DISCONTOOLS

Q fever
Summary

Introduction

1. This note provides a brief summary of an analysis undertaken by a DISCONTOOLS group of experts on Q fever. They reviewed current knowledge on the disease, considered existing disease control tools, identified gaps in their availability, quality and operational use, and determined the research needed to develop new or improved tools for animal-health control while addressing relevant One Health interfaces.
   Full details can be downloaded from the website at http://www.discontools.eu/.

Disease profile and zoonotic relevance

2. Q fever is caused by *Coxiella burnetii*, an obligate intracellular bacterium reported worldwide, although documentation and surveillance remain uneven across regions. Domestic ruminants, especially sheep, goats and cattle, are the main recognised animal reservoirs and the principal sources of human exposure in most documented livestock-associated situations. Infection or exposure has also been reported in other animal species, while detections in ticks and wildlife require careful epidemiological interpretation.
3. Environmental persistence is epidemiologically important. *C. burnetii* DNA is detected in dust, bedding, manure, birth products and other farm-environment matrices, and viable bacteria have been documented in some contaminated settings. However, environmental PCR positivity alone does not demonstrate viable bacteria, current shedding, infectiousness or direct zoonotic risk. Survival, viability and infectivity across natural matrices and field conditions remain insufficiently characterised.
4. In ruminants, the best documented clinical expression is reproductive disease, including placentitis, abortion, stillbirth and weak offspring. High bacterial loads may be shed around abortion or parturition, particularly through placentas, birth fluids and vaginal discharges. Milk, faeces and other matrices may also be positive, but their significance varies according to species, timing, matrix and herd or flock context.
5. In humans, many infections are asymptomatic or mild. Symptomatic acute Q fever usually presents as a febrile flu-like illness; pneumonia or hepatitis may occur and can dominate the clinical presentation in some patients. A minority develop persistent focalized infections, including endocarditis or vascular infection, or post-infectious fatigue. Pregnancy-related outcomes and other less common manifestations may remain insufficiently recognised or quantified.

Risk and preparedness

6. Human infection occurs mainly through inhalation of contaminated aerosols or dust originating from infected animals or contaminated environments. Direct contact with parturient or aborting animals is a well-recognised high-exposure situation, but outbreaks may also occur without direct animal contact, through indirect environmental exposure, windborne or dust-mediated dispersion, contaminated materials or public-facing animal settings.
7. Raw milk products, ticks, pets and other potential exposure routes may be relevant in specific contexts, but their overall contribution remains less clearly established than airborne or environmental exposure from infected ruminants. They should therefore be investigated when relevant without being presented as general drivers of human Q fever occurrence.
8. Three groups should be distinguished for human risk assessment. Highly exposed groups include livestock farmers, veterinarians, animal-health workers, abattoir workers, laboratory staff and people undertaking high-risk animal or environmental interventions. Reported human cases, however, do not necessarily mirror the groups with the highest occupational exposure. In community or environmental outbreaks, residents, visitors, workers in non-traditional exposure settings, or people with little or no direct contact with ruminants may represent an important share of recognised cases, through indirect exposure to contaminated

aerosols, dust or environments. Clinically vulnerable groups include people with pre-existing valvular or vascular conditions, vascular prostheses or aneurysms, and immunocompromised patients, who are at increased risk of severe outcomes or persistent focalized Q fever. Pregnancy requires separate consideration because infection may be associated with adverse pregnancy outcomes.

9. Reported human incidence varies greatly between countries, regions and periods. This reflects true epidemiological differences, but also variation in surveillance systems, diagnostic practices, case definitions, notification pathways and disease awareness. Q fever is likely to remain underdiagnosed and underreported in many settings. Reported incidence should therefore not be interpreted as a direct measure of true burden or zoonotic transmission intensity.
10. Preparedness should not begin only when grouped human cases are confirmed. Serial abortions, clustered parturition, high-shedding situations or evidence of substantial environmental contamination in exposure-relevant settings may justify early One Health attention when they indicate a plausible increased risk of human exposure. Q fever has been identified at EU level among priority zoonoses for coordinated One Health surveillance. Readiness requires predefined alert triggers, clear responsibilities, coordinated diagnostic capacity, sampling procedures, data-sharing pathways, proportionate communication and post-crisis learning.

Available control tools and their limitations

- **Diagnostic**

11. Diagnostic tools are available, including PCR, serology, histopathology, immunohistochemistry and, in specialised laboratories, culture or molecular typing. A key limitation is not simply availability, but validation, harmonisation and interpretation. Results must be considered in relation to the matrix sampled, timing, bacterial load, purpose of testing, species, vaccination status and epidemiological context.
12. PCR assays, particularly those targeting multicopy sequences such as IS*1111*, can provide sensitive detection and are useful for abortion investigations, herd or flock assessment and environmental investigation. Yet detection of *C. burnetii* DNA does not necessarily demonstrate viable bacteria or current transmission risk. Quantitative interpretation may also be influenced by target choice and strain variability. Complementary targets, multiplex approaches and viability- or infectivity-oriented methods require further development and validation.
13. Serology is useful for assessing exposure and herd- or flock-level circulation, but it does not reliably identify active shedding, infectiousness or protection at individual-animal level. Phase I and Phase II serological interpretation is recognised in human medicine but remains insufficiently characterised in ruminants. No validated DIVA strategy for differentiating infected from vaccinated animals is currently available for animal Q fever, limiting interpretation and monitoring in vaccinated populations.

- **Vaccines**

14. Commercial veterinary vaccine options for animal Q fever are currently limited to inactivated whole-cell Phase I vaccines for ruminants, and their availability or distribution is not uniform across countries and settings. These vaccines can reduce abortion risk and bacterial shedding, especially when applied before primary exposure or first pregnancy. However, vaccination does not guarantee sterile immunity or eradicate infection, and its field contribution may be difficult to separate from other measures. It should be integrated with surveillance, biosecurity and monitoring rather than used as a stand-alone solution.

- **Biosecurity**

15. Hygiene, safe management of birth products, reduction of high-risk exposure, manure and bedding management, protection of exposed workers, and protection of visitors to animal-associated settings are relevant components of control. However, field effectiveness is not consistently quantified, especially for complex environmental matrices. Cleaning or

disinfection should not be assumed to eliminate zoonotic risk without considering matrix type, organic matter, handling practices, timing and potential exposure pathways.

- **Pharmaceuticals**

16. Available evidence does not support routine antimicrobial treatment as a reliable means of preventing abortion outbreaks, reducing shedding or controlling environmental contamination in ruminants. Human treatment remains clinically important, but human therapeutic strategies should not be extrapolated to routine veterinary population-level control. The relevant One Health issue is antimicrobial stewardship and avoidance of unnecessary antimicrobial use.

Priority gaps and research needs

17. Priority diagnostic research should focus on fit-for-purpose interpretation as well as tool development. Needs include harmonised matrix-specific sampling strategies, improved interpretation of PCR and serology, environmental viability or infectivity assessment, more robust quantification approaches, DIVA-compatible strategies and decision frameworks combining laboratory, pathological, epidemiological and environmental information.
18. Substantial biological and epidemiological uncertainties remain regarding environmental persistence, viability and infectivity; the contribution of different matrices and exposure pathways; shedding dynamics in ruminants; asymptomatic infection; and the links between strain diversity, host adaptation, virulence, shedding and clinical expression. The roles of ticks, wildlife, pets and other non-ruminant species require context-specific assessment and should not be inferred from infection, exposure or PCR positivity alone.
19. Source investigation remains operationally challenging. Environmental sampling, spatial analysis, meteorological data, genotyping and whole-genome sequencing may support investigation hypotheses, but source attribution usually requires converging human, animal, environmental, temporal and epidemiological evidence. Molecular similarity alone should not be treated as definitive proof of transmission or source attribution.
20. Digital and genomic resources offer useful opportunities for improved surveillance and investigation, provided that data are interpretable and interoperable. Standardised metadata, harmonised vocabularies and links between animal, human, environmental and genomic information are needed. Current datasets remain insufficiently complete and contextualised for routine fine-scale source attribution.

Conclusions for decision makers

21. Q fever remains a neglected but relevant One Health zoonosis. Existing diagnostic, surveillance, vaccination and control tools provide a basis for action, but their usefulness is limited by interpretation difficulties, incomplete harmonisation and weak integration across sectors.
22. The central challenge is to combine animal, environmental, human and molecular signals into timely, proportionate and monitorable decisions. Detection, seropositivity, environmental positivity, shedding or molecular similarity can support interpretation, but none should be treated alone as proof of zoonotic risk, source attribution or control success.
23. Future priorities should include harmonised diagnostic interpretation, environmental viability and persistence studies, surveillance and vaccinated-population monitoring, improved vaccine strategies including DIVA compatibility, comparative genomics, source-investigation capacity and operational One Health preparedness.
24. More effective prevention and control will depend on sustained expertise and funding, interoperable data systems, coordinated readiness before crises occur, and meaningful engagement with farmers, veterinarians, laboratories, public-health authorities and exposed communities. The objective is practical risk reduction that is scientifically justified, proportionate and compatible with animal health, human health, environmental integrity and farming-system feasibility.