Pertanika J. Trop. Agric. Sci. 48 (6): 1831 - 1846 (2025)

TROPICAL AGRICULTURAL SCIENCE

Journal homepage: http://www.pertanika.upm.edu.my/

Review Article

Q Fever in Small Ruminants: A Review on Epidemiology, Risk Factors, and Diagnostic Approaches

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ABSTRACT

Coxiella burnetii, which causes Q fever*,* is a significant zoonotic disease targeting livestock, particularly sheep and goats, with global implications for public health and agriculture. The disease presents diverse epidemiological patterns across regions, with goats often exhibiting higher seroprevalence rates compared to sheep. Transmission occurs primarily through breathing in contaminated airborne particles, with environmental determinants such as farm management practices and wind speed playing crucial roles in disease spread. Risk factors include animal age, flock size, tick infestations, environmental conditions, and poor biosecurity measures. Serological methods, primarily enzyme-linked immunosorbent assay (ELISA), remain widely used for large-scale surveillance due to their cost-effectiveness, sensitivity, and ability to detect past exposure. On the other hand, polymerase chain reaction (PCR) offers higher specificity. It is preferred for detecting active infections and environmental contamination, whereas the immunofluorescence assay (IFA) is a reliable confirmatory test. Emerging molecular techniques, including metagenomic next-generation sequencing (mNGS), surface plasmon resonance (SPR) biosensors, and up-converting phosphor technology-based lateral flow (UPT-LF) assay, demonstrate promise for enhancing diagnostic accuracy and early detection. However, regional disparities in diagnostic approaches, insufficient surveillance data, and gaps in epidemiological research continue to pose significant challenges. Addressing these gaps through integrated diagnostic strategies, affordable PCR implementation, and targeted research on transmission dynamics in livestock, wildlife, and environmental reservoirs is essential. Such efforts will strengthen Q fever control and prevention measures, minimising its impact on public health and livestock productivity.

Keywords: Coxiella burnetii, diagnostic methods, epidemiology, Q fever, risk factors, small ruminants, zoonotic disease

ARTICLE INFO

Article history:
Received: 10 February 2025
Accepted: 10 June 2025
Published: 25 November 2025

DOI: https://doi.org/10.47836/pjtas.48.6.10

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e-ISSN: 2231-8542

INTRODUCTION

Coxiella burnetii, of the order *Legionellales*, causes Q fever, a highly contagious zoonotic disease in livestock. Its chronic effects pose significant challenges to veterinary and healthcare surveillance and care systems (Villari et al., 2018; Clark & Magalhães, 2018; Larson et al., 2019). *C. burnetii* is a widespread intracellular bacterium causing acute and chronic disease, with cattle, sheep, and goats as its main hosts (Yohannes & Mekonen, 2018). Q fever affects arthropods, wildlife, companion animals, and livestock, often asymptomatic in the latter (Salifu et al., 2019). Q fever in livestock is mostly subclinical, where infected animals are mostly asymptomatic with no obvious signs of illness. Symptoms, when present, may include fever, conjunctivitis, arthritis, mastitis, and reproductive issues such as abortion and infertility. In the acute phase, *C. burnetii* tends to localise in certain organs like the liver, lungs, spleen, and bloodstream. In contrast, ongoing bacterial shedding in urine and faeces marks the chronic phase. Reproductive complications like abortions, usually in late pregnancy, with rates ranging from 3% to 80%, stillbirths, low birth weight, and neonatal mortality are common in goats and sheep (Saglam & Sahin, 2016; Tagesu, 2019).

Following a large Q fever outbreak in the Netherlands from 2007 to 2011, a cross-sectional study involving 478 human patients revealed that the health issues extended up to a decade post-infection. About 50% had serious work and physical limitations, over 25% struggled with daily and social activities, and over one-third were found to have stopped working permanently, while fatigue affected 91.2% (Bronner et al., 2020). A Q fever outbreak in 2011 linked to a goat farm in Washington involved 17 herds across Washington, Montana, and Oregon, and the outbreak caused by *C. burnetii* led to 21 human cases. Polymerase chain reaction (PCR) testing confirmed bacterial shedding in 25% of 629 goats, while enzyme-linked immunosorbent assay (ELISA) showed a 12% seroprevalence. This outbreak highlighted the need for strong collaboration between veterinary, medical, and public health sectors for effective zoonotic disease control (Anderson et al., 2015).

C. burnetii can be detected in the air and dust on livestock farms (Espí et al., 2021) while enduring extreme conditions and adhering to dust, increasing the risk of environmental dispersal and outbreaks (Clark & Magalhães, 2018). Q fever is a highly contagious illness that can appear as occasional outbreaks or larger epidemics. It poses a significant health risk, especially to veterinarians, laboratory technicians, farmers, and abattoir workers. In humans, acute infections typically present as self-limiting fever, pneumonia, or hepatitis, while chronic cases can lead to endocarditis (Yohannes & Mekonen, 2018). In Southern Belgium, veterinarians who had frequent contact with livestock showed a higher seroprevalence of Q fever (58.5%) compared to those who dealt exclusively only with companion animals like dogs, cats, and horses (6.25%), indicating that occupational exposure significantly influences the risk of the infection (Pozzo et al., 2016). A Q fever outbreak in an abattoir in Sydney affected eight male workers, with common symptoms including fever (87.5%), lethargy (75%), headaches (62.5%), and nausea or vomiting (62.5%). Notably, one of them died, whereby Q fever was identified as the main contributing factor. The cases were linked to high-risk exposures such as handling birthing materials and slaughtering pregnant animals (Lord et al., 2016). *C. burnetii*, primarily linked to domestic small ruminants as the key origin of human infections, has been weaponised due to its high infectivity, environmental persistence in a spore-like form, and windborne transmission potential, posing a biological warfare threat (Tagesu, 2019). The Centres for Disease Control and Prevention (CDC) has designated *C. burnetii* as a Category B bioterrorism agent, making Q fever reportable in many countries, including the USA, and highlighting its higher prevalence than previously recognised (Bioterrorism Agents/Diseases, 2018; Eldin et al., 2017).

In northwest Italy, a cross-sectional study assessed the individual and flock seroprevalence of *C. burnetii* in small ruminants, addressing the limited data previously based almost solely on records of breeding issues in livestock farms (Rizzo et al., 2016). Coxiellosis results in substantial losses due to miscarriages and the birth of dead offspring in small ruminants (Zahid et al., 2016). Another study in Southeast Iran assessed *C. burnetii* antibody prevalence in small ruminants, revealing high antibody positivity and identifying sheep and goats as significant Q fever reservoirs on the spot (Ezatkhah et al., 2015). Research in Ethiopia detected antibodies against *C. burnetii* in small grazers slaughtered at a slaughterhouse (Yohannes & Mekonen, 2018). Similarly, a study in The Gambia's Kiang West district assessed the extent of *C. burnetii* antibodies in adults and small ruminants, along with *C. burnetii* shedding in small grazers within domestic settings and associated risk factors. Results showed that *C. burnetii* infection is local in humans and animals in the region, with exposure linked to specific settings and shared environments (Bok et al., 2017). Q fever is known to cause abortion in livestock and febrile illness in humans. Outbreaks in Australia and the Netherlands have been related to miscarriages in small ruminant herds. However, limited information exists on Q fever in livestock and humans in Ghana. Therefore, a study was conducted in the Tongu area of Ghana's Volta region to determine the prevalence of Q fever in cattle, sheep, and goats (Johnson et al., 2019).

In South Africa, Q fever is often overlooked as a zoonosis, resulting in substantial losses in livestock and game animals due to reproductive issues (Mangena et al., 2021). A study in Egypt aimed to address the limited data on Q fever by assessing *C. burnetii*-specific antibodies in 299 herds of ruminants and camels. The review also called for more epidemiological studies to better understand Q fever's impact on human health and the market in Egypt (Klemmer et al., 2018). Q fever has drawn renewed attention, particularly following the large outbreak in the Netherlands from 2007 to 2009, emphasising its significance as a looming public health concern. New Zealand is the only country where Q fever is not reported (Pexara et al., 2018). The biggest human Q fever epidemic happened in the Netherlands between 2006 and 2009, rooted in dairy goat herds with abortion matters caused by the infection (Bontje et al., 2016). A study investigated the hosts, origins, and modes of spread associated with the significant Q fever occurrence in the Serbia-Montenegro frontier region (Debeljak et al., 2018). Between 2013 and 2015, an outbreak of abortions in grazing animals linked to Q fever affected the Jimma zone and the city of Ethiopia (Proboste et al., 2021).

EPIDEMIOLOGY

The distribution of Q fever differs significantly across regions and livestock species, based on Table 1. In Asia, studies in Iran and Turkey show sheep are more affected than goats (Ezatkhah et al., 2015; Karagul et al., 2019), whereas in Jordan, goats exhibit a higher seroprevalence than sheep (Lafi et al., 2020). In the Middle Eastern and Sub-Saharan African countries, goats are generally more vulnerable, with a particularly high seroprevalence of

Table 1
Epidemiology of Q fever across different regions

Continent	Country	Species	Sample Size	Seroprevalence (%)	Year of Study	Reference
Africa	Egypt	Goat	311	6.8	2015–2016	Klemmer et al. (2018)
		Sheep	716	8.9		
		Cattle	840	19.3		
		Buffalo	304	11.2		
		Camel	528	40.7		
	Egypt	Goat	39	28.2	2016–2017	Abushahba et al. (2017)
		Sheep	109	25.68		
		Human	35	25.71		
	Ethiopia	Goat	297	48.8	2016	Ibrahim et al. (2021)
		Sheep	269	28.9		
		Cattle	135	9.6		
		Camel	171	55.7		
		Human	190	27.0		
	Ethiopia	Goat	385	51.9	2017–2022	Oakley et al. (2024)
		Sheep	323	39.9		
		Cattle	340	8.8		
		Camel	369	16.3		
		Human (Pastoralist)	323	25.0		
	Ghana	Goat	100	10.0	Not Stated	Johnson et al. (2019)
		Sheep	158	28.4		
		Cattle	204	21.7		
	Guinea	Goat	408	4.4	2017–2019	Troupin et al. (2022)
		Sheep	486	2.3		
		Cattle	463	20.5		
	Kenya	Goat	132	0.76	2019	Kiptanui et al. (2022)
		Sheep	283	1.41		
		Cattle	725	8.14		
	Kenya	Goat	280	18.2	2013	Larson et al. (2019)
		Sheep	100	13.0		

Table 1 *(continue)*

Continent	Country	Species	Sample Size	Seroprevalence (%)	Year of Study	Reference
		Cattle	157	5.7	2013	Larson et al. (2019)
		Camel	312	19.9		
	Kenya	Goat	83	83.1	Not Stated	Nakeel et. al. (2016)
		Sheep	80	57.5		
		Cattle	156	89.7		
		Human	90	26.0		
	South Africa	Sheep	69	4.3	Not Stated	Mangena et al. (2021)**
		Cattle	331	9.4		
		Pig	107	0.9		
	The Gambia	Small Ruminants (Goat & Sheep)	615	24.9	2014	Bok et al. (2017)
		Human	599	3.8-9.7		
Asia	Iran	Goat	241	22.4	2011	Ezatkhah et al. (2015)
		Sheep	127	33.9		
	Jordan	Goat	250	43.3	2015–2017	Lafi et al. (2020)
		Sheep	480	27.0		
	Malaysia	Goat	132	9.9	2019	Jesse et al. (2020)
		Sheep	140	14.3		
	Malaysia	Goat	100	70%	Not Stated	Ahmad et al. (2024)
	Saudi Arabia	Goat	423	34.04	2012–2013	Jarelnabi et al. (2018)
		Sheep	630	12.38		
		Cattle	428	30.67		
		Camel	489	51.53		
	Turkey	Goat	205	10.24	Not Stated	Karagul et al. (2019)
		Sheep	627	14.19		
Europe	France	Goat	349*	41.5	2012–2015	Gache et al. (2017)
		Sheep	522*	25.7		
		Cattle	731*	22.2		
	Italy	Goat	206	19.5	2012	Rizzo et al. (2016)
		Sheep	111	38.7		
		Mixed Flocks (Goat & Sheep)	94	15.9		
	Spain	Goat	135	24.4	2015–2018	Espí et al. (2021)
		Sheep	154	8.4		
		Cattle	163	18.4		
		Iberian Red Deer	83	8.4		
		Cantabrian Chamois	41	7.3		
		Fallow Deer	73	6.9		
		European Wild Boar	73	5.5		
		Roe Deer	57	3.5		
		Human	1312	15.9		

Note. *Number of herds: Seroprevalence (%) calculated between-herds/within-herds
**Study on slaughter-livestock

34.04% reported in Saudi Arabia (Jarelnabi et al., 2018). In Kenya, however, findings are more variable, with one study reporting a lower prevalence in goats (0.76%) compared to sheep (1.41%) (Kiptanui et al., 2022), while the other two studies observed significantly greater rates in goats than in sheep (Nakeel et al., 2016; Larson et al., 2019). This likely reflects regional differences in livestock management and environmental conditions rather than methodological variation.

Research from Italy, Spain, and France in Europe highlights variability across species. In Italy, sheep showed higher seroprevalence than goats (38.7% vs. 19.5%) (Rizzo et al., 2016). In Spain, goats had higher rates (24.4%) than sheep (8.4%) (Espí et al., 2021), while France also reported goats again leading (41.5%) over sheep (25.6%), although the prevalence of the disease in sheep remains notably high (Gache et al., 2017). These differences may reflect variations in veterinary practices or disease surveillance systems between the countries.

In Southeast Asia, limited studies on Q fever have provided valuable insights. One study conducted on goats in Peninsular Malaysia revealed an extremely high seropositivity of 70% among dairy goats from Besut (Ahmad et al., 2024). In contrast, another study in Malaysia found that sheep (14.3%) had higher seroprevalence rates than goats (9.9%) (Jesse et al., 2020). However, the region lacks comprehensive data, highlighting the need for further investigations to better understand the disease's dynamics across species and locations.

A test done on sheep and goats in Egypt found a relatively high seroprevalence of Q fever in sheep (25.68%) and goats (28.2%) but no notable correlation between factors such as location, age, reproductive condition, or history of miscarriages and the rates of Q fever infection (Abushahba et al., 2017). In Nandi County, Kenya, a study found that animal species was the only notable predictor for Q fever, with cattle being more susceptible than sheep and goats. Other factors showed no statistical relevance (Kiptanui et al., 2022). The prevalence in cattle also varies widely, with higher rates in European countries like France (22.2%) (Gache et al., 2017) compared to lower rates in Asian and African countries such as Iran (9.6%) (Ezatkhah et al., 2015) and Kenya (8.14%) (Kiptanui et al., 2022). This variation might result from differences in climate, livestock production systems, or diagnostic practices.

No clear global trend identifies one species as consistently exhibiting the highest Q fever seroprevalence. Rather, species dominance varies by region, underscoring the need for targeted disease control and prevention strategies adapted to local contexts.

RISK FACTORS

Various animal and management-related factors have been linked to Q fever seropositivity across different regions, which can be seen in Table 2. Larger flock size was consistently identified as a risk factor in multiple studies from Jordan (Lafi et al., 2020) and Italy (Rizzo et al., 2016; Villari et al., 2018). Age was another recurring factor, with older goats and sheep tending to be more seropositive in The Gambia, Jordan, and Saudi Arabia (Bok et al., 2017; Lafi et al., 2020; Aljafar et al., 2020). However, a study in Malaysia found that younger animals were more at risk, highlighting that age-related susceptibility to Q fever may vary based on study populations or local management practices (Jesse et al., 2020). Certain exposure-related factors, such as proximity to other flocks, environmental contamination, and contact with companion animals, were also identified as predisposing factors to Q fever risk in small ruminants in some studies (Rizzo et al., 2016; Opaschaitat et al., 2018; Lafi et al., 2020). Many studies identified risk factors unique to their local settings with limited overlap across countries. This suggests that the epidemiology of Q fever is highly context-specific, shaped by regional husbandry practices, environmental conditions, species dynamics, and geographical factors.

Table 2
Reported risk factors for Q fever

Continent	**Country**	**Species**	**Risk Factors**	**Reference**
Africa	Ethiopia	Goat, Sheep, Cattle, Camel	None	Oakley et al. (2024)
		Human (Pastoralist)	Age (<15, ≥49) in households having goats with a history of abortion	
	South Africa	Sheep, Cattle, Pig*	Auction-sourced animals	Mangena et al. (2021)*
	The Gambia	Goat, Sheep	Grazing in village areas, recent lambing, old (age not specified)	Bok et al. (2017)
		Human	The presence of a seropositive animal within their compound	
Asia	Jordan	Goat, Sheep	Large flock size (≥100 animals), older animals (≥2 years), loaned breeding bucks/rams, presence of cats, goats (animal-level)	Lafi et al. (2020)
	Malaysia	Goat, Sheep	Young (age not specified), breed (Barbados Black Belly sheep), production purpose (meat > dairy)	Jesse et al. (2020)
	Saudi Arabia	Goat, Sheep, Cattle	Old (>1 year old), species (goat > sheep/cattle)	Aljafar et al. (2020)
	Saudi Arabia	Sheep	Tick infestation, history of Q fever	Elsohaby et al. (2021)
	Thailand	Goat, Sheep, Cattle, Buffalo, Wild ruminants	Contamination from bedding, manure, and the environment	Opaschaitat et al. (2018)
Europe	Italy	Goat, Sheep	Flock size (>12 animals), mixed flocks, contact with other flocks, farms in the western area, history of infertility	Rizzo et al. (2016)
	Italy	Sheep	Large flock size (>50 animals), high-altitude farms (501–1200 m)	Villari et al. (2018)

Note. *Study on slaughter-livestock

DIAGNOSTIC METHODS

Table 3 refers to the recent diagnostic approaches used for Q fever detection in small ruminants where it shows a dominance of serological methods. ELISA appears to be the most preferred method for screening and determining seroprevalence in studies across different countries, indicating past exposure to infection (Ibrahim et al., 2021). This preference may be attributed to ELISA's cost-effectiveness compared to molecular techniques, particularly large-scale surveillance (Lafi et al., 2020). The method also allows the processing of many samples simultaneously, making it ideal for estimating exposure in populations even when the infection is no longer active. Additionally, ELISA kits are widely available and have been validated for specific animal species. Indirect ELISA remains the most widely utilised, with several commercial kits such as ID Screen®, PrioCHECK™, and IDEXX tests being selected multiple times across diverse geographical settings (Lafi et al., 2020; Abbass et al., 2020; Espí et al., 2021; Ibrahim et al., 2021; Mangena et al., 2021; Ahmad et al., 2024; Saadullah et al., 2024).

Immunofluorescence assay (IFA) is another diagnostic test used to confirm seropositivity by detecting phase-specific antibodies, and it was reported only once in recent studies (Abbass et al., 2020). On the other hand, molecular techniques such as conventional PCR and real-time quantitative PCR (RT-qPCR) are used to detect any ongoing active infection by amplifying specific *C. burnetii* DNA. They were less frequently used in recent years of study and typically in combination with ELISA rather than as standalone diagnostics (Abbass et al., 2020; Mangena et al., 2021). PCR has also been proven to analyse dust and aerosol samples collected from livestock farms, confirming the presence of *C. burnetii* DNA in the environment (Espí et al., 2021).

A study from Malaysia was the only one that used a commercial sandwich-ELISA kit to determine the seroprevalence of Q fever in small ruminants. It was also the only study to report the sensitivity and specificity of the diagnostic kit, demonstrating high diagnostic accuracy with 100% sensitivity and 99.6% specificity (Jesse et al., 2020). Almost no other study reported the sensitivity and specificity of the different diagnostic methods used, which presents a major limitation in assessing and comparing diagnostic tools' performance.

Overall, ELISA remains the primary diagnostic approach for Q fever surveillance in small ruminants. In contrast, molecular diagnostic and confirmatory tests like PCR and IFA are used alongside serological screening rather than independently. Future studies should emphasise reporting the diagnostic accuracy of various diagnostic methods used and consider combining serological and molecular methods to improve the reliability of Q fever detection in small ruminants.

Beyond the commonly used diagnostic methods, a few studies have explored more advanced methods with potential relevance to small ruminants. Metagenomic next-generation sequencing (mNGS) was highlighted for its efficiency in *C. burnetii* pathogen

Table 3
Diagnostic methods used for detection of Coxiella burnetii *in small ruminants*

Diagnostic Method	**Type/Model**	**Target**	**Sample**	**Species**	**Sensitivity/ Specificity**	**Country**	**References**
ELISA (Indirect)	ID Screen® Q Fever Indirect Multi-species (FQS-MS, IDvet, Grabels, France)	Antigen-specific antibodies against *C. burnetii*	Serum	Goat, Sheep	Not reported	Pakistan	Saadullah et al. (2024)
	PrioCHECK™ Ruminant Q Fever Ab Plate Kit (Thermo Fisher Scientific, France)	Q fever-specific antibodies (Phases I+II purified antigens)	Serum	Goat	Not reported	Malaysia	Ahmad et al. (2024)
	PrioCHECK™ Ruminant Q Fever Ab Plate Kit (Thermo Fisher Scientific)	Antibodies against *C. burnetii* (Phases I and II antigens)	Serum	Goat, Sheep, Cattle	Not reported	Spain	Espí et al. (2021)
	ID-vet Q Fever (FQS-MS ver 0514 GB, Grabels, France)	Phases I and II strain	Serum	Goat, Sheep, Cattle, Camel	Not reported	Ethiopia	Ibrahim et al. (2021)
	IDEXX Q Fever 2/Strip Ab test kit (IDEXX Laboratories, Liebefeld-Bern, Switzerland)	IgG antibodies	Serum	Sheep, Cattle, Pig	Not reported	South Africa	Mangena et al. (2021)
	CHEKIT *C. burnetii* Ab ELISA test kit (IDEXX Laboratories, Broomfield, CO, USA)	Phases I and II antibodies	Serum	Goat, Sheep	Not Reported	Jordan	Lafi et al. (2020)
	ID Screen® Q Fever Indirect Multi-species (FQS-MS-2P, IDvet, Grabels, France)	Phase II antibodies (IgM, IgG)	Serum, Milk	Goat, Sheep, Cattle, Human	Not reported	Egypt	Abbass et al. (2020)
ELISA (Sandwich)	*Coxiella burnetii* Q Fever ELISA Kit (Sunlong Biotech Co., Ltd., China)	Q fever specific-antibodies	Serum	Goat, Sheep	100%/99.6%	Malaysia	Jesse et al. (2020)

Table 3 *(continue)*

Diagnostic Method	Type/Model	Target	Sample	Species	Sensitivity/ Specificity	Country	References
PCR	Conventional PCR targeting the IS1111 element	Multi-copy transposase *C. burnetii* IS1111 gene	**Sheep:** Pooled foetal tissues (liver, spleen, lung); **Cattle:** Tissue samples (Mammary gland, uterus, penis, testes, ovary)	Sheep, Cattle	Not reported	South Africa	Mangena et al. (2021)
	Real-Time Quantitative PCR (RT-qPCR)	*C. burnetii* IS1111 repetitive gene	Whole-blood	Goat, Sheep, Cattle, Human	Not reported	Egypt	Abbass et al. (2020)
IFA	*Coxiella burnetii* I+II IFA IgG/IgM/ IgA (Vircell, Spain)	Phase II IgG and IgM anti-*C. burnetii* antibodies	Serum	Goat, Sheep, Cattle, Human	Not reported	Egypt	Abbass et al. (2020)

detection in China's human Q fever outbreak investigation. Although the diagnostic method was primarily applied to human plasma samples, the study also performed mNGS and IFA on goat and cattle blood samples. The detection of *C. burnetii* by mNGS was verified by IFA, supporting the reliability and effectiveness of mNGS as a diagnostic tool for acute Q fever (Huang et al., 2021). Another human Q fever case study from China also proved the application of mNGS in detecting *C. burnetii* within 48 hours, with results validated by IFA (Yang et al., 2022). This highlights the method's rapidity, comprehensiveness, and ability to detect low pathogen loads, which suggests potential for application in livestock animals, including goats and sheep, the key hosts of *C. burnetii,* for early diagnosis and outbreak surveillance when traditional methods fall short.

A study conducted in Bulgaria developed a Surface Plasmon Resonance (SPR)-based biosensor to detect *C. burnetii* antibodies in human serum. Despite being designed for human samples, it underscores the potential of biosensor platforms for rapid, on-site, and user-friendly serological detection of *C. burnetii* by offering a promising alternative to conventional methods requiring proper laboratory settings (Genova-Kalou et al., 2024). Given the challenges of diagnosing Q fever in livestock under field conditions, such biosensor technologies could be great solutions for early detection and surveillance in small ruminants.

An Up-converting Phosphor Technology-based Lateral Flow (UPT-LF) assay was developed in China for rapid and quantitative detection of *C. burnetii* phase I strains, demonstrating high sensitivity, specificity, and field applicability, with successful testing on experimentally infected mice and naturally infected tick samples. Based on the assay's reliable performance in tissue and tick samples and its suitability for field use, it could also potentially be adapted for detecting *C. burnetii* in livestock, including small ruminants, especially in on-site or low-resource settings (Zhang et al., 2020).

CONCLUSION

Q fever remains a significant zoonosis with varying prevalence, particularly in goats and sheep across Africa, Asia, and Europe. Due to its feasibility and cost-effectiveness, ELISA is widely used for serological screening, especially in countries like Malaysia. At the same time, PCR and IFA offer a higher specificity and a valuable and reliable confirmatory test, respectively. However, critical knowledge gaps persist, especially in Southeast Asia, where the detailed epidemiology of *C. burnetii* and risk factors are still unclear. This lack of data hinders disease control, particularly among small ruminants, the primary reservoirs of *C. burnetii.* Holistic studies on seroprevalence and risk factors in this population are urgently needed.

Moreover, the disparity in diagnostic methods across regions is a challenge. ELISA is suitable for large-scale screening, but PCR should be prioritised in high-risk areas for active infection detection. While ELISA is vital in resource-limited settings, complementing it with PCR when feasible will improve diagnostic accuracy. Research into affordable PCR and more advanced methods with rapid on-site detection capability, like SPR-biosensor or UPT-LF implementation in such settings, is crucial. Future studies should also investigate transmission dynamics in wildlife and environmental reservoirs to enhance outbreak control. Addressing these diagnostic and transmission gaps will be essential for preventing future outbreaks and reducing the impacts of Q fever on public health and livestock production.

ACKNOWLEDGEMENT

This review was performed under the Faculty of Veterinary Medicine, Universiti Putra Malaysia, with funding support from GP-IPS/2025/9816400. The authors acknowledge the Department of Veterinary Services (DVS), Malaysia, for their collaborative support.

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