

Rickettsiales AND *Coxiella burnetii* INFECTIONS IN CAMELIDS: A REVIEW

U. Wernery

Central Veterinary Research Laboratory, Dubai, UAE

Overview

The members of the *Rickettsiales* Order are very small, non-motile, pleomorphic, obligate intracellular Gram-negative bacteria. They are coccobacilli or short rods, which are visible under light microscope best at 100 x oil magnification. *Rickettsiales* and *Coxiella* stain poorly with Gram but better with Giemsa and Romanowsky stains. Most of these bacteria do not grow on inert media. They require living cells for their replication and are normally cultured in tissue cultures (Munderloh *et al*, 2003), preferable tick cell cultures or in yolk sac of embryonated hen eggs (Passos, 2012).

The genus includes many species also associated with human disease, including those in the spotted fever and typhus group. The *Rickettsiae* that are pathogens to human beings are subdivided into three major groups based on clinical characteristics of the disease:

Spotted fever group with 8 species

Typhus group with 3 species

Scrub typhus group with 3 species

Rocky Mountain spotted fever caused by *Rickettsia rickettsii* for example is common in Mexico and North and South America and is transmitted by rodents, dog ticks like *Dermacentor* and *Amblyomma* species. In human beings the disease is characterised by fever, muscle pain, severe headache and occasionally by a myocarditis (Markey *et al*, 2013).

The classification of this group of bacteria is complex and complicated and not finalised, yet. For example, several species in the *Anaplasmataceae* family have been redesigned, as they previously included haemotrophic bacteria, which are now confirmed to be closely related to *Mycoplasma* as they also lack a cell wall.

The *Rickettsiales* Order comprises of two families of veterinary significance which are *Rickettsiaceae* and *Anaplasmataceae* (Markey *et al*, 2013). The family

Rickettsiaceae possesses a cell wall, but members of the *Anaplasmataceae* family lack a peptidoglycan layer.

Significant re-classification of the Order has occurred several times over the years, which are mainly based on DNA sequencing in particular 16S and 23S-r RNA gene sequence comparisons. The classification is not yet complete.

The source of rickettsia taxonomy can be found in the latest (2004) edition of the Bergey's Manual of Systematic Bacteriology or under Schoch *et al* (2020), NCBI Taxonomy: a comprehensive update on curation, resources and tools. Database Oxford 2020: baaa062. Pub Med: 32761142 PMC: PMC 7408187. This database gives an overview of *Rickettsiales* currently known. Most of them are either unclassified, uncultured or 'candidates' waiting for their classification; in total more 100 different species. However, the newest classification of *Rickettsiales* comprises the family *Rickettsiaceae* into two genera: *Rickettsia* and *Orientea*; both with no veterinary importance, but responsible for zoonotic diseases of human beings; while the family *Anaplasmataceae* have five genera: *Anaplasma*, *Ehrlichia*, *Neorickettsia*, *Aegyptianella* and *Wolbachia*.

Only few species of the *Anaplasmataceae* are pathogens of veterinary significance which are listed in Table 1.

As can be seen from this Table, none of them is mentioned to produce disease in camelids.

Coxiella burnetii, the cause of Q fever, is now closely related to *Legionella* species and *Francisella tularensis* and is therefore dealt here in a separate section.

Natural Habitat and Pathogenesis

Members of the *Rickettsiales* are bacteria of arthropods which are replicating in the gut cells before spreading to other organs, such as salivary glands and ovaries. The requirement for an invertebrate vector, distinguishes these microorganisms from other bacterial species. This is unique. Infection

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