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INTEGRATING LIVESTOCK HEALTH, FARMER PRACTICES AND EPIDEMIOLOGICAL SURVEILLANCE FOR *CHLAMYDIA PECORUM*: A ONE HEALTH FRAMEWORK FOR DISEASE DETECTION AND PREVENTION

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Abstract

Chlamydia pecorum is an important veterinary pathogen associated with infections in livestock and wildlife, with documented relevance to cattle, sheep, pigs and koalas. Its epidemiological significance is complicated by variation in clinical presentation, the occurrence of subclinical infection, limitations of some serological approaches, and substantial genetic diversity among strains. Molecular methods, particularly species-specific quantitative polymerase chain reaction (qPCR), ompA characterization and multilocus sequence typing (MLST), have strengthened the capacity to detect and characterize C. pecorum. Nevertheless, laboratory surveillance alone does not constitute a complete disease-prevention system. Recognition of abnormal animal health by farmers, perceptions of disease risk, health literacy, veterinary-service utilisation, farmer–veterinarian communication and biosecurity practices influence the pathway through which suspected disease becomes formally investigated. The present article develops an integrated One Health framework connecting these social, veterinary and molecular dimensions of C. pecorum surveillance. The framework was reconstructed from the supplied research material and supported by verified literature on C. pecorum, livestock disease surveillance, molecular epidemiology, farmer biosecurity and One Health. The proposed system begins with farmer recognition and reporting, progresses through veterinary assessment and sample collection, and incorporates species-specific molecular detection followed, where appropriate, by molecular characterization. Surveillance information is then intended to inform targeted biosecurity and continued monitoring. Because the supplied source does not contain completed empirical observations, participant data, laboratory results or statistical analyses, the present article does not claim empirical effectiveness of the framework. Instead, it provides a publication-ready conceptual and methodological structure for future integrated research. The framework contributes a practical mechanism for connecting farm-level behaviour with laboratory and epidemiological surveillance within a One Health system.

1. Introduction

Livestock diseases are rarely controlled effectively through a single diagnostic or management intervention. Disease emergence and persistence are influenced by interactions among pathogens, animals, farmers, production systems, veterinary services, environmental conditions and patterns of animal movement. These relationships are particularly important for infectious diseases that may circulate without producing readily recognizable clinical signs. Within this broader context, *Chlamydia pecorum* represents a relevant veterinary-health challenge because infection has been identified in several livestock species and wildlife hosts and because molecular investigations have demonstrated substantial diversity among isolates.

C. pecorum is an obligate intracellular bacterium that has been associated with disease in domestic livestock and wildlife. Research has documented its importance in sheep and cattle and has also demonstrated its relevance to koala health. Molecular epidemiological investigations have shown that isolates obtained from different hosts can exhibit distinct genetic characteristics, highlighting the importance of understanding infection at both the clinical and population levels (Jelocnik et al., 2013). More recent livestock research has continued to demonstrate substantial strain diversity, particularly among bovine isolates, while identifying relationships between *ompA* profiles and MLST results (Hagenbuch et al., 2024).

The epidemiology of *C. pecorum* is complicated y diagnostic limitations. Serological evidence of exposure does not necessarily provide species-specific confirmation because cross-reactivity between chlamydial organisms can complicate interpretation. Bommana et al. (2019), for example, demonstrated limitations of commercial serological assays in Australian livestock and concluded that species-specific qPCR and peptide-based serological approaches provided greater specificity than some conventional whole-cell antigen tests. Longitudinal research has also demonstrated the value of molecular detection for investigating the temporal dynamics of *C. pecorum* infection in livestock (Bommana et al., 2018).

Molecular epidemiology provides an additional level of information. Jelocnik et al. (2013) developed a *C. pecorum*-specific multilocus sequence analysis approach and used it to investigate genetic relationships among isolates from sheep, cattle and koalas. Subsequent genomic and molecular studies have reinforced the observation that *C. pecorum* populations are genetically diverse. Hagenbuch et al. (2024) reported high diversity among bovine strains in Switzerland and identified congruence between *ompA* typing and MLST in livestock isolates. However, recent reviews have also noted limitations associated with relying on *ompA* alone because of its polymorphism and recombination, supporting the use of complementary molecular approaches when epidemiological resolution is required.

Although diagnostic and molecular research has advanced considerably, surveillance begins before a sample reaches a laboratory. A farmer may first observe reproductive abnormalities, reduced productivity, abnormal clinical signs or other changes in animal health. Whether that observation results in veterinary consultation depends partly on knowledge, risk perception, accessibility of veterinary services and communication between farmers and veterinary professionals. Biosecurity practices can similarly be influenced by knowledge, perceived barriers, available resources and interactions with animal-health professionals. Evidence from livestock systems outside *C. pecorum* research demonstrates that farmer behaviour is an important component of infectious-disease prevention and should be considered alongside technical disease-control measures.

This issue is particularly relevant to a One Health approach. The Quadripartite organizations—the Food and Agriculture Organization of the United Nations, United Nations Environment Programme, World Health Organization and World Organisation for Animal Health—define One Health as an integrated approach that recognizes the interdependence of human, animal, plant and ecosystem health. The One Health Joint Plan of Action emphasizes coordinated surveillance, communication, capacity development and multisectoral action (FAO, UNEP, WHO, & WOAH, 2022). In August 2026, the

Quadripartite organizations extended implementation of the Joint Plan of Action through 2029, reinforcing the continuing policy relevance of integrated One Health systems (WHO, 2026).

The research gap addressed by the present framework is therefore not the absence of molecular methods for *C. pecorum*. Rather, it concerns the limited integration of molecular surveillance with farmer-level knowledge, health literacy, risk perception, veterinary-service utilisation and biosecurity behaviour. The aim of this article is to develop a One Health framework that connects these dimensions into a continuous pathway from farm-level disease recognition to molecular detection, epidemiological interpretation and prevention.

2. Research Objectives and Questions

The central objective of the proposed research is to integrate livestock health, farmer practices and epidemiological surveillance into a coherent One Health framework for the detection and prevention of *C. pecorum* infection. More specifically, the framework seeks to examine how farmer knowledge and health literacy may influence recognition of livestock-health problems and how risk perception may influence decisions concerning veterinary consultation and preventive behaviour. It further seeks to integrate farmer–veterinarian communication and veterinary-service utilisation into the surveillance process and to connect farm-level observations with molecular detection and epidemiological characterization.

The framework is guided by four research questions. First, how can farmer knowledge, health literacy and perceived livestock-disease risk be incorporated into *C. pecorum* surveillance? Second, how can veterinary-service utilisation and communication between farmers and veterinary professionals contribute to earlier recognition and investigation of suspected infection? Third, how can molecular detection and molecular epidemiology be integrated with farm-level disease information? Fourth, what combination of farmer practices, veterinary engagement and surveillance activities could support evidence-informed prevention?

These questions are intended to guide empirical implementation. They should not be interpreted as having been statistically answered by the supplied material because no completed empirical dataset was provided.

3. Literature Review

3.1 Livestock infection and epidemiological complexity

The existing literature establishes *C. pecorum* as a relevant pathogen of livestock and wildlife. Its importance is not limited to a single host species, and molecular studies have demonstrated relationships among isolates obtained from sheep, cattle and koalas. Jelocnik et al. (2013) examined 35 isolates using multilocus sequence analysis and demonstrated genetic relationships among isolates from different hosts. Their findings illustrated the usefulness of molecular approaches for understanding *C. pecorum* epidemiology beyond conventional clinical diagnosis.

The epidemiological picture has subsequently become more complex. Comparative genomic research demonstrated genetic differences among koala, cattle and sheep strains (Bachmann et al., 2014). Research in Switzerland further identified *C. pecorum* in ruminant and porcine samples and found substantial diversity in bovine strains (Hagenbuch et al., 2024). These findings indicate that surveillance systems need to consider both detection and characterization.

3.2 Diagnostic surveillance

The distinction between exposure and active infection is important when developing surveillance systems. Bommana et al. (2018) investigated *C. pecorum* infection longitudinally in prime lamb production and demonstrated the value of combining molecular and serological information. Their findings illustrate that different diagnostic approaches can provide different forms of epidemiological information.

Bommana et al. (2019) subsequently examined commercial serological assays and demonstrated the potential for cross-reactivity between chlamydial organisms. In their study, *C. pecorum* DNA was identified by species-specific qPCR in animals with chlamydial

serological evidence. The authors consequently cautioned against interpreting whole-cell antigen serological results as definitive evidence of infection by a particular chlamydial species. This evidence supports the proposed framework's emphasis on species-specific molecular confirmation.

3.3 Molecular epidemiology

Molecular epidemiology can extend surveillance from detection toward understanding transmission and population structure. The MLST approach developed by Jelocnik et al. (2013) provided a method for comparing *C. pecorum* isolates across livestock and wildlife hosts. However, molecular marker selection remains important. Recent synthesis of *C. pecorum* research has identified limitations in relying exclusively on *ompA*, particularly because of high polymorphism and recombination. Consequently, *ompA* typing can be useful but should be interpreted alongside additional markers or whole-genome approaches where resources permit.

Hagenbuch et al. (2024) provide contemporary evidence for this integrated molecular approach. Their investigation of Swiss livestock found considerable diversity in bovine strains and reported congruence between *ompA* typing and MLST among livestock strains. Such evidence supports incorporating molecular characterization into surveillance when positive samples and appropriate laboratory resources are available.

3.4 Farmer behaviour and biosecurity

The laboratory component of surveillance cannot be separated from farm-level decision-making. Farmer knowledge influences recognition of disease, while risk perception may influence whether a farmer considers a particular event sufficiently serious to contact a veterinary professional. Veterinary-service accessibility and communication can then determine whether a suspected problem progresses toward diagnostic investigation.

Evidence from Pakistan demonstrates that livestock-health surveillance can be influenced by gaps in farmer knowledge and veterinary consultation. Although a study conducted in Punjab investigated ticks and tick-borne diseases rather than *C. pecorum*, it demonstrated the relevance of farmer awareness and veterinary engagement within a One Health context. Such evidence is useful for conceptual development but cannot be interpreted as evidence that the same behavioural patterns exist specifically for *C. pecorum*.

Biosecurity is similarly multidimensional. It includes management of animal movement, isolation of potentially affected animals, hygiene, disinfection, facility management and appropriate veterinary consultation. Farmer implementation may depend not only on knowledge but also on cost, practicality, infrastructure and perceived disease risk. The proposed framework therefore avoids assuming that education automatically produces behaviour change and instead treats farmer behaviour as an interaction between knowledge, perception, communication and structural conditions.

3.5 One Health integration

The proposed framework is aligned with the broader One Health approach because it treats disease surveillance as a system rather than an isolated laboratory activity. The Quadripartite One Health Joint Plan of Action identifies coordinated action, surveillance, communication and capacity-building as components of effective One Health implementation (FAO et al., 2022). This framework is particularly relevant where livestock production intersects with environmental systems, animal movement, veterinary services and human communities.

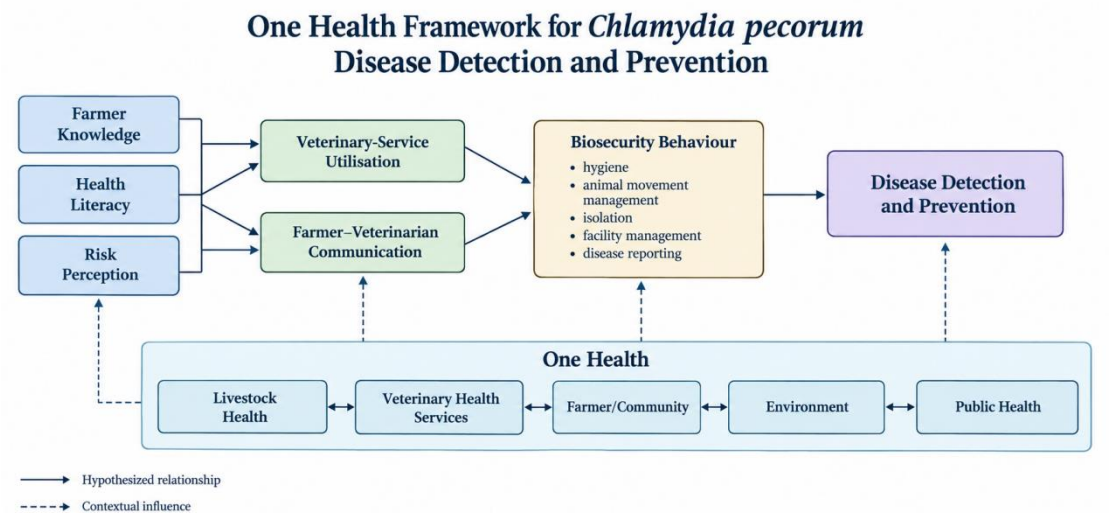
4. Theoretical and Conceptual Framework

The framework combines a behavioural pathway with an epidemiological surveillance pathway. At the farmer level, knowledge and health literacy are conceptualized as factors that may influence risk perception. Risk perception may subsequently affect veterinary-service utilisation and communication with veterinary professionals. These interactions can influence biosecurity behaviour and the likelihood that abnormal livestock-health events are reported.

The epidemiological pathway begins with farmer recognition of an abnormal health event. Veterinary assessment provides an intermediate

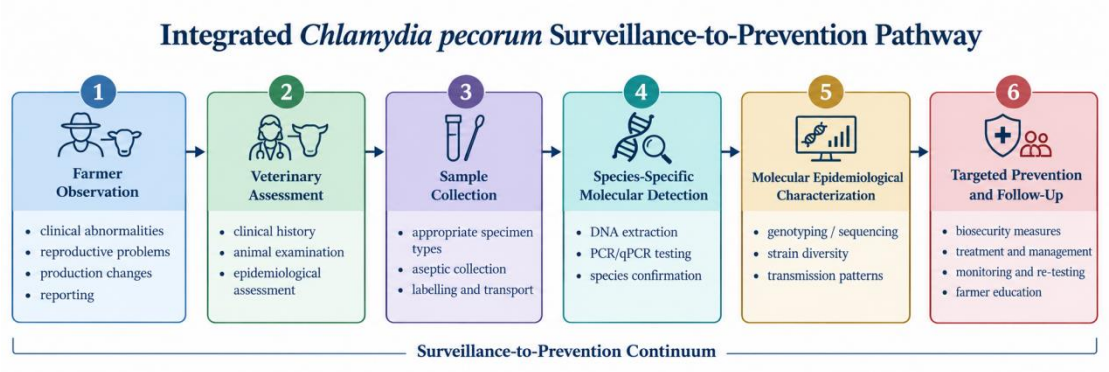
stage through which clinical history, animal examination and epidemiological information can be used to determine whether laboratory investigation is appropriate. Sample collection then connects farm-level surveillance to molecular detection. Species-specific qPCR provides a potential mechanism for identifying *C. pecorum*, while *ompA* typing and MLST may provide additional epidemiological information for confirmed samples.

Figure 1: One Health Framework for Chlamydia pecorum Disease Detection and Prevention



The second component of the framework is the surveillance feedback loop. Farmer observation leads to veterinary assessment, followed by sample collection and laboratory investigation. Where *C. pecorum* is detected, molecular characterization may provide epidemiological information that can be combined with farm-level information. The resulting information can inform targeted prevention and subsequent monitoring.

Figure 2: Integrated Chlamydia pecorum Surveillance-to-Prevention Pathway



"Species-Specific Molecular Detection," show "*C. pecorum*-specific qPCR." Under "Molecular Epidemiological Characterization," show "*ompA* typing" and "MLST." Under "Targeted Prevention," show "biosecurity," "animal movement management," "hygiene," and "continued surveillance." Add a large curved feedback arrow from the final stage back to the first stage labelled "Continuous Surveillance and Feedback." White background, publication-quality vector style, clear typography, no numerical data and no invented laboratory parameters.

5. Methodology

5.1 Research design and setting

The supplied research material represents an integrated One Health framework rather than a

completed empirical dataset. Accordingly, the methodological structure is presented as a proposed research design and is not described as a completed field study. The framework is suitable for implementation as a mixed-methods epidemiological investigation in livestock-producing communities.

The proposed research setting would consist of livestock production environments in which farmers maintain relevant domestic animal species and have access, to varying degrees, to veterinary services. The available source does not provide a confirmed final geographic sampling frame, therefore no specific province, district, village or farm count is reported as completed study information.

5.2 Farmer component

The farmer component is intended to investigate knowledge and awareness of livestock disease, health literacy, perceived disease risk, veterinary-service utilisation, farmer–veterinarian communication and biosecurity behaviour. The proposed assessment would examine how farmers recognize disease events, how they interpret perceived risks and what factors influence decisions to seek veterinary assistance.

Because the supplied material does not identify a validated questionnaire, the exact instrument, number of items, scoring system and psychometric properties cannot be stated. These details should be established and validated before empirical implementation.

5.3 Veterinary and laboratory component

The proposed veterinary pathway begins with recognition of a potentially abnormal animal-health event. Veterinary professionals would assess clinical history and relevant epidemiological information and determine whether sample collection is appropriate.

The laboratory component is conceptually based on species-specific molecular detection. Previous studies provide support for the use of *C. pecorum*-specific qPCR, particularly where serological cross-reactivity creates uncertainty (Bommana et al., 2019). Positive samples could subsequently be considered for molecular characterization using *ompA* typing and MLST, consistent with published *C. pecorum* epidemiological research (Jelocnik et al., 2013; Hagenbuch et al., 2024).

The supplied material does not specify exact sample types, DNA extraction kits, primer sequences, cycling conditions, equipment, Ct thresholds or quality-control parameters. These should therefore not be invented and would need to be documented in an empirical protocol.

5.4 Data integration

The central methodological feature is integration. Farmer-level information would provide context for animal-health events, veterinary information would provide clinical and epidemiological interpretation, and molecular information would provide pathogen-specific evidence. Linking these data streams would allow future researchers to examine whether patterns in farmer behaviour and veterinary engagement correspond with laboratory-confirmed infection.

Table 1. Proposed Study Domains and Measurement Components

Domain	Main construct	Proposed information	Evidence status
Farmer	Disease knowledge	Awareness and recognition of livestock disease	Proposed
Farmer	Health literacy	Ability to understand and use animal-health information	Proposed
Farmer	Risk perception	Perceived likelihood and seriousness of disease	Proposed
Veterinary	Service utilisation	Frequency and circumstances of veterinary consultation	Proposed
Communication	Farmer–veterinarian interaction	Information exchange and advice received	Proposed

Biosecurity	Preventive behaviour	Hygiene, isolation and animal movement practices	Proposed
Laboratory	Molecular detection	Species-specific detection of *C. pecorum*	Proposed
Molecular epidemiology	Strain characterization	*ompA* and MLST where applicable	Proposed
Surveillance	Feedback	Follow-up and prevention after detection	Proposed

6. Results

6.1 Status of results

The supplied research material does not contain a completed empirical dataset. Therefore, the Results section cannot legitimately report a participant count, prevalence estimate, statistical association, p-value, confidence interval or laboratory positivity rate for the present study. The results presented here are instead framework-derived results, meaning that they represent the integrated structure generated from the supplied research objectives and supported literature.

The first result is the identification of a multi-stage surveillance pathway. The framework places farmer observation at the beginning of surveillance rather than treating laboratory diagnosis as the starting point. This is important because clinical or production changes are often initially observed at farm level. Veterinary assessment provides the bridge between observation and laboratory investigation, while molecular testing provides pathogen-specific evidence.

The second result is the integration of behavioural and diagnostic domains. Rather than considering farmer knowledge and laboratory surveillance as unrelated components, the framework proposes that they operate sequentially and interactively. Knowledge and health literacy can affect recognition; risk perception can influence reporting; veterinary communication can influence diagnostic access; and biosecurity behaviour can influence prevention.

The third result is the inclusion of molecular epidemiology after species-specific detection. This reflects evidence demonstrating that *C. pecorum* isolates can be genetically diverse and that molecular characterization can contribute to understanding strain relationships.

Table 2. Framework-Derived Surveillance Results

Framework stage	Information generated	Intended epidemiological function
Farmer observation	Recognition of abnormal animal-health events	Initiation of surveillance
Risk assessment	Farmer perception of disease importance	Explanation of reporting behaviour
Veterinary assessment	Clinical and epidemiological information	Determination of diagnostic need
Sample collection	Biological material for testing	Connection between field and laboratory surveillance
qPCR	Species-specific molecular evidence	Confirmation of *C. pecorum* detection
ompA/MLST	Molecular characterization	Epidemiological comparison
Biosecurity response	Preventive management	Reduction of potential transmission opportunities
Follow-up	Continued observation/testing	Surveillance feedback

6.2 Evidence from previous research informing the framework

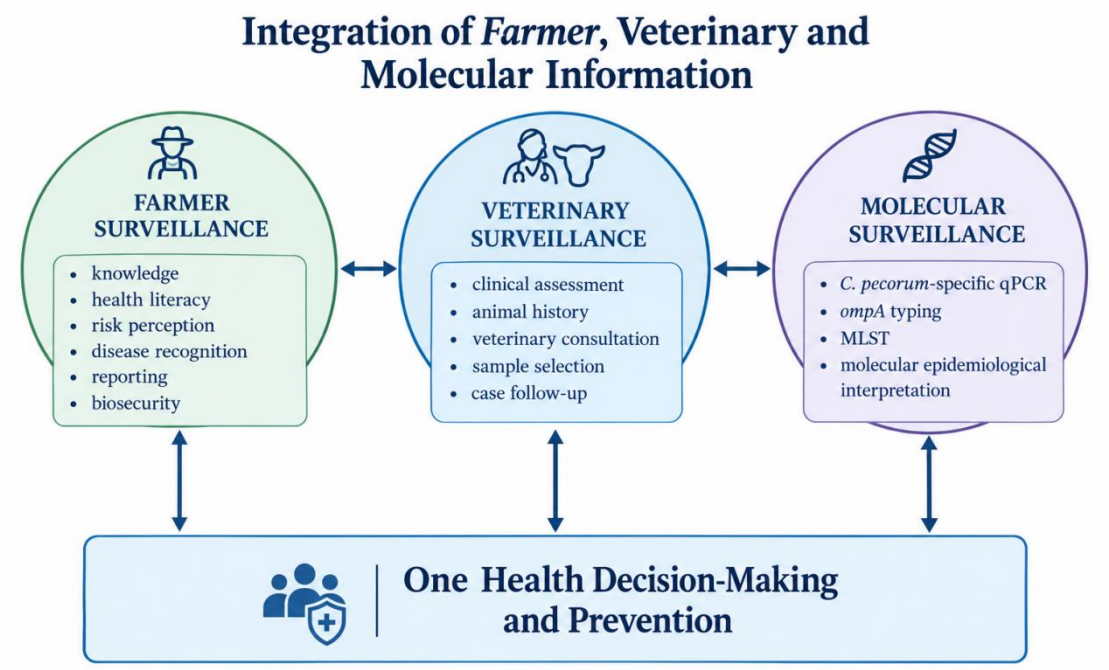
The framework is supported by empirical studies, but their findings must not be represented as results of the present study. For example, Jelocnik et al. (2013) used 35 isolates in their molecular epidemiological study, while Bommana et al. (2018) investigated infection

dynamics longitudinally in prime lamb production. Bommana et al. (2019) investigated 173 sera in a study of commercial serological assays. These numbers belong to those published studies and are therefore not included as sample sizes for the present framework.

Table 3. Selected Empirical Evidence Supporting Framework Components

Study	Research focus	Principal relevance to present framework
Jelocnik et al. (2013)	MLST of C. *pecorum* isolates from sheep, cattle and koalas	Supports molecular epidemiological characterization
Bommana et al. (2018)	Longitudinal molecular and serological dynamics	Supports integrated diagnostic surveillance
Bommana et al. (2019)	Evaluation of commercial serological assays	Supports species-specific molecular confirmation
Hagenbuch et al. (2024)	Molecular diversity in Swiss livestock	Supports combined *ompA*/MLST surveillance
FAO et al. (2022)	One Health Joint Plan of Action	Supports multisectoral integration

Figure 3: Integration of Farmer, Veterinary and Molecular Information



7. Discussion

The principal contribution of the framework is its integration of disease recognition, veterinary engagement, laboratory confirmation and molecular epidemiology into a single surveillance architecture. Existing C. *pecorum* research provides strong evidence for the value of molecular approaches, but the process through which animals enter laboratory surveillance is comparatively less emphasized in pathogen-focused studies.

The diagnostic evidence provides a clear rationale for species-specific detection. Bommana et al. (2019) demonstrated that serological interpretation can be complicated by cross-reactivity and concluded that species-specific qPCR provides greater specificity for identifying C. *pecorum*. The implication for the present framework is that farmer or veterinary recognition should ultimately be connected to a diagnostic method capable of distinguishing the

target pathogen from related chlamydial organisms.

The molecular component also has epidemiological significance. The work of Jelocnik et al. (2013) demonstrated the usefulness of MLST for investigating genetic relationships among *C. pecorum* isolates. More recent evidence from Switzerland demonstrated substantial diversity among bovine strains and congruence between *ompA* and MLST profiles (Hagenbuch et al., 2024). The framework consequently treats molecular characterization as an extension of surveillance rather than simply a laboratory endpoint.

At the same time, molecular testing cannot compensate for failures earlier in the surveillance chain. If a farmer does not recognize an abnormal event, does not perceive it as sufficiently important or cannot access veterinary assistance, an infected animal may never enter diagnostic surveillance. This is why farmer knowledge, health literacy and risk perception are incorporated into the framework.

The behavioural component should, however, be interpreted cautiously. Knowledge does not necessarily produce preventive behaviour. Biosecurity decisions can be constrained by financial resources, infrastructure, labour, production practices, veterinary access and perceived disease risk. The framework therefore conceptualizes biosecurity as an outcome of multiple interacting factors rather than as a direct consequence of farmer education.

The proposed model also supports the One Health principle of integrating information across sectors. The Quadripartite One Health Joint Plan of Action emphasizes collaboration, communication and coordinated surveillance across human, animal and environmental systems (FAO et al., 2022). The framework translates this broad principle into a pathogen-specific surveillance structure in which farmer observations, veterinary information and molecular evidence can be linked.

For livestock systems in Pakistan, this approach may be particularly relevant because veterinary and farmer-level surveillance capacity can vary across production environments. However, the present framework should not be interpreted as evidence that a particular level of farmer knowledge or biosecurity currently exists in Pakistan. Disease-specific field research is required before such conclusions can be made.

Another important implication concerns surveillance feedback. A positive molecular result should not represent the endpoint of surveillance. Instead, it should initiate an epidemiological interpretation and appropriate follow-up. Depending on the empirical findings and veterinary assessment, this may include reviewing animal movement, improving hygiene, isolating affected animals or conducting additional surveillance. The precise intervention should be determined by evidence and veterinary assessment rather than assumed by the conceptual model.

8. Practical and Theoretical Implications

The framework has practical implications for veterinary services because it provides a structure for incorporating farmer-reported information into diagnostic decision-making. A standardized approach could help veterinary professionals document not only clinical signs but also relevant management practices, recent animal movement and the circumstances surrounding disease recognition.

For farmers, the framework indicates that education should extend beyond pathogen awareness. Effective programmes may need to address recognition of abnormal animal-health events, appropriate reporting, veterinary consultation, hygiene, isolation and movement management. Such interventions should also consider the practical barriers that farmers face.

For laboratories, the framework emphasizes the importance of connecting molecular results to epidemiological information. A qPCR-positive result can confirm the presence of *C. pecorum*, but additional molecular characterization may provide information useful for investigating relationships among isolates.

At the theoretical level, the framework contributes an integrated model in which behavioural and biological surveillance are treated as complementary rather than competing approaches. It therefore operationalizes One Health at the level of a specific livestock pathogen.

9. Limitations

The principal limitation is the absence of completed empirical data in the supplied research material. Consequently, the framework cannot demonstrate prevalence, risk factors, statistical associations or intervention effectiveness. The absence of a documented sample size and sampling frame also prevents assessment of representativeness.

A second limitation is that the precise questionnaire or interview instrument was not provided. Therefore, the proposed constructs of knowledge, health literacy, risk perception and biosecurity behaviour require operational definitions and validation before empirical data collection.

A third limitation concerns laboratory methodology. Exact specimen types, extraction procedures, primer sequences, qPCR parameters and molecular typing protocols were not provided in the supplied material. These details must be established according to the final laboratory protocol and relevant standards before implementation.

Finally, the framework is broader than the evidence base for *C. pecorum*-specific farmer behaviour. Evidence from other livestock diseases can support conceptual development but should not be interpreted as direct evidence about *C. pecorum*.

10. Future Research

Future empirical research should first validate a farmer-level instrument measuring knowledge, health literacy, perceived disease risk, veterinary consultation and biosecurity behaviour. The instrument should be tested for reliability and validity before large-scale use.

A second priority is the collection of paired farmer and animal-health data. Farmer responses should be linked, where ethically and practically possible, with veterinary observations and laboratory findings. This would allow researchers to determine whether reported practices correspond with objectively observed infection patterns.

Third, future studies should establish geographically defined livestock surveillance sites and investigate differences between production systems. Longitudinal designs would be particularly valuable because they could examine whether changes in farmer behaviour or biosecurity precede changes in infection detection.

Fourth, molecular surveillance should be integrated with animal movement information where legally and ethically permissible. This could help determine whether particular molecular profiles are associated with specific production or movement networks.

Fifth, future research should evaluate the incremental value of *ompA*, MLST and, where feasible, whole-genome sequencing. Recent literature suggests that reliance on a single molecular marker may provide incomplete information concerning evolutionary relationships.

Finally, intervention studies should examine whether structured farmer–veterinarian communication and targeted biosecurity education improve disease reporting and surveillance participation. Such interventions should be evaluated empirically rather than assumed to be effective.

11. Conclusion

The proposed One Health framework integrates livestock health, farmer practices, veterinary engagement and molecular epidemiological surveillance into a unified approach to *Chlamydia pecorum* detection and prevention. Its central premise is that surveillance should begin at the farm rather than at the laboratory. Farmer recognition and reporting can initiate veterinary assessment, veterinary assessment can guide appropriate sampling, molecular testing can establish pathogen-specific evidence, and molecular characterization can provide additional epidemiological information.

The framework is supported by established research demonstrating the diagnostic value of species-specific molecular detection, the genetic diversity of *C. pecorum*, and the utility of molecular epidemiological methods. It is also consistent with the broader One Health approach promoted by the Quadripartite organizations.

Importantly, the framework is not presented as a completed empirical intervention study. The supplied source does not contain sufficient participant, laboratory or statistical data to

establish prevalence, associations or intervention effectiveness. The contribution of the present article is therefore the development of an integrated research architecture that can be empirically tested.

By connecting farmer behaviour with veterinary and molecular surveillance, the framework provides a pathway through which future research can investigate not only whether *C. pecorum* is present, but also how disease events are recognized, reported, investigated and ultimately incorporated into prevention strategies. This integration may provide a stronger foundation for disease detection and control than isolated approaches that examine laboratory, behavioural or veterinary dimensions independently.

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