

The relevance of the wild reservoir in zoonotic diseases: the relationship between Iberian wildlife and *Coxiella burnetii*.

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Abstract

Throughout history, wildlife has been an important source of infectious diseases transmissible to humans. Q fever is a worldwide zoonosis caused by an obligate intracellular bacterium, *Coxiella burnetii* with only anecdotal reports of human-to-human transmission. The epidemiology of human infections always reflects the circulation of *C. burnetii* in animal reservoirs. Q fever occurs as sporadic cases, usually after identifiable at-risk activities (farming, slaughterhouse work, or rural tourism), however, as a rule, it is infected livestock, particularly goats and sheep, the most important sources of zoonotic Q fever outbreaks in humans. Nonetheless the origin of several human Q fever cases continues to be unclear. Human impacts on habitats, biodiversity and climate could be responsible for changes in the patterns of interaction between domestic animals, wildlife and humans, allowing wild animals to be involved in the epidemiology of Q fever and thus serving as important reservoirs to domestic animals and humans. These factors combined with the identification of shared genotypes between wildlife and humans in the Iberian Peninsula, makes it possible for wild reservoirs to play an important role in the increase in cases of Q fever in Spain

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Throughout history, wildlife has been an important source of infectious diseases transmissible to humans. Q fever is a worldwide zoonosis caused by an obligate intracellular bacterium, *Coxiella burnetii*, with only anecdotal reports of human-to-human transmission. The epidemiology of human infections always reflects the circulation of *C. burnetii* in animal reservoirs. Q fever occurs as sporadic cases, usually after identifiable at-risk activities (farming, slaughterhouse work, or rural tourism), however, as a rule, it is infected livestock, particularly goats and sheep, the most important sources of zoonotic Q fever outbreaks in humans. Nonetheless the origin of several human Q fever cases continues to be unclear. Human impacts on habitats, biodiversity and climate could be responsible for changes in the patterns of interaction between domestic animals, wildlife and humans, allowing wild animals to be involved in the epidemiology of Q fever and thus serving as important reservoirs to domestic animals and humans. These factors combined with the identification of shared genotypes between wildlife and humans in the Iberian Peninsula, makes it possible for wild reservoirs to play an important role in the increase in cases of Q fever in Spain

Letter to the editor

An original article has recently been published in Transboundary and Emerging Diseases entitled ‘Unravelling animal exposure profiles of human Q fever cases in Queensland, Australia, using natural language

processing’ by Clark and others (<https://doi.org/10.1111/tbed.13565>; Clark et al., 2020), to which we have some comments.

In this paper, the authors applied natural language processing to an 18-year data set of Q fever notifications in Queensland, Australia, to investigate whether patients belonging to different demographic groups commonly report different potential exposure pathways. Identifying potential exposure pathways is necessary to design effective interventions and aid outbreak prevention.

Q fever is a worldwide zoonosis caused by an obligate intracellular bacterium, *Coxiella burnetii* (Angelakis and Raoult, 2011). With only anecdotal reports of human-to-human transmission, the epidemiology of human infections always reflects the circulation of the bacterium in animal (domestic and wild) reservoirs. The prevalence of Q fever is highly variable from one country to another, due to mainly epidemiological and geographical disparities. In areas of endemicity, as Australia and Spain, Q fever occurs as sporadic cases, usually after identifiable at-risk activities (farming, slaughterhouse work, or rural tourism), however, as a rule, it is infected livestock, particularly goats and sheep, the most important sources of zoonotic Q fever outbreaks in humans. Nonetheless the origin of several human Q fever cases continues to be unclear. Besides domestic livestock, a diversity of possible wildlife reservoirs has been identified through molecular and serological surveys, including wild mammals, birds and even ticks (Toledo et al., 2009; Cooper, Stephens, Ketheesan, & Govan, 2013; González-Barrio and Ruiz-Fons, 2019). Throughout history, wildlife has been an important source of infectious diseases transmissible to humans. Today, zoonoses with a wildlife reservoir constitute a major public health problem, affecting all continents, an example is the SARS-CoV 2 that it has been able to cross the inter-species barrier to emerge as the most devastating human pandemic of our time. The total number of zoonoses is unknown, some 1,415 known human pathogens have been catalogued and 62% are of zoonotic origin (Billinis, 2013). Human impacts on habitats, biodiversity and climate could be responsible for changes in the patterns of interaction between domestic animals, wildlife and humans, allowing wild animals to be involved in the epidemiology of most zoonoses and thus serving as important reservoirs for the transmission of zoonotic agents to domestic animals and humans (González-Barrio and Ruiz-Fons, 2019). These changing patterns may also be behind the re-emergence of enzootic zoonoses such as Q fever that, although with a lower pandemic potential, it may become a serious health problem. Within Europe, Spain has reported the highest number of human Q fever cases annually since 2016 (0.8 cases per 100.000 population). In 2018, more than a third of the overall number of cases were notified from Spain (ECDE, 2019). In addition, Spain is the country where more studies in relation to Q fever have been conducted on wildlife and where more reservoirs of the bacteria have been confirmed (González-Barrio and Ruiz-Fons, 2019). In my opinion, these factors combined with the identification of shared genotypes between wildlife and humans in Iberian Peninsula (González-Barrio et al., 2016a,b,c) makes it possible that wild reservoirs, in this case ticks, deer, rabbits and micromammals (Toledo et al., 2009; González-Barrio et al., 2015a,b) among others, may play an important role in the increase of Q fever cases in Spain.

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Conflicts of Interest : The authors declare no conflict of interest.

References

- Angelakis, E. & Raoult, D. (2011). Q fever. *Vet Microbiol* 2011 140, 297–309.
- Billinis, C. (2013) Wildlife diseases that pose a risk to small ruminants and their farmers. *Small Ruminant Research* , 110, 67-70, <https://doi.org/10.1016/j.smallrumres.2012.11.005>.
- Clark, N.J., Tozer, S., Wood, C., Firestone, S.M., Stevenson, M., Caraguel, C., Chaber, A.L., Heller, J., Soares Magalhães, R.J. (2020) Unravelling animal exposure profiles of human Q fever cases in Queensland, Australia, using natural language processing. *Transbound Emerg Dis* , <https://doi.org/10.1111/tbed.13565>

- Cooper, A., Stephens, J., Ketheesan, N., & Govan, B. (2013). Detection of *Coxiella burnetii* DNA in wildlife and ticks in northern Queensland, Australia. *Vector-borne Zoonotic Dis*, 13(1), 12–16. <https://doi.org/10.1089/vbz.2011.0853>
- European Centre for Disease Prevention and Control. Q fever. In: ECDC. Annual epidemiological report for 2018. Stockholm: ECDC 2019.
- González-Barrio, D., Maio, E., Vieira-Pinto, M., & Ruiz-Fons, F. (2015a). European rabbits as reservoir for *Coxiella burnetii* .*Emerging Infectious Diseases* , 21, 1055–1058.<https://doi.org/10.3201/eid2106.141537>
- González-Barrio, D., Velasco Ávila, A. L., Boadella, M., Beltrán-Beck, B., Barasona, J. A., Santos, J. P. V., ... Ruiz-Fons, F. (2015b). Host and environmental factors modulate the exposure of free-ranging and farmed red deer (*Cervus elaphus*) to *Coxiella burnetii* .*Applied and Environment Microbiology* , 81, 6223–6231. <https://doi.org/10.1128/AEM.01433-15>
- Gonzalez-Barrio, D.; Jado, I., Fernandez-de-Mera, I.G., Fernandez-Santos, M.R., Rodriguez-Vargas, M., Garcia-Amil, C., Beltran-Beck, B., Anda, P., Ruiz-Fons, F. (2016a). Genotypes of *Coxiella burnetii* in wildlife: disentangling the molecular epidemiology of a multi-host pathogen. *Environ Microbiol Rep*, 8, 708–714. <https://doi.org/10.1111/1758-2229.12431>
- Gonzalez-Barrio, D., Hagen, F., Tilburg, J. J. H. C., & Ruiz-Fons, F. (2016b). *Coxiella burnetii* genotypes in Iberian wildlife.*Microbial Ecology* , 72, 890–897.<https://doi.org/10.1007/s00248-016-0786-9>
- Gonzalez-Barrio, D., Garcia, J. T., Jado, I., Olea, P. P., Vinuela, J., & Ruiz-Fons, F. (2016c). Have Small Mammals Been Neglected as *Coxiella Burnetii* Reservoirs? Berlin, Germany: 12th Conference of the European Wildlife Disease Association.
- Gonzalez-Barrio, D., Vieira-Pinto, M., & Ruiz-Fons, F. (2017) *Coxiella burnetii* in European game species: Challenges for human health. In J. C. C. Simoes, S. F. Anastacio & G. J. Da Silva (Eds.), *The Principles and Practice of Q Fever. The one Health Paradigm* (pp. 245–272). New York, NY: Nova Science Publishers.
- Gonzalez-Barrio, D. & Ruiz-Fons, F. (2019). *Coxiella burnetii* in wild mammals: A systematic review. *Transbound Emerg Dis*, 66, 662–671.
- Toledo, A., Jado, I., Olmeda, A.S., Casado-Nistal, M.A., Gil, H., Escudero, R., Anda, P. (2009). Detection of *Coxiella burnetii* in ticks collected from central Spain. *Vector-Borne Zoonotic Dis* , 9 (5), 465–468. <https://doi.org/10.1089/vbz.2008.0070>.