



Figure S1. Phylogenetic relationship of *Amblyomma* ticks collected from tortoises (that could not be identified to species level using morphological keys), and other *Amblyomma* congeners. The maximum likelihood phylogenetic trees were based on **(A)** ITS2 (1,008 bp) and **(B)** 16S rRNA (402 bp). Phylogenetic analyses for ITS2 was performed in PhyML v. 2.2.4 with General-time-reversible (GTR) substitution models over 1000 bootstrap replicates. For 16S rRNA, phylogenetic analyses was performed in MEGA-X with Tamura-Nei model applying 1000 bootstrap replicates. Only bootstrap values exceeding 65% are shown. The identified sequences are highlighted in red.