



A Narrative Review

Three Decades of *Coxiella burnetii* in Pakistan: A Narrative Review

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ABSTRACT

Background: *Coxiella burnetii*, the etiological agent of Q fever, is a globally distributed zoonotic pathogen with significant public health implications, particularly in agrarian economies. Despite its known prevalence in various regions, there remains a paucity of consolidated epidemiological data specific to Pakistan, limiting effective surveillance and intervention strategies. **Objective:** This study aimed to comprehensively evaluate the epidemiological trends, geographical distribution, host and environmental reservoirs, and methodological frameworks of *C. burnetii* research in Pakistan, with a particular focus on prevalence patterns and public health implications. **Methods:** A narrative review design was employed, encompassing a systematic literature search across PubMed, Scopus, Web of Science, and Google Scholar up to April 2025. Studies were included if they focused on *C. burnetii* in Pakistan and were published in English. A total of 15 studies were selected after screening (n = 15). Data were extracted on study location, design, sampling strategy, sample size, host species, and prevalence rates. Ethical standards were maintained following the Declaration of Helsinki. Data were synthesized using Microsoft Excel and analyzed descriptively via GraphPad Prism. **Results:** The review found a notably higher concentration of studies in Punjab province (80%) with random sampling being the dominant methodology (87%). Sheep and goats showed the highest mean blood prevalence (41.23% and 38.86%, respectively), with notable tick vector involvement and soil-based environmental persistence (16.97%). Human samples showed a mean prevalence of 14.57%, reinforcing zoonotic risk. Clinically, underdiagnosis remains a challenge due to nonspecific symptomatology and lack of routine screening. **Conclusion:** *C. burnetii* poses a significant and underrecognized zoonotic threat in Pakistan, especially in high-density livestock areas. Findings support the need for a One Health approach integrating veterinary, environmental, and clinical surveillance to mitigate disease transmission and inform targeted interventions in human healthcare.

Keywords: *Coxiella burnetii*, Q Fever, Zoonoses, Pakistan, Seroprevalence, Molecular Detection, One Health

INTRODUCTION

The growing burden of tick-borne diseases has emerged as a global concern due to their dual threat to both human and animal health, with zoonotic pathogens increasingly recognized as significant contributors to public health risks (1). Among these, *Coxiella burnetii*, the etiological agent of Q fever, is a highly infectious, pleomorphic, intracellular Gram-negative bacterium that exhibits remarkable environmental resistance and a complex transmission ecology. Its primary tropism for macrophages, coupled with the ability to form spore-like morphotypes, enables it to persist in harsh conditions such as

high temperatures and desiccation, which enhances its environmental stability and zoonotic transmission potential (2). In animals, particularly ruminants, *C. burnetii* is associated with a spectrum of reproductive disorders including abortion, stillbirths, and infertility, often without overt clinical signs, making it difficult to detect without targeted surveillance (3). In humans, Q fever can manifest as an acute febrile illness with nonspecific symptoms or progress to chronic infections involving endocarditis and hepatitis, especially in immunocompromised individuals (4). Occupational exposure

among veterinarians, abattoir workers, farmers, and laboratory personnel significantly increases the risk of infection (5), while ticks—both soft and hard—play a pivotal role in maintaining and transmitting the pathogen in wildlife-livestock-human interfaces across diverse ecological landscapes (6).

Globally, over 40 tick species have been confirmed as vectors for *C. burnetii*, capable of acquiring the bacterium via blood meals and transmitting it during subsequent feedings or through the dispersal of contaminated excreta as aerosols (7). Transmission to humans is primarily airborne, but also occurs through direct contact with contaminated birth products, raw milk, meat, or environmental materials such as dust or soil (8). Ruminants, particularly sheep, goats, and cattle, are the principal reservoirs, often shedding large quantities of the pathogen in urine, feces, milk, and placental tissues during parturition, even in the absence of clinical disease (9). While earlier studies in Pakistan reported seroprevalence rates of up to 26.8% in humans (10, 11), the actual burden remains underestimated due to limited diagnostic capacity, underreporting, and low clinical suspicion among healthcare providers (12). This is compounded by the absence of a national surveillance program or coordinated public health strategy addressing Q fever, resulting in fragmented and geographically limited epidemiological data (13).

Over the past three decades, sporadic efforts in Pakistan have employed both serological and molecular tools to assess the prevalence of *C. burnetii* in various hosts and environments. However, most studies are localized, predominantly conducted in Punjab, and lack methodological uniformity and national representation. Although molecular diagnostics such as PCR and ELISA-based serological assays have improved detection, their application remains restricted by resource constraints and logistical challenges.

Unlike countries that have implemented integrated One Health surveillance systems, Pakistan's epidemiological landscape is characterized by gaps in spatial coverage, strain characterization, and transmission dynamics (14). The need for a comprehensive synthesis of existing data is critical to assess the burden of disease, identify high-risk populations, and inform policy-making.

This review addresses the existing research gap by synthesizing the available literature on the prevalence, geographic distribution, host range, and sampling strategies used in the study of *C. burnetii* in Pakistan between 1987 and 2025. By evaluating the strengths and limitations of past research, this review aims to offer a clearer picture of the zoonotic threat posed by Q fever in the country and to recommend strategic directions for future surveillance and control. The central question guiding this review is: How has the epidemiological understanding of *Coxiella burnetii* evolved in Pakistan over the past three decades, and what are the implications for developing a coordinated One Health surveillance and intervention strategy?

RESULTS

The narrative review comprehensively assessed epidemiological trends, geographical distribution, methodologies, and

prevalence data related to *Coxiella burnetii* research in Pakistan from 1987 to 2025 (Table 1). The first documented study on *C. burnetii* in Pakistan dates back to 1987, with sparse subsequent research activity up to 2015. Specifically, only two studies were published between 1987 and 2010, followed by one publication between 2011 and 2015. A marked increase in research output has been observed recently, evidenced by four studies published between 2016 and 2020, and eight studies published between 2021 and 2024. The geographical distribution of research indicates a significant concentration in Punjab province, accounting for twelve out of fifteen reviewed studies. Conversely, Sindh, Khyber Pakhtunkhwa, and northern Pakistan were represented by only one study each, highlighting notable geographical gaps in epidemiological data.

The review identified that cross-sectional designs predominantly featured in the reviewed studies, frequently employing molecular or serological methodologies (Table 1). Seven studies exclusively utilized a cross-sectional molecular-based approach, two combined cross-sectional serological and molecular methods, and four studies relied exclusively on cross-sectional serological analyses.

Only one study employed a purely epidemiological-serological approach. This preference for cross-sectional designs reflects an emphasis on point prevalence rather than longitudinal or experimental studies that could elucidate transmission dynamics and temporal epidemiological trends more effectively.

In terms of sampling methodologies, random sampling was overwhelmingly favored, with thirteen studies adopting this approach. More structured sampling methods, such as grid-based sampling (one study) and three-stage sampling design (one study), were notably rare. The limited use of advanced sampling strategies underscores a methodological gap, suggesting the need for more rigorous sampling frameworks in future research to improve the reliability and epidemiological robustness of findings (Figure 1).

Animal hosts, sheep exhibited the highest mean prevalence in blood samples (41.23%), followed closely by goats (38.86%) and dromedary camels (31.30%). In cattle, cows demonstrated a notably higher prevalence (32.12%) compared to buffaloes (12.5%). Human blood samples had a mean prevalence of 14.57%, highlighting significant zoonotic implications.

The prevalence data indicate widespread distribution of *C. burnetii* across diverse animal reservoirs, vectors, raw meat products, and environmental samples within Pakistan (Table 2, Figure 2). Among Vector-based studies, focusing on ticks, revealed the highest mean prevalence rates in ticks from sheep (35.5%) and goats (22.85%). A significantly lower prevalence was reported in ticks associated with Indian long-eared hedgehogs (2%), indicating varying degrees of vector-host interaction. The examination of raw meat samples also underscored significant public health concerns.

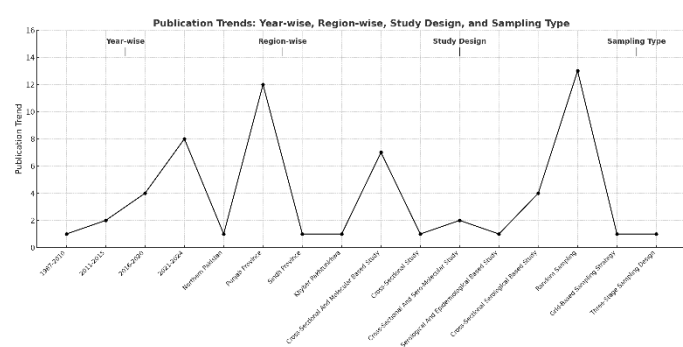
Meat from sheep showed the highest prevalence rate (33.2%), followed by goats (27.6%), cattle (12%), and buffaloes (8%), emphasizing the risks associated with handling and consumption of contaminated meat products.

Table 1: Trends of Publications Related to *Coxiella burnetii* Research in Pakistan (1987–2024)

Categories	Year/Area/Design	Number of Studies
Year-wise Distribution	1987–2010	2
	2011–2015	1
	2016–2020	4
	2021–2024	8
Area-wise Distribution	Northern Pakistan	1
	Punjab	12
	Sindh	1
	Khyber Pakhtunkhwa	1
Study Design	Cross-Sectional Molecular	7
	Cross-Sectional Serological	4
	Cross-Sectional Sero-Molecular	2
	Epidemiological Serological	1
	Cross-Sectional (general)	1
Sampling Type	Random Sampling	13
	Grid-based Sampling	1
	Three-Stage Sampling	1

Table 2: Mean Prevalence (%) of *Coxiella burnetii* in Various Sample Types in Pakistan

Sample Type	Host/Source	Mean Prevalence (%)
Blood	Sheep	41.23
	Goats	38.86
	Dromedary Camels	31.30
	Cows	32.12
	Buffaloes	12.50
	Humans	14.57
Ticks	Sheep	35.50
	Goats	22.85
	Indian Long-eared Hedgehogs	2.00
Raw Meat	Sheep	33.20
	Goats	27.60
	Cattle	12.00
	Buffaloes	8.00
Soil	Environmental (Soil Samples)	16.97


Figure 1: Trends of publication related to *C. burnetii* (1987–2024), emphasizing study design and sampling methodology patterns.

Environmental persistence was confirmed through soil sample analyses, revealing an average prevalence of 16.97%, underscoring the importance of environmental reservoirs in disease transmission and potential aerosolized contamination routes. The prevalence data underscore the urgent need for

integrated One Health surveillance strategies, particularly in Punjab province where research and reported prevalence rates are concentrated. Variability across Pakistan's regions necessitates further comprehensive and geographically diverse research to establish a complete national epidemiological profile. Future studies should incorporate longitudinal and experimental designs to improve understanding of transmission dynamics, genetic diversity, and molecular epidemiology.

Implementing advanced sampling methodologies and strengthening laboratory capacity for molecular diagnostics and strain typing are crucial steps towards developing targeted interventions. Biosecurity enhancement in agricultural settings, public education on handling animal products, and active vector control measures are pivotal to managing the zoonotic risks associated with *C. burnetii*. This review highlights the critical need for precise, context-specific intervention strategies to effectively mitigate the public health burden posed by Q fever in Pakistan.

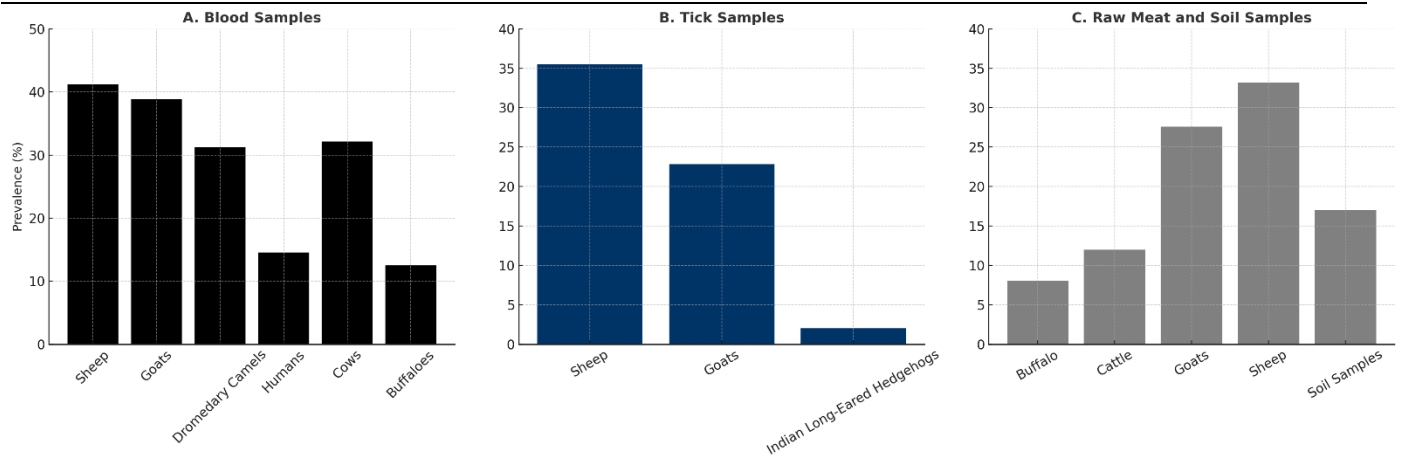


Figure 2: Mean prevalence of *C. burnetii* in blood, vector (tick), meat, and soil samples across various hosts and environments.

DISCUSSION

The findings of this review reaffirm the widespread presence and zoonotic potential of *Coxiella burnetii* in Pakistan, revealing important epidemiological trends that reflect both progress and persistent gaps in national surveillance. The observed rise in publication frequency over the last decade indicates increasing awareness and prioritization of Q fever within the scientific community. This trend aligns with global patterns in emerging zoonoses research, yet the concentration of studies in Punjab, with minimal representation from other provinces, suggests an uneven distribution of investigative efforts. Comparatively, earlier research in regions like Northern and Southern Europe demonstrated more geographically comprehensive surveillance systems, allowing for broader epidemiological modeling and risk assessment (1). The methodological preference for cross-sectional studies in Pakistan, though valuable for estimating point prevalence, limits the ability to interpret temporal changes and causative links, a constraint similarly noted in low-resource settings elsewhere (2, 24).

The consistently high prevalence of *C. burnetii* in sheep, goats, and camels across various biological samples echoes findings from Middle Eastern and North African studies, which identified small ruminants as primary reservoirs and sources of human infection (3). These similarities underscore the relevance of regional livestock management practices in shaping pathogen transmission dynamics. However, the relatively lower prevalence rates observed in human subjects in this review, while suggestive of limited zoonotic spillover, may also reflect underdiagnosis due to lack of routine clinical screening and the pathogen's non-specific symptomatology. This diagnostic ambiguity has been a recurring challenge in Q fever research globally and has prompted recommendations for targeted serological surveillance in high-risk populations, such as farmers, abattoir workers, and veterinary staff (4). The review's identification of ticks as significant vectors further strengthens the case for integrated vector-host surveillance, a strategy increasingly advocated in One Health frameworks, especially where environmental reservoirs such as soil have also been implicated (5, 23–27).

In addition to the clinical implications, the findings highlight theoretical considerations related to environmental

persistence. The detection of *C. burnetii* in soil samples supports aerosol transmission as a plausible mechanism, reinforcing prior work from European outbreak investigations that identified contaminated dust as a significant exposure pathway during dry seasons (6). This route of transmission adds complexity to control efforts, especially in densely populated livestock zones with poor biosecurity infrastructure. Moreover, the high prevalence of the pathogen in raw meat samples—particularly from sheep and goats—raises concerns not only for occupational exposure but also for foodborne transmission. While cooking and pasteurization effectively neutralize the pathogen, improper meat handling practices and consumption of undercooked products could contribute to human infections, as suggested in past food safety studies (28–31).

Although the study provides valuable insights, several limitations must be acknowledged. The sample size across studies, while collectively substantial, varies significantly by host type and geographic region, limiting the generalizability of prevalence estimates. The overrepresentation of Punjab may introduce regional bias, and the scarcity of structured, stratified sampling designs diminishes the strength of extrapolated data. Furthermore, the lack of longitudinal studies prevents an assessment of seasonal or interannual variation, which is crucial for modeling outbreaks and informing vaccination or vector control campaigns. The exclusive inclusion of English-language publications might have led to the omission of relevant data published in local or regional journals (32, 33).

Despite these limitations, the review's strength lies in its comprehensive synthesis of both historical and recent data, offering a consolidated reference point for policymakers, researchers, and clinicians. It also demonstrates the feasibility of integrating molecular, serological, and environmental surveillance techniques, supporting a more holistic understanding of *C. burnetii* epidemiology in resource-constrained contexts. To advance current knowledge, future research should prioritize geographically inclusive sampling, longitudinal designs, and genomic characterization of circulating *C. burnetii* strains to discern patterns of diversity and resistance. Additionally, incorporating community-based participatory approaches and health education interventions could improve awareness and early detection, reducing the

burden of undiagnosed or misdiagnosed Q fever cases. The findings of this review substantiate the endemic nature of *C. burnetii* in Pakistan and reveal clear epidemiological hotspots and host-pathogen interactions. The evidence supports a call to action for enhanced One Health surveillance, capacity-building in diagnostic infrastructure, and the development of national strategies tailored to livestock-dense, high-risk zones. Addressing these gaps is critical not only for preventing zoonotic transmission but also for mitigating broader public health risks associated with neglected bacterial pathogens (8, 33).

CONCLUSION

This narrative review highlights the endemic presence and significant zoonotic potential of *Coxiella burnetii* across diverse hosts, vectors, and environmental sources in Pakistan, with a clear predominance in the Punjab province. The findings underscore a pressing need for enhanced surveillance and diagnostic capacity, particularly within healthcare and veterinary systems, to identify and mitigate risks associated with Q fever. The high prevalence in livestock and ticks, coupled with environmental persistence, presents critical implications for human health, especially for individuals in close contact with animals or exposed to contaminated aerosols. Clinically, these results advocate for the integration of *C. burnetii* screening into differential diagnosis protocols for febrile illnesses, while reinforcing the importance of occupational health safeguards. From a research standpoint, the study calls for geographically broader, longitudinal, and molecularly driven investigations to elucidate transmission dynamics and inform targeted interventions. Overall, this review provides a foundational step toward establishing a coordinated, One Health-based surveillance framework to reduce the burden of Q fever in Pakistan's human and animal populations.

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