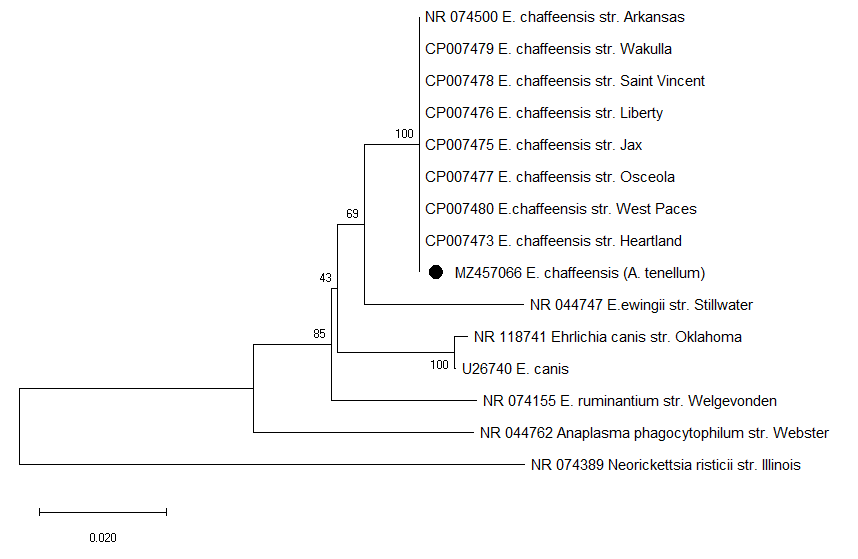


**Supplement 1.** Phylogenetic tree of **Mitochondrial 16S ribosomal RNA** gene from *Amblyomma tenellum*, inferred using the Maximum Likelihood method based on the General Time Reversible model with a discrete Gamma distribution (1.0). The bootstrap consensus tree inferred from 1000 replicates, a total of 376 nucleotides were analyzed. The square corresponds to the sequence obtained from *A. tenellum* in this study. (GenBank accession number: MZ457070).



**Supplement 2.** Phylogenetic tree of **16srRNA** gene from *Ehrlichia chaffeensis*, inferred using the Neighbor-Joining method. The bootstrap consensus tree inferred from 1000 replicates, a total of 418 nucleotides were analyzed. The circle ● corresponds to the sequence obtained in this study. (GenBank accession number: MZ457066).