Mycoplasma and *Eperythrozoon* (Mycoplasmataceae). Comments on a recent paper

In papers on the taxonomy of a number of species of haemoparasitic bacteria of the genera *Eperythrozoon* and *Haemobartonella*, Neimark *et al.* (2001, 2002, 2004) (and others such as Messick *et al.*, 2002) formally proposed the transfer of these species from the order *Rickettsiales* to the order *Mycoplasmatales*, family *Mycoplasmataceae*. This supported the earlier studies of Neimark & Kocan (1997) and Rikihisa *et al.* (1997). The proposal was based mainly on comparisons of 16S rRNA gene sequences. The evidence for the transfer of these bacteria to the *Mycoplasmatales* is convincing. However, we do not think that the molecular evidence presented justifies the fusion of the genera *Eperythrozoon* and *Haemobartonella* with the genus *Mycoplasma*, as we discussed in a recent paper (Uilenberg *et al.*, 2004). Indeed, not only are the gene sequences that were compared only a very small portion of the genome, but the percentage similarity between 16S rRNA gene sequences of *Eperythrozoon wenyonii* and one of its closest relatives, *Mycoplasma fastidiosum*, is relatively low at only about 77 %, well below the level expected for micro-organisms belonging to the same genus (Uilenberg *et al.*, 2004). In their 1997 paper, Neimark and Kocan had already found a similarly low relationship between *E. wenyonii* and the *Mycoplasma pneumoniae* group (Neimark & Kocan, 1997). Moreover, there are other differences between members of the genera *Eperythrozoon* and (classical) *Mycoplasma*, such as habitat and probably their mode of transmission (although for most of the members of the genus *Eperythrozoon*, it is still not known how they are transmitted).

In a recent study, Neimark *et al.* (2005) showed that in a phylogenetic tree based on 16S rRNA gene sequences, the type species of the genus *Eperythrozoon*, *Eperythrozoon*

coccoides, is also close to the *Eperythrozoon* (and *Haemobartonella*) species that were transferred earlier to the genus *Mycoplasma*. The 16S rRNA gene sequence similarity of *E. coccoides* and its closest relative of the (classical) *Mycoplasma* species, *M. fastidiosum*, is only 80·2 %, which is slightly higher than that of *E. wenyonii*, but nevertheless means that the type species of *Eperythrozoon* is not sufficiently close to the (classical) *Mycoplasma* species to justify the fusion of the genera *Eperythrozoon* and *Mycoplasma*. In addition, we have aligned the 16S rRNA gene sequences (published on the NCBI website) of another species of 'classical' *Mycoplasma*, *Mycoplasma mycoides* subsp. *mycoides* SC (small colonies) (MmmSC, causal agent of contagious bovine pleuropneumonia), with those of *E. coccoides* as well as those of a member of the *Mycoplasmataceae* belonging to another genus, *Ureaplasma parvum* serovar 3, strain ATCC 700970 (GenBank accession no. NC_002162). Based on 16S rRNA gene sequences, the similarity of MmmSC and *E. coccoides* is even less than that between MmmSC and *U. parvum*, 72·1 and 78·1 %, respectively. Furthermore, we have found, using this same criterion, that the similarity of MmmSC and a species of a different family and even a different order of the class *Mollicutes*, *Spiroplasma citri* (family *Spiroplasmataceae*, order *Entomoplasmatales*) is greater than that between MmmSC and *E. coccoides*, at 87 and 72·1 %, respectively.

Finally, we have also aligned the 16S rRNA gene sequences of MmmSC and a phytoplasma, Onion yellow phytoplasma OY-M (GenBank accession no. NC_005303); their similarity (using solely this criterion) is also closer than that of MmmSC and *E. coccoides*, 78·9 and 72·1 %. In fact, the logical consequences of the proposals of Neimark and co-workers would be the abolition of the family *Spiroplasmataceae* and the order *Entomoplasmatales* and the transfer of

Ureaplasma, *Spiroplasma* and phytoplasma to the genus *Mycoplasma*, rather than the transfer of the genus *Eperythrozoon* to the genus *Mycoplasma*!

It is evident that taxonomy based solely on comparing 16S rRNA gene sequences is insufficient. It is also clear that *Eperythrozoon* and *Mycoplasma* should be considered as different taxa, even if only on the basis of such a comparison. It has not even been shown that the genus *Eperythrozoon* belongs in the same family as the genus *Mycoplasma*. A direct consequence of the taxonomic opinion expressed in this letter is that the validly published names *Eperythrozoon* and *Mycoplasma* may continue to be used as separate genera, within the class *Mollicutes*, possibly in one and the same family, the *Mycoplasmataceae*.

Another point is that of priority. The genus name *Eperythrozoon*, created in 1928, has priority over *Mycoplasma*, published in 1929. As the study reported by Neimark *et al.* (2001) did not include the type species of *Eperythrozoon*, *E. coccoides*, the question of priority did not have to be addressed. Following the publication of their 2005 paper (Neimark *et al.*, 2005), which includes the type species, this question cannot now be avoided. If the proposal for the fusion of the genera *Eperythrozoon* and *Mycoplasma* were to be taken seriously, all members of the genus *Mycoplasma* should be renamed *Eperythrozoon* and not the other way around. Neimark *et al.* (2005) request that the priority of *Eperythrozoon* over *Mycoplasma* be waived, in order to avoid confusion. Quoting our 2004 paper (Uilenberg *et al.*, 2004), Neimark *et al.* (2005) state that we proposed that all *Mycoplasma* species should be renamed *Eperythrozoon*. What we really said in that publication is that, if it were to be shown that *E. coccoides* also belongs to the mycoplasmas (as is now the case), the transfer of the genus *Eperythrozoon* to the genus *Mycoplasma* (with which we do not

agree, as stated very clearly in our paper), would create problems of priority (in addition to not being justified).

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