

Figure S1. Phylogenetic analysis of *Rickettsia* based on 16S rRNA gene variation. Neighbor-joining trees constructed via Tamura-Nei2 model using Geneious. Numbers at branches represent bootstrap values of 1000 replicates (values > 50 are shown). A). The trimmed 404 bp ASV of *Rickettsia* was analysed with Geneious. Top 10 hits from BLAST output were selected from GenBank. B). The trimmed 122 bp amplicon sequence of *Rickettsia* via Sanger sequencing was analysed with Geneious. Top 10 hits from BLAST output were selected from GenBank.

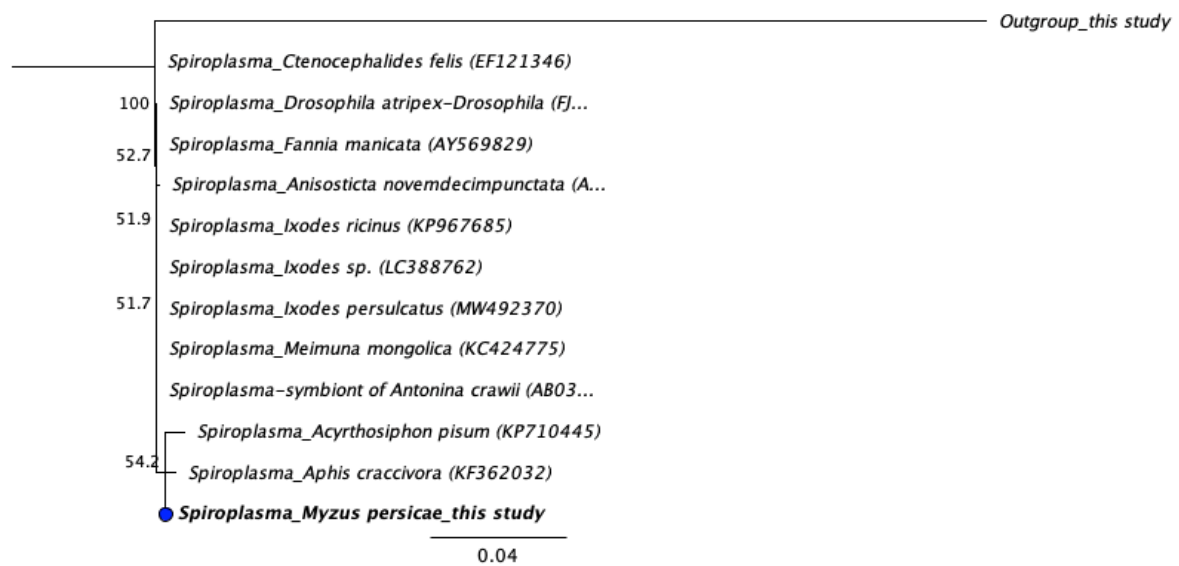


Figure S2. Phylogenetic analysis of *Spiroplasma* based on 16S rRNA gene variation. Neighbor-joining trees constructed via Tamura-Nei2 model using Geneious. Numbers at branches represent bootstrap values of 1000 replicates (values > 50 are shown). The trimmed 364 bp amplicon sequence of *Spiroplasma* via Sanger sequencing was analysed with Geneious. Top 10 hits from BLAST output were selected from GenBank.