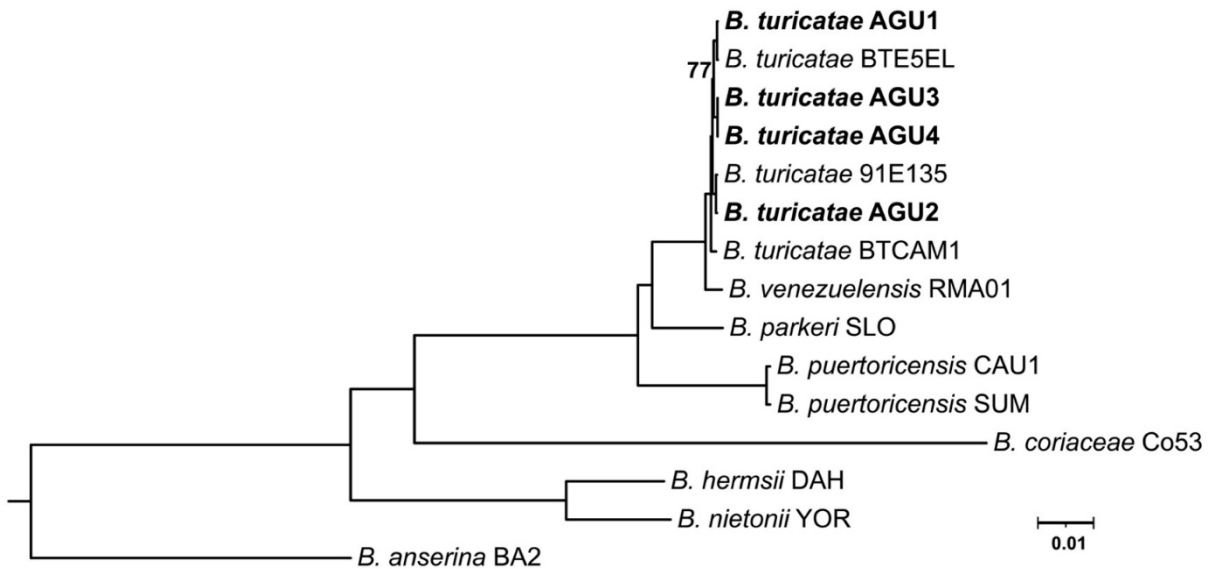


Borrelia turicatae in Ticks from Animals in a Public Park, Aguascalientes, Mexico

Appendix



Appendix Figure. The isolates are shown in bold, and other relapsing fever *Borrelia* genomes were included in the analyses, and *Borrelia anserina* BA2 was used as the outgroup. The tree was generated with an edge-linked proportional partition model with 1,000 ultra-fast bootstraps replicates. Scale bar indicates 0.01 substitutions per site. GenBank RefSeq accessions for previously assembled genomes used for this analysis are: *B. anserina* BA2 (GCF_023035575.1), *B. hermsii* DAH (GCF_023035675.1), *B. nietonii* YOR (GCF_023035795.1), *B. coriaceae* Co53 (GCF_023035295.1), *B. puertoricensis* SUM (GCF_023035875.1), *B. puertoricensis* CAU1 (GCF_051132515.1), *B. parkeri* SLO (GCF_023035815.1), *B. venezuelensis* (GCF_023035835.1), *B. turicatae* 91E135 (GCF_023035855.1), *B. turicatae* BTE5EL (GCF_023035415.1), *B. turicatae* BTCAM1 (GCF_036362965.1). Phylogenomic analysis of *B. turicatae* isolates AGU1–4 was conducted as previously described (7), using panaroo v1.5.1 and IQ-TREE2 v2.3.6, and the results were visualized in iTOL v7.