First human case of severe septicaemia associated with *Mycoplasma capricolum* subsp. *capricolum* infection

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Introduction: The bacterium *Mycoplasma capricolum* subsp. *capricolum* is known as a pathogen in goats. There have been no reports on a zoonotic potential so far.

Case presentation: A case of septicaemia and meningoencephalitis in a 62-year-old patient has been associated with infection by *M. capricolum* subsp. *capricolum*. No other infectious agent could be detected.

Conclusion: Although it was impossible to identify the source of infection, coincidental contact with small ruminants or consumption of food products from goats during a tourist trip may have played a role.

Introduction

The wall-less bacterium *Mycoplasma capricolum* subsp. *capricolum* is known as an agent of respiratory disease, mastitis and arthritis in small ruminants. It has also been associated with contagious agalactia of goats, a syndrome affecting mammary glands, joints and eyes, which occurs in small ruminant flocks of Mediterranean countries and many other regions (DaMassa et al., 1987, 1992; Bergonier et al., 1997; Gómez-Martín et al., 2013). As a species, *M. capricolum* subsp. *capricolum* is highly adapted to goats, even though there are also reports on findings in sheep (Al-Momani et al., 2006) and South American camelids (Pitcher & Nicholas, 2005). Here, to the best of our knowledge, we report the first case of a human infection with *M. capricolum* subsp. *capricolum*.

Case report

A 62-year-old man presented symptoms of recurrent fever and severe limb pain, which was diagnosed as septicaemia and meningoencephalitis combined with bilateral asymptomatic pneumonia and pleural effusion. The symptoms had emerged at the end of a tourist visit to the Cape Verde Islands around New Year’s Day 2014. After his return to Germany, the patient was hospitalized for 2 weeks. On day 6 after admission, sinusitis and blepharoconjunctivitis were additionally diagnosed; bacterial infection was identified (see below) and meningitis was suspected. Therefore, combined antibiotic treatment with ceftriaxon (for 8 days), roxithromycin and doxycyclin (each for 3 weeks) was started. At the time of discharge from hospital, 2 weeks after admission, the symptoms had disappeared.

Blood examination revealed thrombocytopenia and several elevated inflammation parameters, such as leukocytes, monocytes, neutrophils, erythrocyte sedimentation rate and C-reactive protein. The following viral infections could be excluded after nucleic acid testing and serology: influenza A and B, Dengue, Chikungunya and cytomegalovirus. Antibody ELISAs for *Brucella* and *Coxiella* proved negative. No malaria antigen was detected. Whilst bacterial culture from cerebrospinal fluid was negative, initial blood culture on Columbia Agar containing 7 % sheep blood (Oxoid) was weak, but could be improved on Mycoplasma/Ureaplasma Agar (Oxoid), as well as in liquid culture media (BD Bactec Plus Aerobic/Aerobic; Becton Dickinson). Partial sequencing of the isolates from 10 experiments revealed identical results. Based on the 16S rRNA locus (GenBank accession number KP718739) and a partial sequence of the 23S rRNA (GenBank accession...
number KP718740), the isolate designated 14DL0024 was identified as *M. capricolum* subsp. *capricolum*. The genome sequence of the strain has also become available under GenBank accession number LBMF01000000 (Seersholm *et al.*, 2015).

The *M. capricolum* subsp. *capricolum* strain isolated was further characterized using multilocus sequence typing (MLST), which is based on partial sequences of seven housekeeping genes (Fischer *et al.*, 2012). The sequences were concatenated and aligned to reference sequences of the *Mycoplasma mycoides* cluster. We reconstructed a maximum-likelihood phylogeny tree based on the 3816 nt sequence alignment using PhyML 3.0 (Guindon *et al.*, 2010). To assess statistical support for the resulting phylogeny, we performed 1000 bootstrap replicates assuming a GTR+G+I model of nucleotide substitution. The tree was drawn using FigTree 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/) and is shown in Fig. 1. The patient isolate 14DL0024 clearly clustered within the clade of *M. capricolum* subsp. *capricolum* and was separated from its closest relative *M. capricolum* subsp. *capripneumoniae*.

To find out whether specific antibodies had been generated, we examined a patient serum sample taken 3 weeks after the end of antibiotic treatment using Western blotting. A serum sample from an earlier time point was not available. Whole-cell antigens used included the patient strain 14DL0024, the type strains of closely related members of the *Mycoplasma mycoides* cluster, i.e. *M. mycoides* subsp. *mycoides*, *M. mycoides* subsp. *capri*, *M. capricolum* subsp. *capripneumoniae*, *Mycoplasma agalactiae*, as well as *Mycoplasma pneumoniae*. The results in Fig. 2 provide evidence of the patient serum containing antibodies reacting with a number of antigens of *M. capricolum* subsp. *capricolum*, but also with those of the related mycoplasmal agents. The serum of a randomly chosen healthy blood donor, which served as a control, failed to show any reactive bands (data not shown).

**Fig. 1.** Simplified phylogenetic tree based on concatenated sequences (3816 nt) from the seven genomic loci (*adk*, *gmk*, *gyrB*, *pdhC*, *pgi*, *recA*, *rpoB*) of the MLST scheme for strains of the *Mycoplasma mycoides* cluster. The alignment included sequences from 10 strains each of *M. capricolum* subsp. *capricolum* (Mcc), *Mycoplasma capricolum* subsp. *capripneumoniae* (Mccp), *Mycoplasma mycoides* subsp. *mycoides* (Mmm), *Mycoplasma mycoides* subsp. *capripneumoniae* (Mmc), and *M. leachii*.
herds during their hiking tours. The patient’s known heavy-smoker status may have contributed to the severity of the infection. It is also pertinent to note that the goat population on the Cape Verde Islands is large, and that both the number of goats and goat milk production have doubled in the last 10 years (http://faostat3.fao.org/home/E). Therefore, the probability of human exposure to goat-adapted bacteria, such as *M. capricolum* subsp. *capricolum*, should have increased as well.

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**References**


