Table S3. Summary of previous reports of most abundant operational taxonomic units (OTUs) from *Amblyomma americanum*.

| OTU | Classification  (Class) | GenBank ID | Closest GenBank BLAST Hit  (GenBank ID, % identity) | Previous Reports from Ticks? | Notes |
| --- | --- | --- | --- | --- | --- |
| 1 | Genus *Coxiella* (Gammaproteobacteria) | KJ130495 | *Coxiella* endosymbiont of *A. americanum*  (AY939824.1, 99%) | *A. americanum* [1] | Considered primary symbiont of *A. americanum* [2]. Related symbionts found in many other tick species [reviewed in 3]. |
| 2 | Genus *Rickettsia* (Alphaproteobacteria) | KJ130496 | *R. amblyommii*  (NR\_074471.1, 99%) | *A. americanum* [4]  Other *Amblyomma*, eg. *A. cajennense* and *A. coelebs* [5] | Many additional citations exist; some are given in the main article. |
| 3 | Genus *Midichloria* 1 (Alphaproteobacteria) | KJ130497 | *M. mitochondrii* strain AamerB  (JQ678691.1, 100% ) | *A. americanum* [6]  *A. triste* [7]  *A. tuberculatum* [8]  *D. andersoni* [9]  *Ha. punctate* [8]  *Hy. marginatum* [8]  *Hy. truncatum* [8]  *I. ricinus* [8]  *I. uriae* [8]  *Rh. turanicus* [8]  *Rh. bursa* [8] | A likely facultative symbiont [10]. |
| 4 | Genus *Borrelia*  (Spirochaetes) | KJ130498 | *B. lonestari*  (AY166715.1, 100%) | *A. americanum* [11]  *C. capensis* [12] | *C. capensis*’s *Borrelia* has not been definitively identified as *B. lonestari*, but available evidence supports this identification. |
| 5 | Genus *Francisella* (Gammaproteobacteria) | KJ130499 | *Francisella* spp. both pathogenic and symbiotic (e.g. JQ764629.1, 100%) | *A. americanum* [reviewed in 13]  *A. maculatum* [14]  *Dermacentor* spp. [reviewed in 3]  *Hy. marginatum* [15] | Widespread symbiont of many tick species, but *A. americanum* is not known to carry a symbiotic form. |
| 6 | Genus *Midichloria* 2 (Alphaproteobacteria) | KJ130500 | *M. mitochondrii* strain AamerC  (JQ678692.1, 100%) | *A. americanum* [6]  *A. triste* [7]  *A. tuberculatum* [8]  *D. andersoni* [9]  *Ha. punctate* [8]  *Hy. marginatum* [8]  *Hy. truncatum* [8]  *I. ricinus* [8]  *I. uriae* [8]  *Rh. turanicus* [8]  *Rh. bursa* [8] | A likely facultative symbiont [10]. |
| 7 | Genus *Ehrlichia* (Alphaproteobacteria) | KJ130501 | *Ehrlichia* spp.  (e.g. U96436.1, 100%) | *A. americanum* [reviewed in 13]  *D. variabilis* [16]  *Rh. sanguineus* [17] |  |
| 8 | Order Bacillales 1  (Bacilli) | KJ130502 | *Bacillus* spp.  (e.g. EU530599.1, 100%) | *A. americanum* [18,19]  *A. testudinarium* [20]  *Ha. formosensis* [20]  *I. ovatus* [20]  *I. persulcatus* [20]  *I. ricinus* [20,21]  *I. scapularis* [19]  *Rh. microplus* [22] | Common environmental bacteria, but also known symbionts of other arthropods. Notably *Bacillus* protects against fungal pathogens in bees [reviewed in 23]. |
| 9 | Family Enterobacteriaceae (Gammaproteobacteria) | KJ130503 | Many genera; 60% of sequences classified to *Yersinia*  (e.g. BX936398.1, 100%) | *A. americanum* [18,19,24]  *I. scapularis* [19] | Many insect symbionts belong to this family (e.g. *Sodalis* [25], *Wigglesworthia* [26], *Buchnera* [27]), but it also contains common and diverse environmental bacteria [28] and pathogens [29]. |
| 10 | Genus *Pseudomonas* 1  (Gammaproteobacteria) | KJ130504 | *Pseudomonas* spp.  (e.g. KF147045.1, 100%) | *A. americanum* [18,24]  *I. ricinus* [21]  *Rh. microplus* [22] | Common environmental bacteria. Demonstrated *in vitro* lysis of vector-borne parasites by some species [30] |
| 11 | Genus *Wolbachia* (Alphaproteobacteria) | KJ130505 | *Wolbachia* strains  (e.g. KC522606.1, 99%) | *A. americanum* [31]  *I. ricinus* [21,32]  *I. scapularis* [33]  *Rh. microplus* [22]  *Rh. sanguineus* [34] | Widespread symbiont of many arthropods known for reproductive manipulation of hosts and protective abilities [reviewed in 35]. |
| 12 | Order Rhizobiales 1  (Alphaproteobacteria) | KJ130506 | Many genera; 52% of sequences classified to Bradyrhizobiaceae  (e.g. GU125653.2, 99%) | *A. americanum* [36]  *I. ricinus* [21] | Common nitrogen-fixing plant symbionts [reviewed in 37], but also found in association with ants [38,39]. |
| 13 | Family Burkholderiaceae (Betaproteobacteria) | KJ130507 | Many genera; 78% of sequences classified to *Burkholderia*  (e.g. KF059270.1, 100%) | *A. americanum* [19,24]  *I. ricinus* [21]  *I. scapularis* [19,40] | *Burkholderia* exist as free-living [41], plant symbionts [42], arthropod symbionts [43], and vertebrate pathogens [44]. |
| 14 | Family “Gp1” *incertae sedis*  (Acidobacteria) | KJ130508 | Unidentified clones  (e.g. HQ598755.1, 100%) | *A. variegatum* [20] | “Gp1” bacteria are iron oxidizers previously found in environmental samples, like iron-rich ground water [45]. |
| 15 | Genus *Rhodobaca* (Alphaproteobacteria) | KJ130509 | Unidentified clones  (e.g. AB297418.1, 100%) | No | Genus containing anoxygenic purple nonsulfur bacteria usually associated with lake waters and soil [46]. Never previously reported in association with ixodid ticks, but its closest phylogenetic relatives in the genus *Rhodobacter* have been (*I. scapularis* [19], *Rh. microplus* [22], and *I. ricinus* [21]). |
| 16 | Order Bacillales 2  (Bacilli) | KJ130510 | Unidentified clones  (e.g. JF968215.1, 100%) | *A. americanum* [18,19]  *A. testudinarium* [20]  *Ha. formosensis* [20]  *I. ovatus* [20]  *I. persulcatus* [20]  *I. ricinus* [20,21]  *I. scapularis* [19]  *Rh. microplus* [22] | Common environmental bacteria, but also known symbionts of other arthropods. Notably *Bacillus* protects against fungal pathogens in bees [reviewed in 23]. |
| 17 | Genus *Pseudomonas* 2 (Gammaproteobacteria) | KJ130511 | *Pseudomonas* spp.  (e.g. GQ232466.1, 100%) | *A. americanum* [18,24]  *I. ricinus* [21]  *Rh. microplus* [22] | Common environmental bacteria. Demonstrated in vitro lysis of vector-borne parasites by some species [30]. |
| 18 | Genus *Nitriliruptor* (Actinobacteria) | KJ130512 | *N. alkaliphilus*  (NR\_044203.1, 100%) | References to unclassified Actinobacteria:  *A. americanum* [18,19]  *A. variegatum* [20]  *D. variabilis* [40]  *I. scapularis* [21,40] | *Nitriliruptor* has been previously documented from soil samples [47,48]. Actinobacteria are common environmental bacteria and eukaryote-associates [reviewed in 49]. |
| 19 | Genus *Methylobacterium* (Alphaproteobacteria) | KJ130513 | *Methylobacterium* spp.  (e.g. AB698724.1, 100%) | *A. americanum* [18]  *I. ricinus* [21] | Common environmental bacteria associated with soil and plants [e.g. 50]. It is known from the human mouth [51] and skin [52] microbiome and may also be pathogenic [53]. |
| 20 | Order Rhizobiales 2 (Alphaproteobacteria) | KJ130514 | Unidentified clones  (e.g. JQ047240.1, 100%) | *A. americanum* [24]  *D. variabilis* [40]  *I. ricinus* [21]  *I. scapularis* [40]  *Rh. microplus* [22] | Common nitrogen-fixing plant symbionts [reviewed in 37], but also found in association with ants [38,39]. |
| 21 | Family Sphingomonadaceae (Alphaproteobacteria) | KJ130515 | *Sphingomonas* spp.; 97% of sequences classified to *Sphingomonas*  (e.g. KF542913.1, 100%) | *A. americanum* [19,36]  *I. ricinus* [21]  *I. scapularis* [19] | *Sphingomonas* spp. are known arthropod associates, including mosquitoes (*Aedes aegypti*) [54] and termites (*Macrotermes natalensis* and *Nasutitermes* sp.) [55]. |
| 22 | Order Bacillales 3  (Bacilli) | KJ130516 | Unidentified clones  (e.g. AB637120.1, 100%) | *A. americanum* [18,19]  *A. testudinarium* [20]  *Ha. formosensis* [20]  *I. ovatus* [20]  *I. persulcatus* [20]  *I. ricinus* [20,21]  *I. scapularis* [19]  *Rh. microplus* [22] | Common environmental bacteria, but also known symbionts of other arthropods. Notably *Bacillus* protects against fungal pathogens in bees [reviewed in 23]. |
| 23 | Order Actinomycetales (Actinobacteria) | KJ130517 | *Mycobacterium* spp.; 99% of sequences classified to *Mycobacterium*  (e.g. KF224994.1, 100%) | *A. americanum* [19]  *D. variabilis* [40]  *I. ricinus* [21]  *I. scapularis* [19] | Common environmental bacteria (soil, water). Also common pathogens of wildlife (birds, mammals) [56]. |

The OTU number ranks the groups in order of decreasing abundance. In the classification column, the lowest taxon that all sequences within the OTU could be assigned to is provided first, followed by the class assignment in parentheses. Numbers are added to this column to differentiate OTUs classified to otherwise identical taxons; these are the same numbers used in the main paper. GenBank IDs are given for a representative sequence from each OTU, which was defined as the sequence with the smallest maximum distance from all other sequences in the OTU. The closest GenBank BLAST Hit was found by comparing the representative sequence against the GenBank database and reporting the hit with the highest identity. If there was no single best hit, this is indicated by the example designation before the GenBank ID number. The fifth column contains references for tick species from which these OTUs have previously been reported and is not exhaustive. Tick genus abbreviations are as follows: *A. Amblyomma, C. Carios, D. Dermacentor, Ha. Haemaphysalis, Hy. Hyalomma, I. Ixodes,* and *Rh. Rhipicephalus*.

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