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Authors: Katharina Hoelzle, Regina Hofmann-Lehmann, Ludwig E. Hoelzle

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Candidatus Mycoplasma haemobos, a new bovine haemotrophic Mycoplasma species?

Katharina Hoelzle*, Regina Hofmann-Lehmannb, Ludwig E. Hoelzlea

aInstitute of Veterinary Bacteriology, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 260, 8057 Zurich, Switzerland
bClinical Laboratory, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 260, 8057 Zurich, Switzerland

*Corresponding author at: Institute of Veterinary Bacteriology, Tel.: +41 44 6358635; email: khoelzle@vetbakt.uzh.ch

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After reading the letter to the editor from G. Uilenberg on 'Candidatus Mycoplasma haemobos', which was published in Veterinary Microbiology (Uilenberg, 2009), we would like to make a few comments and add novel insights on bovine haemotrophic mycoplasma (syn. haemoplasma) infections based on recent results. Furthermore we would hereby like to call on the research community to provide us with “old” isolates of bovine haemotrophic mycoplasmas.

Uilenberg’s letter based on the fact that recently various research groups found a novel bovine haemotrophic mycoplasma species by applying PCR, 16S rDNA sequencing and phylogenetic analyses: in Switzerland, the group of Hofmann-Lehmann (Hofmann-Lehmann et al., 2004), in China and Japan, Tagawa and co-workers (2008), and in Germany, the
group of Hoelzle (Hoelzle et al., 2010). This novel bovine haemoplasma species clearly differs from the classical bovine haemotrophic *Mycoplasma wenyonii* in its 16S rDNA (identity of 81.2%); thus the provisional name ‘*Candidatus* Mycoplasma haemobos’ was suggested (Tagawa et al., 2008). Phylogenetically the novel bovine species ‘*Candidatus* M. haemobos’ belongs to the “haemofelis” cluster that includes, e.g., the feline *Mycoplasma haemofelis*, and the canine *Mycoplasma haemocanis* species; it does not cluster with *M. wenyonii*, the other bovine haemoplasma species from which the 16 rDNA has yet been sequenced (Tagawa et al., 2008; Hoelzle et al., 2010).

In the letter mentioned the author stated that it is quite possible that the novel bovine haemotrophic mycoplasma is identical with one of the bovine species described earlier. He noted that in the pre-PCR and pre-sequencing era four different haemoplasma species (syn. *Eperythrozoon, Haemobartonella*) had been described in cattle, i.e. “*Haemobartonella bovis*” (Brocklesby, 1970), *Eperythrozoon wenyonii* (Adler and Ellenbogen 1934), “*Eperythrozoon teganodes*” (Hoyte, 1962), and “*Eperythrozoon tuomii*” (Tuomi and von Bonsdorff, 1967; Tuomi and Tanskanen, 1980). These species were found to differ morphologically, in cross-immunity tests and their localisation (erythrocytes, thrombocytes, free in the blood plasma). Remarkably, in 1980 only *E. wenyonii* (*M. wenyonii*), but not the other species described had been included in the 1980 Approved List of Bacterial Names.

The letter encouraged us to contact the author as well as researchers from other institutes who had worked with these agents earlier on. We aimed at analysing the 16S rDNA of the bovine haemoplasma species previously described, i.e. “*E. teganodes*”, “*E. tuomii*”, and “*H. bovis*” from the blood of infected animals. We know from literature (Messick, 2004) as well as from our own electron microscopic investigations of *M. suis* that haemotrophic mycoplasmas are able to adopt several shapes, i.e. spheres, commas, rods, rings, tanged (“frying pan”) forms, and multiple forms. Moreover, the morphology of haemotrophic mycoplasmas alters in the course of infection as has been published, e.g. for *Mycoplasma ovis* (Gulland et al., 1987). Therefore, only genetic analysis of the 16S rDNA of the uncultivable bacteria “*E. teganodes*”, “*H. bovis*”, and “*E. tuomii*” could clarify whether any of
them are identical with ‘Candidatus M. haemobos’ or whether the latter is a new and distinct species. These analyses, however, can only be done if “old” isolates of “E. teganodes”/“E. tuomii” or “H. bovis” are made available. So far, only the Utrecht Centre for Tick-borne Diseases (UCTD, Prof. Frans Jongejan; Utrecht University, The Netherlands) was able to send us DNA of “E. teganodes” from their stock originating from cattle in the Netherlands. In the case of “E. tuomii” or “H. bovis” no material has been available so far. The sequence analysis of the 16S rDNA of “E. teganodes” revealed 99.8% identity to M. wenyonii (GenBank Acc. No. AF016546), and 81.2% identity to ‘Candidatus M. haemobos’ (GenBank Acc. No. EF460765).

Therefore, we arrived at the following preliminary conclusions: (1) Currently, ‘Candidatus M. haemobos’ must be considered a new species and (2) “E. teganodes”, or at least the isolate that was made available so far, and M. (E.) wenyonii are genetically consistent yet phenotypically different types of one and the same bacterium, or alternatively two distinct bacteria species with identical 16s rDNA sequences. The 16S rDNA sequence identity may not be sufficient to guarantee species identity (Fox et al., 1992). Of course, the interpretation of the result of a single isolate is delicate. To further elucidate this issue we herewith urge other institutes to participate in our search for “E. teganodes”, “E. tuomii” and “H. bovis” isolates, and to test these in cooperation with us.

In this context we would like to put up for discussion whether the new species name ‘Candidatus M. haemobos’ indeed should correctly be changed to ‘Candidatus M. haemobovis’ (the correct latin genitive of bos is bovis) according to the Rules of the International Code of Nomenclature of Bacteria (Lapage et al., 1992).

References


