion of the observed heterogeneity. Although region, host species, and diagnostic method explained 38.5% of the between-study variance, more than 60% of the heterogeneity remained unexplained, suggesting the influence of unmeasured ecological and methodological factors (e.g., sampling design, herd structure, animal age distribution, and diagnostic cut-offs).

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Variable	Odds Ratio	95% CI	*P-value*
Intercept (Ref: Serological, Animals, North-centre)	0.19	0.1-0.36	0.001
Method: Molecular (vs. Serological)	0.45	0.2-1.02	0.057
Host: Humans (vs. Animals)	0.34	0.06-1.8	0.199
Host: Vectors (vs. Animals)	0.87	0.32-2.37	0.775
Region: South-eastern (vs. North-centre)	9.41	3.15-28.06	< 0
Region: North-eastern	1.08	0.47-2.41	0.851
Region: North-western	0.69	0.2-2.38	0.55
Region: South-centre	1.43	0.36-5.57	0.605
Region: South-western	1.11	0.21-5.68	0.905
Region: Northern	0.81	0.03-20.89	0.9

Table V. Odds ratios (ORs), 95% confidence intervals (CIs), and P-values for risk factors associated with C. Burnetii in different hosts and regions. Ref = Reference category for categorical variables; OR = Odds Ratio; CI = Confidence Interval; p-values < 0.05 are considered statistically significant; For the "Intercept," reference categories are: Serological method, Animals as host, and North-Centre region.

The south-eastern region emerged as the strongest predictor of *C. burnetii* prevalence. Studies conducted in this region exhibited significantly higher prevalence compared to the north-centre reference group (Odds Ratio = 9.41, $p < 0.001$), which is consistent with the high infection rates observed in camels, the predominant livestock species in this area.

Diagnostic method also influenced prevalence estimates. Molecular methods (PCR) tended to yield lower prevalence compared to serological assays (Odds Ratio = 0.45, $p = 0.05$), a borderline significant finding. This result reflects the expected difference between techniques that measure past exposure (serology) versus active infection (PCR).

Humans displayed a trend toward lower prevalence compared to animals (OR = 0.34), although this difference was not statistically significant in the multivariable model ($p = 0.20$), likely due to the limited number of human datasets ($k = 4$). Several factors may explain the lower prevalence in humans: (1) humans are accidental, dead-end hosts rather than reservoirs; (2) many human infections are asymptomatic or present with non-specific febrile illnesses that often go undiagnosed; and (3) several human studies included in this review employed molecular detection in specific clinical settings (for example, endocarditis patients), which captures a narrower window of positivity compared with broader serological screening.

After adjustment for region, host, and diagnostic method, no significant linear trend in prevalence over time was observed ($p = 0.63$) (Figure 4).

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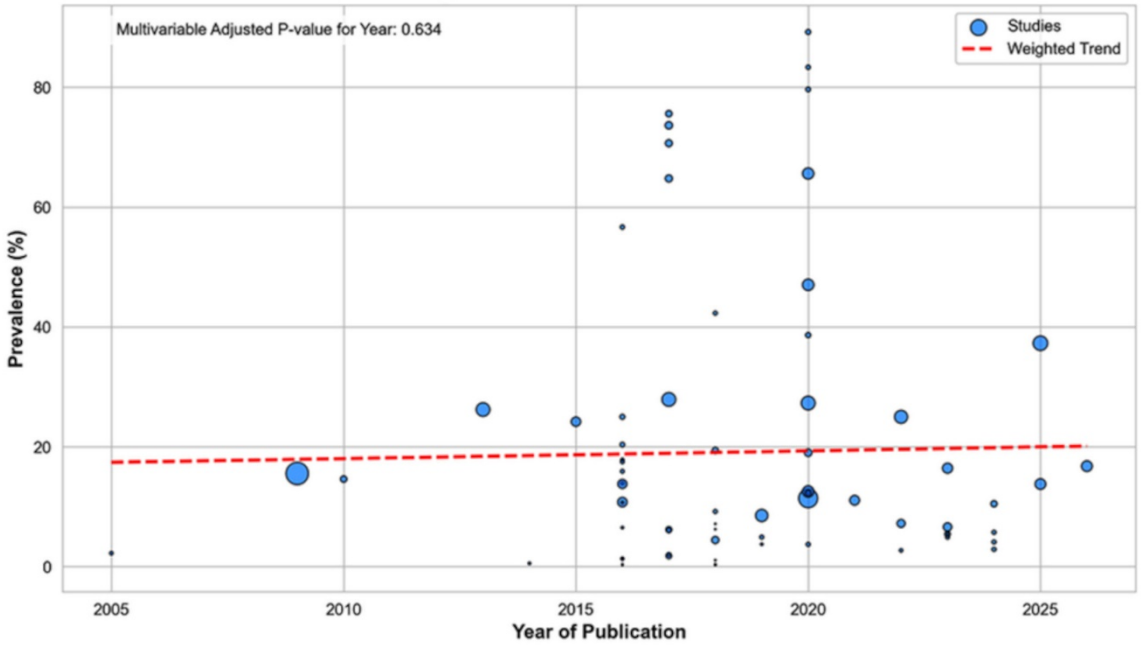

Figure 4. Temporal trend of prevalence (2005–2026).

Publication bias assessment

Visual inspection of the funnel plot revealed some asymmetry, with a gap in the lower-left quadrant suggesting a potential underrepresentation of small studies reporting low prevalence (Figure 5). Egger's regression test produced a *p-value* of 0.052 (Intercept = -1.56; 95% CI: -3.13 to 0.01). Although this result is borderline, it indicates that small studies with negative findings may be slightly underrepresented in the literature.

Interpretation of these findings suggests that, despite the observed visual asymmetry, the statistical evidence for publication bias is marginal and does not reach the conventional significance threshold of 0.05. Overall, this indicates that the pooled estimates are likely robust and not substantially influenced by missing small studies.

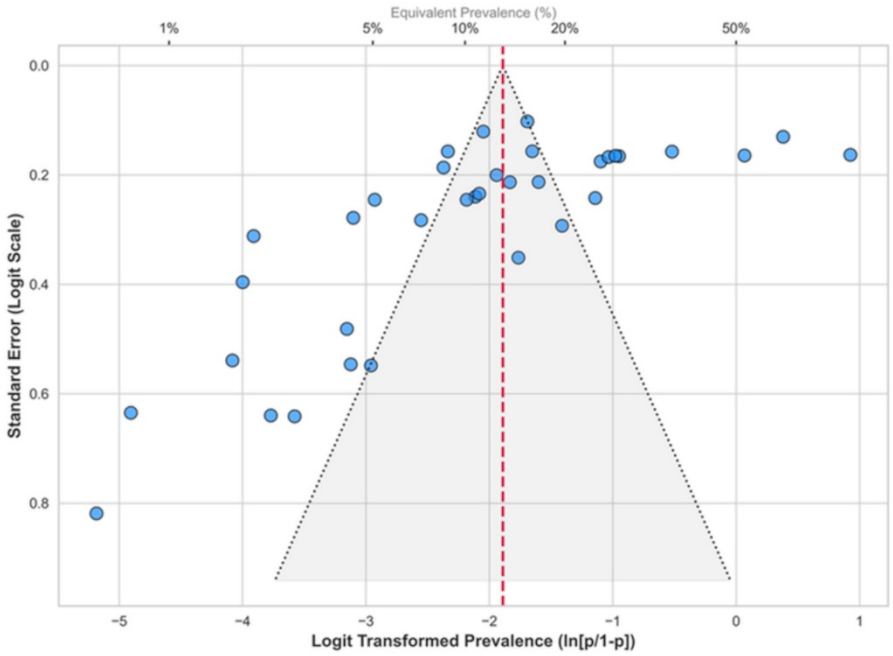

Figure 5. Funnel plot illustrating publication bias.

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Discussion

Coxiella burnetii is a globally distributed zoonotic pathogen whose complex ecology strongly supports the need for a One Health approach. In Algeria, Q fever has long been endemic. The first human cases were reported in Algiers in 1948, followed by outbreaks among military personnel in Batna (1955–1957) and Tlemcen (1958) (Pierrou et al., 1956; Bento et al., 2023). Despite this historical background, Q fever remains under-recognised in the country. Recent serosurveys nonetheless indicate substantial human exposure, including a seroprevalence of 15.5% in an agropastoral area of Setif Province, suggesting ongoing transmission. Livestock constitute the principal reservoirs of *C. burnetii* (Lacheheb and Raoult, 2009). Nationwide surveys conducted between 2011 and 2013 detected at least one infected animal in 58% of sheep and goat flocks, with an individual seroprevalence of 14.1% (Khaled et al., 2016). Cattle populations in north-eastern Algeria show comparable evidence of widespread exposure, with herd-level seroprevalence ranging from 11% to 37% and individual seroprevalence between 11.4% and 37% (Menadi et al., 2020, 2022). Collectively, these findings indicate extensive circulation of *C. burnetii* among Algerian livestock, while human infections remain largely undiagnosed.

Hospital-based investigations support this under-recognition. In Algiers, 4.3% of patients presenting with unexplained febrile illness were seropositive for *C. burnetii* (Ghaoui et al., 2023), underscoring the pathogen's contribution to febrile syndromes in the absence of routine diagnostic testing. From a One Health perspective, this mismatch between high animal exposure and low reported human incidence reflects limited clinical awareness, restricted access to specific diagnostics, and the absence of systematic human surveillance**,** as also observed in several African and Middle Eastern countries (Rahaman et al., 2019; Bento et al., 2023).

Dromedary camels emerge as particularly important reservoirs in Algeria. Multiple studies report extremely high seroprevalence in south-eastern provinces, with 71–75% of camels testing positive by ELISA (Benaissa et al., 2017; Bellabidi et al., 2020). In a survey of 184 camels in southern arid regions, seroprevalence reached 75.5% (Bellabidi et al., 2020). Identified risk factors include advanced age, large herd size, and tick infestation (Benaissa et al., 2017; Bellabidi et al., 2020). These findings are consistent with data from Egypt and Sudan, where camel seroprevalence frequently exceeds 60%, emphasising the major role of camels in Q fever ecology across the North African and Saharo–Sahelian region (Devaux et al., 2020).

Ticks parasitising camels, particularly *H. dromedarii* and *H. impeltatum*, frequently harbour *C. burnetii* DNA; 11.7% of camel ticks were PCR-positive in one study (Bellabidi et al., 2020). Genotyping revealed close similarity between strains detected in camels, ticks, and Mediterranean human isolates, suggesting that camels contribute to the maintenance of local transmission cycles. Nomadic husbandry practices, arid climatic conditions, intense dust exposure, and high camel densities likely amplify these dynamics**,** facilitating airborne dissemination during animal handling and parturition. Overall, the Sahara–Sahelian ecosystem of southern Algeria appears to constitute a hyperendemic focus for Q fever, with camels and their ticks acting as major amplifiers and posing spillover risks to humans and other livestock (Benaissa et al., 2017; Bellabidi et al., 2020).

Sheep and goats are also key reservoirs and play a major role in environmental contamination. The national survey by Khaled et al. (2016) confirmed bacterial shedding in birthing products and vaginal swabs, with 21.3% of aborted females testing PCR-positive, exceeding the seroprevalence estimate (14.1%). Regional studies corroborate these findings: flock-level seroprevalence reached 35.9% in Constantine (Hireche et al., 2020) and 66.7% in Ain Defla, with individual seroprevalence of 24.9% (Belhouari et al., 2022). Goat seroprevalence in north-eastern Algeria was lower (8.7%), consistent with values reported elsewhere in the country (Bento et al., 2023).

Ecologically, lambing and kidding periods involve the congregation of animals and shedding of highly infectious birth materials (Van den Brom et al., 2015). Wind dispersal of contaminated dust from barns and pastures facilitates airborne transmission (Clark and Soares Magalhães, 2018), while mixed farming systems allow interspecies transmission cycles (Zheng et al., 2026). These mechanisms mirror those described in European outbreaks, where small ruminants were the primary drivers of human epidemics, but occur in Algeria within a distinct agro-ecological context characterised by extensive rather than intensive farming systems (Pal et al., 2025).

Cattle appear moderately exposed compared with camels and small ruminants. In Setif, 11.4% of adult cows were seropositive (Menadi et al., 2020), while bulk tank milk surveys showed 37% of dairy herds ELISA-positive (Menadi et al., 2022). However, PCR detection was much lower: only 6.98% of cows with reproductive disorders were PCR-positive in blood, and 9% of milk samples contained detectable DNA (Menadi et al., 2022). Agreement between serology and PCR was poor (Cohen's $\kappa \approx 0.08$), reflecting different epidemiological windows. Serology captures cumulative exposure, whereas PCR detects active infection or intermittent shedding, which may be missed depending on sampling timing and matrix (de Souza Ribeiro Mioni et al., 2019), although inhalation of contaminated aerosols

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remains the dominant transmission route (Gale et al., 2015). Infection has also been associated with reproductive disorders in cattle, including abortions and infertility, though causality is not always definitive (Gisbert et al., 2024a, 2024b).

Ticks constitute additional ecological components of Q fever transmission. In Algeria, *Hyalomma* ticks collected from camels harbour *C. burnetii* genotypes related to Mediterranean strains (Bellabidi et al., 2020). While ticks may maintain infection within animal populations, their direct role in human transmission remains poorly documented, with aerosol inhalation considered the principal route (Ullah et al., 2022). Nevertheless, vector control may contribute to reducing infection persistence in livestock.

Human Q fever is likely substantially under-detected in Algeria. Most data derive from small hospital-based or occupational studies, and there is no systematic surveillance or mandatory reporting. A recent hospital study found 4.3% seropositivity and 1.4% PCR positivity among patients with unexplained fever (Ghaoui et al., 2024). The non-specific clinical presentation—fever, pneumonia, hepatitis—combined with limited diagnostic capacity and low clinical awareness, likely leads to underdiagnosis. Rural populations and livestock workers are expected to be at higher risk, yet remain insufficiently studied (Bento et al., 2023).

Marked spatial heterogeneity characterises Q fever epidemiology in Algeria. High seroprevalence in camels dominates the south-eastern Sahara, whereas lower but variable prevalence occurs in northern and high-plateau regions among sheep and cattle (Hireche et al., 2020; Belhouari et al., 2022; Menadi et al., 2022). This north–south gradient reflects Algeria's unique position at the interface between the Mediterranean basin and the Sahara–Sahel, combining climatic extremes, diverse livestock systems, and variable human–animal contact patterns**.** Internationally, Algeria presents a distinctive epidemiological profile. Compared with Europe, where surveillance is well established following large outbreaks and transmission is mainly driven by small ruminants, Algeria shows similarly high or higher levels of animal exposure but markedly lower detection of human cases. In contrast to Egypt and Sudan, where camel-associated Q fever is increasingly recognised, Algeria lacks integrated human surveillance despite comparable camel seroprevalence. This divergence underscores the critical gap between animal infection and human case detection in the Algerian context(Larson et al., 2019).

Divergent serological and molecular prevalence estimates further complicate interpretation. Serology reflects cumulative exposure, while PCR detects active infection or shedding. Methodological heterogeneity (diagnostic kits, cut-offs, sampled matrices) and age bias toward adult animals also affect estimates. Consequently, national prevalence figures must be interpreted cautiously, and meta-analyses are challenged by substantial heterogeneity.

Direct comparison between serological and molecular prevalence estimates must be interpreted with caution. Serology reflects cumulative exposure and may remain positive for prolonged periods after infection, whereas PCR detects current infection or shedding, which is often transient and matrix-dependent. Consequently, differences in prevalence between these diagnostic approaches do not necessarily reflect true epidemiological contrasts but rather differences in biological windows of detection. Pooling these data within the same meta-analytic framework may therefore inflate heterogeneity and complicate interpretation.

Taken together, these findings underscore the urgent need for a coordinated One Health strategy in Algeria. Integrated human–animal surveillance, strengthened laboratory capacity (IFA and PCR), targeted vaccination of small ruminants where feasible, improved biosecurity during parturition, milk pasteurisation, vector control, and ecological risk mapping are essential components of effective control. Establishing national One Health coordination platforms could formalise collaboration between public health, veterinary, and environmental sectors, enabling targeted interventions in high-risk zones and species and improving prevention and control of Q fever in Algeria (Rahaman et al., 2019, 2021).

This study represents the first systematic review and meta-analysis quantifying the prevalence of *C. burnetii* in Algeria across humans, animals, and vectors within a One Health framework. The inclusion of both serological and molecular data provides a comprehensive overview of exposure and active infection.

However, several limitations must be acknowledged. The small number of human datasets limits the precision of pooled estimates in this subgroup. Considerable heterogeneity was observed across studies, likely reflecting differences in sampling strategies, diagnostic assays, ecological conditions, and host demographics. The inclusion of both serological and molecular data, although informative, may contribute to methodological heterogeneity. In addition, potential publication bias and the underrepresentation of small studies with negative findings cannot be entirely excluded.

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Conclusion

This systematic review and meta-analysis demonstrates that Q fever is endemic in Algeria across animal, human, and vector populations. Substantial regional variation was observed, highlighting the influence of ecological and husbandry-related factors on disease distribution. Camels emerged as a particularly important reservoir, exhibiting consistently high seroprevalence, which suggests a hyper-endemic circulation in this host species.

Despite evidence of widespread animal exposure, human data remain scarce and fragmented, pointing to a significant detection and surveillance gap. Furthermore, the considerable heterogeneity across studies—driven by differences in diagnostic methods, study design, and sampling strategies—underscores the need for methodological harmonisation.

Strengthening integrated One Health surveillance, standardising diagnostic approaches, and expanding human epidemiological investigations are essential steps to better characterise transmission dynamics and mitigate the public health impact of *C. burnetii* in Algeria.

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Ethical approval

This study did not require ethical approval because it involved the analysis of data extracted from previously published studies, with no new human or animal subjects involved.

Conflict of interest

The authors declare that they have no conflict of interest.

Author Contributions

Conceptualisation: SY; Methodology: SY, KTNA; Formal analysis: SY; Investigation: SY, RF, OS; Writing original draft preparation: SY, RF, OS; Writing, review and editing: NO, NAKT; Visualisation: NO, NAKT; Supervision: NO, NAKT; Funding acquisition: Not applicable. All authors have read and agreed to the published version of the manuscript.

Data availability

The data used in this systematic review and meta-analysis were extracted from previously published studies, all of which are cited in the reference list.

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References

Abdelhadi, F., Ameur, A., Abdellatif, N., Benallou, B., Meliani, S., Smail, N., & Mahmoud, D. (2015). Abortion in cattle on the level of Tiaret area (Algeria). Global Veterinaria, 14(5), 638–645. https://doi.org/10.5829/idosi.gv.2015.14.05.93224.

Abdelkadir, K., Ait-Oudhia, K., & Khelef, D. (2017). Seroprevalence of chlamydial abortion and Q fever in ewes

aborted in the North-West of Algeria. Journal of Veterinary Medicine and Animal Health. 9. 246-249. https://doi.org/10.5897/JVMAH2016.0474.

Abdelkadir, K., Palomar, A. M., Portillo, A., Oteo, J. A., Ait-Oudhia, K., & Khelef, D. (2019). Presence of Rickettsia aeschlimannii, 'Candidatus Rickettsia barbariae' and Coxiella burnetii in ticks from livestock in Northwestern Algeria. Ticks and tick-borne diseases, 10(4), 924–928. https://doi.org/10.1016/j.ttbdis.2019.04.018.

Agag, S., Kaidi, R., & Khelef, D. (2016). Séroprévalence de la fièvre Q chez les bovins de la région de Bejaïa (Algérie). Revue d'élevage Et De médecine vétérinaire Des Pays Tropicaux, 69(4), 155–159. https://doi.org/10.19182/remvt.31200.

Angelakis, E., & Raoult, D. (2010). Q Fever. Veterinary microbiology, 140(3-4), 297–309. https://doi.org/10.1016/j.vetmic.2009.07.016.

Angelakis, E., Mediannikov, O., Socolovschi, C., Mouffok, N., Bassene, H., Tall, A., Niangaly, H., Doumbo, O., Znazen, A., Sarih, M., Sokhna, C., & Raoult, D. (2014). Coxiella burnetii-positive PCR in febrile patients in rural and urban Africa. International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases, 28, 107–110. https://doi.org/10.1016/j.ijid.2014.05.029.

Ansel, S., Samir, B., Karima, B., Abdellah, M. C., Amine, A., Rachid, K., Miroud, K., & Ait-Oudhia, K. (2020). Coxiella burnetii in horses of Algeria: Seroprevalence and associated risk factors. World Vet J, 10(4), 602–608. https://doi.org/10.54203/scil.2020.wvj72.

Aouadi, A., Leulmi, H., Boucheikhchoukh, M., Benakhla, A., Raoult, D., & Parola, P. (2017). Molecular evidence of tick-borne hemoprotozoan-parasites (Theileria ovis and Babesia ovis) and bacteria in ticks and blood from small ruminants in Northern Algeria. Comparative immunology, microbiology and infectious diseases, 50, 34–39. https://doi.org/10.1016/j.cimid.2016.11.008.

Arricau-Bouvery, N., & Rodolakis, A. (2005). Is Q fever an emerging or re-emerging zoonosis?. Veterinary research, 36(3), 327–349. https://doi.org/10.1051/vetres:2005010.

Belhouari, A., Souames, S., Berrama, Z., & Ouchene, N. (2022). Seroprevalence of Q fever among ewes and associated risk factors in Ain Defla region, North-central Algeria. Comparative immunology, microbiology and infectious diseases, 87, 101853. https://doi.org/10.1016/j.cimid.2022.101853.

Bellabidi, M., Benaissa, M. H., Bissati-Bouafia, S., Harrat, Z., Brahmi, K., & Kernif, T. (2020). Coxiella burnetii in camels (Camelus dromedarius) from Algeria: Seroprevalence, molecular characterization, and ticks (Acari: Ixodidae) vectors. Acta tropica, 206, 105443. https://doi.org/10.1016/j.actatropica.2020.105443.

Benaissa, M. H., Ansel, S., Mohamed-Cherif, A., Benfodil, K., Khelef, D., Youngs, C. R., Kaidi, R., & Ait-Oudhia, K. (2017). Seroprevalence and risk factors for Coxiella burnetii, the causative agent of Q fever in the dromedary camel (Camelus dromedarius) population in Algeria. The Onderstepoort journal of veterinary research, 84(1), e1–e7. https://doi.org/10.4102/ojvr.v84i1.1461.

Benslimani, A., Fenollar, F., Lepidi, H., & Raoult, D. (2005). Bacterial zoonoses and infective endocarditis, Algeria. Emerging infectious diseases, 11(2), 216–224. https://doi.org/10.3201/eid1102.040668.

Bento, J. T., Dahmane, A., Santos-Silva, S., Reghaissia, N., Almeida, D., & Mesquita, J. R. (2023). Antibody-Based Assessment of Coxiella burnetii Circulation in Algerian Goat Herds. Animals : an open access journal from MDPI, 13(18), 2926. https://doi.org/10.3390/ani13182926.

Bessas, A., Leulmi, H., Bitam, I., Zaidi, S., Ait-Oudhia, K., Raoult, D., & Parola, P. (2016). Molecular evidence of vector-borne pathogens in dogs and cats and their ectoparasites in Algiers, Algeria. Comparative immunology, microbiology and infectious diseases, 45, 23–28. https://doi.org/10.1016/j.cimid.2016.01.002.

Clark, N. J., & Soares Magalhães, R. J. (2018). Airborne geographical dispersal of Q fever from livestock holdings to human communities: a systematic review and critical appraisal of evidence. BMC infectious diseases, 18(1), 218. https://doi.org/10.1186/s12879-018-3135-4.

Cutler, S. J., Bouzid, M., & Cutler, R. R. (2007). Q fever. The Journal of infection, 54(4), 313–318. https://doi.org/10.1016/j.jinf.2006.10.048
18.

de Souza Ribeiro Mioni, M., Ribeiro, B. L. D., Peres, M. G., Teixeira, W. S. R., Pelícia, V. C., Motta, R. G., Labruna, M. B., Ribeiro, M. G., Sidi-Boumedine, K., & Megid, J. (2019). Real-time quantitative PCR-based detection of Coxiella burnetii in unpasteurized cow's milk sold for human consumption. Zoonoses and public health, 66(6), 695–700. https://doi.org/10.1111/zph.12609.

Dechicha, A., Gharbi, S., Kebbal, S., Chatagnon, G., Tainturier, D., Ouzrout, R., & Guetarni, D. (2010). Serological survey of etiological agents associated with abortion in two Algerian dairy cattle breeding farms. Journal of Veterinary Medicine and Animal Health. 2(1). 001-005.

Derdour, S. Y., Hafsi, F., Azzag, N., Tennah, S., Laamari, A., China, B., & Ghalmi, F. (2017). Prevalence of the Main Infectious Causes of Abortion in Dairy Cattle in Algeria. Journal of veterinary research, 61(3), 337–343. https://doi.org/10.1515/jvetres-2017-0044.

Devaux, C. A., Osman, I. O., Million, M., & Raoult, D. (2020). Coxiella burnetii in Dromedary Camels (Camelus dromedarius): A Possible Threat for Humans and Livestock in North Africa and the Near and Middle East?. Frontiers in veterinary science, 7, 558481. https://doi.org/10.3389/fvets.2020.558481.

Djellata, N., Yahimi, A., Hanzen, C., Saegerman, C., & Kaidi, R. (2019). Prevalence and factors associated with a higher or lower risk of exposure to Coxiella burnetii, Chlamydia abortus and Toxoplasma gondii in dairy cows that have aborted in Algeria. Prévalences et facteurs associés à un risque augmenté ou diminué d'exposition à Coxiella burnetii, Chlamydia abortus et Toxoplasma gondii chez la vache laitière ayant avorté en Algérie. Revue scientifique et technique (International Office of Epizootics), 38(3), 761–786. https://doi.org/10.20506/rst.38.3.3025.

Duron, O., Noël, V., McCoy, K. D., Bonazzi, M., Sidi-Boumedine, K., Morel, O., Vavre, F., Zenner, L., Jourdain, E., Durand, P., Arnathau, C., Renaud, F., Trape, J. F., Biguezoton, A. S., Cremaschi, J., Dietrich, M., Léger, E., Appelgren, A., Dupraz, M., Gómez-Díaz, E., … Chevillon, C. (2015). The Recent Evolution of a Maternally-Inherited Endosymbiont of Ticks Led to the Emergence of the Q Fever Pathogen, Coxiella burnetii. PLoS pathogens, 11(5), e1004892. https://doi.org/10.1371/journal.ppat.1004892.

Gale, P., Kelly, L., Mearns, R., Duggan, J., & Snary, E. L. (2015). Q fever through consumption of unpasteurised milk and milk products - a risk profile and exposure assessment. Journal of applied microbiology, 118(5), 1083–1095. https://doi.org/10.1111/jam.12778.

Ghaoui, H., Achour, N., Saad-Djaballah, A., Belacel, S. I., Bitam, I., & Fournier, P. E. (2023). Q Fever in Unexplained Febrile Illness in Northern Algeria. Microbiology Research, 14(4), 1589-1595. https://doi.org/10.3390/microbiolres14040109.

Ghaoui, H., Bitam, I., Zaidi, S., Achour, N., Zenia, S., Idres, T., & Fournier, P. E. (2024). Molecular detection and MST genotyping of Coxiella burnetii in ruminants and stray dogs and cats in Northern Algeria. Comparative immunology, microbiology and infectious diseases, 106, 102126. https://doi.org/10.1016/j.cimid.2024.102126.

Gisbert, P., Garcia-Ispierto, I., Quintela, L. A., & Guatteo, R. (2024a). Coxiella burnetii and Reproductive Disorders in Cattle: A Systematic Review. Animals: an open access journal from MDPI, 14(9), 1313. https://doi.org/10.3390/ani14091313.

Gisbert, P., Hurtado, A., & Guatteo, R. (2024b). Efficacy and Safety of an Inactivated Phase I Coxiella burnetii Vaccine to Control Q Fever in Ruminants: A Systematic Review. Animals : an open access journal from MDPI, 14(10), 1484. https://doi.org/10.3390/ani14101484.

Hamlili, F. Z., Laroche, M., Diarra, A. Z., Lafri, I., Gassen, B., Boutefna, B., Davoust, B., Bitam, I., & Parola, P. (2022). MALDI-TOF MS Identification of Dromedary Camel Ticks and Detection of Associated Microorganisms, Southern Algeria. Microorganisms, 10(11), 2178. https://doi.org/10.3390/microorganisms10112178.

Hireche, S., Agabou, A., & Bouaziz O. (2020). Seroprevalence of Coxiella burnetii among ewes and associated risk factors in Constantine (Northeastern Algeria). Journal of the Hellenic Veterinary Medical Society, 71(3), 2383–2390. https://doi.org/10.12681/jhvms.25100.

Khaled, H., Sidi-Boumedine, K., Merdja, S., Dufour, P., Dahmani, A., Thiéry, R., Rousset, E., & Bouyoucef, A. (2016). Serological and molecular evidence of Q fever among small ruminant flocks in Algeria. Comparative immunology, microbiology and infectious diseases, 47, 19–25. https://doi.org/10.1016/j.cimid.2016.05.002.

Lacheheb, A., & Raoult, D. (2009). Seroprevalence of Q-fever in Algeria. Clinical microbiology and infection: the official publication of the European Society of Clinical Microbiology and Infectious Diseases, 15 Suppl 2, 167–168. https://doi.org/10.1111/j.1469-0691.2008.02211.x.

Ladjal, R., Ameur, A., & Khaldi, F. (2025). Study on the main abortive diseases of sheep in the El Bayadh region, Algeria. International journal of ecosystems and ecology science (IJEES). 15. 209-214. https://doi.org/10.31407/ijees15.626.

Larson, P.S., Espira, L., Grabow, C., Wang, C.A., Muloi, D., Browne, A.S., Deem, S.L., Fèvre, E.M., Foufopoulos, J., Hardin, R., Eisenberg, J.N.S. (2019). The sero-epidemiology of Coxiella burnetii (Q fever) across livestock species and herding contexts in Laikipia County, Kenya. Zoonoses and Public Health, 66(3), 316–324. https://doi.org/10.1111/zph.12567.

Leulmi, H., Aouadi, A., Bitam, I., Bessas, A., Benakhla, A., Raoult, D., & Parola, P. (2016). Detection of Bartonella tamiae, Coxiella burnetii and rickettsiae in arthropods and tissues from wild and domestic animals in northeastern Algeria. Parasites & vectors, 9, 27. https://doi.org/10.1186/s13071-016-1316-9.

Louni, M., Mana, N., Bitam, I., Dahmani, M., Parola, P., Fenollar, F., Raoult, D., & Mediannikov, O. (2018a). Body lice of homeless people reveal the presence of several emerging bacterial pathogens in northern Algeria. PLoS neglected tropical diseases, 12(4), e0006397. https://doi.org/10.1371/journal.pntd.0006397.

Louni, M., Amanzougaghene, N., Mana, N., Fenollar, F., Raoult, D., Bitam, I., & Mediannikov, O. (2018b). Detection of bacterial pathogens in clade E head lice collected from Niger's refugees in Algeria. Parasites & vectors, 11(1), 348. https://doi.org/10.1186/s13071-018-2930-5.

Maurin, M., & Raoult, D. (1999). Q fever. Clinical microbiology reviews, 12(4), 518–553. https://doi.org/10.1128/CMR.12.4.518.

Menadi, S. E., Chisu, V., Santucciu, C., Di Domenico, M., Curini, V., & Masala, G. (2022). Serological, Molecular Prevalence and Genotyping of Coxiella burnetii in Dairy Cattle Herds in Northeastern Algeria. Veterinary sciences, 9(2), 40. https://doi.org/10.3390/vetsci9020040.

Menadi, S. E., Mura, A., Santucciu, C., Ghalmi, F., Hafsi, F., & Masala, G. (2020). Seroprevalence and risk factors of Coxiella burnetii infection in cattle in northeast Algeria. Tropical animal health and production, 52(3), 935–942. https://doi.org/10.1007/s11250-019-02083-x.

Merdja, S.E., Dahmani, A., Khaled, H., & Bouyoucef, A. (2026). Concurrent seroprevalence of the zoonotic diseases Q fever and brucellosis and their association with abortion in small ruminants from Medea province, northern Algeria. Journal of Zoonotic Diseases, 2026, 10 (1): x. https://doi.org/10.22034/jzd.2026.21074.

Million, M., Thuny, F., Richet, H., & Raoult, D. (2010). Long-term outcome of Q fever endocarditis: a 26-year personal survey. The Lancet. Infectious diseases, 10(8), 527–535. https://doi.org/10.1016/S1473-3099(10)70135-3.

Pal, M., Zende, R., Abdisa, W., Regassa, M., Mekonnen, M., Tesfaye, H., Panicker, N. (2025). Current status of Q fever and its public health implications: A comprehensive review. American Journal of Medical and Biological Research, 13(1), 1–11.

Pierrou, M., Mimoune, G., & Vastel, G. (1956). Une importante épidémie de fièvre Q (175 cas) observée à Batna (Algérie) [An extensive epidemic of Q fever (175 cases) studied at Batna (Algeria)]. La Presse medicale, 64(21), 471–473.

Radja, Z., Hezil, D., & Ghalmi, F. (2022). Contribution to the study of q fever in cattle: seroepidemiological survey in Jijel, Algeria. Agricultura. 120(3-4).81-87. https://doi.org/10.15835/agrisp.v120i3-4.14210.

Rahal, M., Tahir, D., Eldin, C., Bitam, I., Raoult, D., & Parola, P. (2018). Genotyping of Coxiella burnetii detected in placental tissues from aborted dairy cattle in the north of Algeria. Comparative immunology, microbiology and infectious diseases, 57, 50–54. https://doi.org/10.1016/j.cimid.2018.06.001.

Rahal, M., Medkour, H., Diarra, A. Z., Bitam, I., Parola, P., & Mediannikov, O. (2020). Molecular identification and evaluation of Coxiella-like endosymbionts genetic diversity carried by cattle ticks in Algeria. Ticks and tick-borne diseases, 11(5), 101493. https://doi.org/10.1016/j.ttbdis.2020.101493.

Rahal, M., Salhi, O., Ouchetati, I., Khelifi Touhami, N. A., & Ouchene, N. (2025). Global epidemiology and molecular typing of Coxiella burnetii: A systematic review of Q fever in humans and animals. Comparative immunology, microbiology and infectious diseases, 123, 102401. https://doi.org/10.1016/j.cimid.2025.102401.

Rahaman, M. R., Milazzo, A., Marshall, H., & Bi, P. (2019). Is a One Health Approach Utilized for Q Fever Control? A Comprehensive Literature Review. International journal of environmental research and public health, 16(5), 730. https://doi.org/10.3390/ijerph16050730.

Rahaman, M. R., Milazzo, A., Marshall, H., Chaber, A. L., & Bi, P. (2021). Q fever vaccination: Australian animal science and veterinary students' One Health perspectives on Q fever prevention. Human vaccines & immunotherapeutics, 17(5), 1374–1381. https://doi.org/10.1080/21645515.2020.1829900.

Rodolakis, A., Berri, M., Héchard, C., Caudron, C., Souriau, A., Bodier, C. C., Blanchard, B., Camuset, P., Devillechaise, P., Natorp, J. C., Vadet, J. P., & Arricau-Bouvery, N. (2007). Comparison of Coxiella burnetii shedding in milk of dairy bovine, caprine, and ovine herds. Journal of dairy science, 90(12), 5352–5360. https://doi.org/10.3168/jds.2006-815.

Rodolakis A. (2009). Q fever in dairy animals. Annals of the New York Academy of Sciences. 1166: 90–93. https://doi.org/10.1111/j.1749-6632.2009.04511.x.

Schimmer, B., Luttikholt, S., Hautvast, J. L., Graat, E. A., Vellema, P., & Duynhoven, Y. T. (2011). Seroprevalence and risk factors of Q fever in goats on commercial dairy goat farms in the Netherlands, 2009-2010. BMC veterinary research, 7, 81. https://doi.org/10.1186/1746-6148-7-81.

Smith, T. A., Driscoll, T., Gillespie, J. J., & Raghavan, R. (2015). A Coxiella-like endosymbiont is a potential vitamin source for the Lone Star tick. Genome biology and evolution, 7(3), 831–838. https://doi.org/10.1093/gbe/evv016.

Sprong, H., Tijsse-Klasen, E., Langelaar, M., De Bruin, A., Fonville, M., Gassner, F., Takken, W., Van Wieren, S., Nijhof, A., Jongejan, F., Maassen, C. B., Scholte, E. J., Hovius, J. W., Emil Hovius, K., Spitalská, E., & Van Duynhoven, Y. T. (2012). Prevalence of Coxiella burnetii in ticks after a large outbreak of Q fever. Zoonoses and public health, 59(1), 69–75. https://doi.org/10.1111/j.1863-2378.2011.01421.x.

Tissot-Dupont, H., & Raoult, D. (2008). Q fever. Infectious disease clinics of North America, 22(3), 505–ix. https://doi.org/10.1016/j.idc.2008.03.002.

Ullah, Q., Jamil, T., Saqib, M., Iqbal, M., & Neubauer, H. (2022). Q Fever-A Neglected Zoonosis. Microorganisms, 10(8), 1530. https://doi.org/10.3390/microorganisms10081530.

Yahiaoui, W., Afri-Bouzebda, F., Bouzebda, Z. & Dahmani, A. (2013). Sondage sérologique de la fièvre Q chez les ovins par la méthode ELISA et prévalence des avortements dans la région de Ksar El Boukhari. Tropicultura. Vol. 32. 22-27.

Yahiaoui, F., Kardjadj, M., Mohammedi, S., & Ben-Mahdi, M. H. (2025). Seroprevalence of Abortion-Related infectious diseases and associated risk factors among Brucellosis-free herds in Northern central Algeria. BMC veterinary research, 21(1), 185. https://doi.org/10.1186/s12917-025-04655-6.

Zemmouri, L., Besbaci, M., Adel, M., & Lafri, M. (2020). Sero-epidemiological Investigation of the Major Abortive Bacterial Agents in Ewes of M'Sila Governorate, Algeria. Bulletin of University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca. Veterinary Medicine. 77. 24-34. https://doi.org/10.15835/buasvmcn-vm:2020.0004.

Zheng, Z. M., Zadoks, R. N., Kim, P. S., Bosward, K. L., & Brookes, V. J. (2026). A scoping review of Coxiella burnetii transmission models in ruminants. Preventive veterinary medicine, 246, 106715. https://doi.org/10.1016/j.prevetmed.2025.106715.