

The criteria to include a 18S RNA gene sequence of a piroplasmid species into the tree and subsequently list it in the tables as well-defined isolates, species and/or species complexes is based on a number of careful considerations that are based on the following:

- (i) we focused in this study on piroplasmid infecting domestic animals and principally disregarded piroplasmid species infecting wildlife. However, an exception was made whenever a wildlife piroplasmid species seemed to be closely related with a piroplasmid species infecting domestic animals and when its inclusion was necessary to get a thorough understanding and overview of the evolutionary origin and evolution/phylogeny within the context of the phylogenetic lineages of piroplasmid species that infect domestic animals.
- (ii) we report on piroplasmids species/isolates that are well-defined based on their 18S RNA gene. We regard piroplasmid isolates in this review as well-defined when a nearly full length 18S RNA gene sequence has been reported, which allowed us to integrate it and show its placement in our trees without loss of tree stability. The trees that we show are all based on 18S RNA gene sequences that are at least 1200 nt, but in general even much longer (see list of 18S rRNA gene sequences in Supp. Data 2).
- (iii) there is a considerable number of piroplasmid species that seem to infect a large number of different vertebrate hosts (e.g. *B. microti*, *B. canis*, *B. vogeli*, *T. equi* among others). We decided in the context of this review to focus on the principally and commonly accepted vertebrate hosts, in which parasite propagation occurs. While we make in our manuscript reference to accidental vertebrate hosts we do not pretend to give a complete listing on this issue for the following reasons.
 - First, the significance of accidental infections is unknown (it has been proposed that they represent spill-over infections promoted due to human-caused high density of domestic animals in farms or the zoo; alternatively, they might represent dead-end hosts in which they do not further propagate).
 - Second, accidental infections have been reviewed in some detail and discussed under different perspectives in other recent reviews and studies (e.g. Schnittger et al. 2012, Uilenberg et al. 2019, Bishop et al 2020, Penzhorn et al 2020).
 - Third, it would extend this review unnecessarily and clarity would get lost as there are numerous examples of accidental infections.
 - Forth, we made an exception to rule (iii) when a nearly-full length 18S RNA genes has been reported even though the natural vertebrate host may probably not be known. These sequences have been integrated in our trees and are of interest since they represent potentially novel species that deserve further species description and classification.