

Table S1. Molecular identification of *Francisella* sp. endosymbiont isolated from *H. dromedarii* collected from camels in Abu Dhabi, UAE based on DNA similarity between 16S rRNA gene and GenBank species using NCBI BLAST.

Best Match Species	Accession Number	Sequence Identity %	Sequence Coverage %	E-value ^a	Host	Country
Uncultured <i>Francisella</i> sp. clone FraApaulo	MN998649.1	98.59	100	0.0	<i>Amblyomma paulopunctatum</i>	France
<i>Francisella</i> endosymbiont	JQ764629.1	98.59	100	0.0	<i>Dermacentor auratus</i>	Thailand
<i>Ornithodoros moubata</i> symbiont	AB001522.1	98.59	100	0.0	<i>Ornithodoros moubata</i>	Japan
Uncultured <i>Francisella</i> sp. clone FraAscul	MN998650.1	98.47	100	0.0	<i>Amblyomma sculptum</i>	France
<i>Francisella</i> endosymbiont	JQ764628.1	98.47	100	0.0	<i>Dermacentor auratus</i>	Thailand
Uncultured <i>Francisella</i> sp. clone FraAhume3	MN998638.1	98.35	100	0.0	<i>Amblyomma humerale</i>	France
Uncultured <i>Francisella</i> sp. clone FraAhume2	MN998637.1	98.35	100	0.0	<i>Amblyomma humerale</i>	France
Uncultured <i>Francisella</i> sp. clone FraAhume1	MN998636.1	98.35	100	0.0	<i>Amblyomma humerale</i>	France
Uncultured <i>Francisella</i> sp. clone 627HBF ZOTU 13a	MN088353.1	98.35	100	0.0	<i>Haemaphysalis bancrofti</i>	Australia
Uncultured <i>Francisella</i> sp. clone 297HBF ZOTU 13a	MN088349.1	98.35	100	0.0	<i>Haemaphysalis bancrofti</i>	Australia
<i>Francisella</i> endosymbiont of <i>Ornithodoros porcinus</i>	AF166257.1	98.35	100	0.0	<i>Ornithodoros porcinus</i>	USA
Uncultured bacterium clone he_23	KX465127.1	98.35	100	0.0	Tick	China
Uncultured bacterium clone he_17	KX465125.1	98.35	100	0.0	Tick	China
Uncultured bacterium clone he_6	KX465118.1	98.35	100	0.0	Tick	China
Uncultured bacterium clone he_5	KX465117.1	98.35	100	0.0	Tick	China
Uncultured bacterium clone he_1	KX465115.1	98.35	100	0.0	Tick	China
<i>Francisella</i> endosymbiont isolate XJ-S3	KX852466.1	98.35	100	0.0	<i>Hyalomma asiaticum</i>	China
<i>Francisella</i> endosymbiont isolate XJ-S1	KX852464.1	98.35	100	0.0	<i>Hyalomma asiaticum</i>	China
Uncultured <i>Francisella</i> sp.	MN998635.1	98.24	100	0.0	<i>Amblyomma goeldii</i>	France
Uncultured <i>Francisella</i> sp.	MN998634.1	98.24	100	0.0	<i>Amblyomma goeldii</i>	France
Uncultured <i>Francisella</i> sp.	MN998633.1	98.24	100	0.0	<i>Amblyomma goeldii</i>	France
Uncultured <i>Francisella</i> sp. clone FraAvari	MN998648.1	98.24	100	0.0	<i>Amblyomma varium</i>	France
Uncultured <i>Francisella</i> sp. clone 297HBF ZOTU 13a	MN088357.1	98.24	100	0.0	<i>Haemaphysalis bancrofti</i>	Australia
<i>Francisella</i> endosymbiont of <i>Hyalomma marginatum</i>	AF166257.1	98.24	100	0.0	<i>Rhipicephalus bursa</i>	Italy
<i>Francisella</i> -like endosymbiont	MH645205.1	98.24	100	0.0	<i>Hyalomma aegyptium</i>	Turkey
<i>Francisella</i> -like endosymbiont	MH645204.1	98.24	100	0.0	<i>Hyalomma aegyptium</i>	Turkey
<i>Francisella</i> -like endosymbiont	MH645203.1	98.24	100	0.0	<i>Hyalomma aegyptium</i>	Turkey
<i>Francisella</i> -like endosymbiont	MH645202.1	98.24	100	0.0	<i>Hyalomma aegyptium</i>	Turkey
<i>Francisella</i> -like endosymbiont	MH645201.1	98.24	100	0.0	<i>Hyalomma aegyptium</i>	Turkey

^a The typical threshold for a good E-value from a BLAST search is 10⁻⁵ or lower.

Table S2. Molecular identification of Uncultured *Rickettsia* sp. isolated from *H. dromedarii* collected from camels in Abu Dhabi, UAE based on DNA similarity between *ompA* gene and GenBank species using NCBI BLAST.

Best Match Species	Accession Number	Sequence Identity %	Sequence Coverage %	E-value*	Host	Country
Uncultured <i>Rickettsia</i> sp. clone C269_18	MK522488.1	99.80	100	0.0	<i>Amblyomma parvum</i>	Brazil
<i>Candidatus Rickettsia andeanae</i> clone Caxias	KY628370.1	99.80	100	0.0	<i>Amblyomma parvum</i>	Brazil
<i>Candidatus Rickettsia andeanae</i> haplotype BQ-RS	KX434737.1	99.80	100	0.0	<i>Amblyomma tigrinum</i>	Brazil
<i>Candidatus Rickettsia andeanae</i> clone 4	KX158267.1	99.80	100	0.0	<i>Amblyomma maculatum</i>	USA
<i>Candidatus Rickettsia andeanae</i> clone 3	KX158266.1	99.80	100	0.0	<i>Amblyomma maculatum</i>	USA
<i>Candidatus Rickettsia andeanae</i> isolate Agripino Enciso	KF179352.1	99.80	100	0.0	<i>Amblyomma parvum</i>	Paraguay
<i>Candidatus Rickettsia andeanae</i> isolate Ap	KF030932.1	99.80	100	0.0	<i>Amblyomma parvum</i>	Brazil
Uncultured <i>Rickettsia</i> sp. clone ALAIN-001-2011	KF156874.1	99.80	100	0.0	<i>Hyalomma dromedarii</i>	UAE
<i>Rickettsia</i> endosymbiont of <i>Amblyomma maculatum</i> strain SH_B4	JX134638.1	99.80	100	0.0	<i>Amblyomma maculatum</i>	USA
<i>Candidatus Rickettsia andeanae</i> isolate At2	MT968426.1	99.80	100	0.0	<i>Amblyomma tigrinum</i>	Brazil
<i>Candidatus Rickettsia andeanae</i> isolate At2	JQ690599.1	99.80	100	0.0	<i>Haemaphysalis</i> sp.	USA
<i>Candidatus Rickettsia amblyommii</i> isolate 61A	JQ690625.1	94.78	98	0.0	<i>Haemaphysalis</i> sp.	USA
<i>Candidatus Rickettsia andeanae</i> isolate G614	KX576678.1	99.76	83	0.0	<i>Amblyomma tigrinum</i>	Argentina
<i>Candidatus Rickettsia amblyommii</i> isolate GP4A	KM652487.1	94.27	99	0.0	Hard ticks	Panama
<i>Candidatus Rickettsia amblyommii</i> isolate 23B	JQ690590.1	94.76	97	0.0	<i>Haemaphysalis</i> sp.	USA
Uncultured <i>Rickettsia</i> sp. clone SH_MG7	JQ914762.1	94.08	99	0.0	<i>Amblyomma maculatum</i>	USA

Table S3. Molecular identification of *T. annulata* isolated from *H. anatolicum* collected from cows in Sharjah, UAE based on DNA similarity between *ssrRNA* gene and GenBank species using NCBI BLAST.

Best Match Species	Accession Number	Sequence Identity %	Sequence Coverage %	E-value ^a	Host	Country
<i>Theileria annulata</i>	MT341858.1	99.62	99	0.0	<i>Bos taurus</i>	Italy
<i>Theileria annulata</i>	MT341857.1	99.62	99	0.0	<i>Bos taurus</i>	Italy
<i>Theileria annulata</i> isolate T178	MT318160.1	99.62	99	0.0	Ruminants	Pakistan
<i>Theileria annulata</i> isolate T79	MT318159.1	99.62	99	0.0	Ruminants	Pakistan
<i>Theileria annulata</i> isolate T33	MT318158.1	99.62	99	0.0	Ruminants	Pakistan
<i>Theileria annulata</i> isolate Ticks, No 46	MN227669.1	99.62	99	0.0	Ticks	Egypt
<i>Theileria annulata</i> isolate Ticks, No 45	MN227668.1	99.62	99	0.0	Ticks	Egypt
<i>Theileria annulata</i> isolate Ticks, No 44	MN227667.1	99.62	99	0.0	Ticks	Egypt
<i>Theileria annulata</i> isolate Ticks, No 24	MN227666.1	99.62	99	0.0	Ticks	Egypt
<i>Theileria annulata</i> isolate 355	MN223736.1	99.62	99	0.0	Unpublished data	Egypt
<i>Theileria annulata</i> clone 5-31	AY508465.1	99.62	99	0.0	Cattle	Turkey
<i>Theileria annulata</i> isolate Turkey 4	AY508464.1	99.62	99	0.0	Cattle	Turkey
<i>Theileria annulata</i> isolate Turkey 3	AY508463.1	99.62	99	0.0	Cattle	Turkey
<i>Theileria annulata</i>	EU083801.1	99.43	99	0.0	<i>Bos taurus</i>	China
<i>Theileria annulata</i>	M64243.1	99.43	99	0.0	Bovine	USA

Table S4. Molecular identification of *T. ovis* isolated from *H. anatolicum* collected from goats in Sharjah, UAE based on DNA similarity between *ssrRNA* gene and GenBank species using NCBI BLAST.

Best Match Species	Accession Number	Sequence Identity %	Sequence Coverage %	E-value ^a	Host	Country
<i>Theileria ovis</i> isolate HBOY1	MN394810.1	99.81	99	0.0	<i>Bos grunniens</i>	China
<i>Theileria ovis</i> isolate HXTS1	MN394809.1	99.81	99	0.0	Tibetan sheep	China
<i>Theileria ovis</i> isolate HBTS1	MN394808.1	99.81	99	0.0	Tibetan sheep	China
<i>Theileria ovis</i> isolate SH. T1	MN712508.1	99.81	99	0.0	Sheep	Iraq
<i>Theileria ovis</i> isolate SH. T5	MN704656.1	99.81	99	0.0	Sheep	Iraq
<i>Theileria ovis</i> isolate THOD2	MN625903.1	99.81	99	0.0	Donkey	Egypt
<i>Theileria ovis</i> isolate THOB2	MN625887.1	99.81	99	0.0	Buffalo	Egypt
<i>Theileria ovis</i> isolate THOSH5	MN625886.1	99.81	99	0.0	Sheep	Egypt
<i>Theileria ovis</i> isolate SH.S2	MN544931.1	99.81	99	0.0	Sheep	Iraq
<i>Theileria ovis</i> isolate 3kz7	MN493111.1	99.81	99	0.0	Sheep	Turkey
<i>Theileria</i> sp. Iwate 141 gene	AB602888.1	99.81	99	0.0	<i>Cervus nippon</i>	Japan
<i>Theileria</i> sp. Iwate 276 gene	AB602887.1	99.81	99	0.0	<i>Cervus nippon</i>	Japan
<i>Theileria</i> sp. Iwate 228 gene	AB602886.1	99.81	99	0.0	<i>Cervus nippon</i>	Japan
<i>Theileria</i> sp. Iwate 194 gene	AB602885.1	99.81	99	0.0	<i>Cervus nippon</i>	Japan
<i>Theileria</i> sp. Iwate 169 gene	AB602883.1	99.81	99	0.0	<i>Cervus nippon</i>	Japan

Table S5. Prevalence of microbes in *Hyalomma* ticks in UAE.

Sr. No.	Farm Locations	Samples (Camels)	Samples (Cows)	Samples (Sheep)	Samples (Goats)	Total Samples	<i>Francisella</i> sp. (positive samples)	<i>Rickettsia</i> sp. (positive samples)	<i>Theileria annulata</i> (positive samples)	<i>Theileria ovis</i> (positive samples)
Abu Dhabi										
1.	Al-Foah, UAEU	2	-	-	-	2	1	-	-	-
2.	Beda Bent Saud	6	-	-	-	6	1	-	-	-
3.	Livestock Market, Al Ain	11	-	4 (36)	-	15	1	-	-	-
4.	Nahel Town	24	-	-	-	24	2	2	-	-
5.	Omghafa	84	-	-	-	84	3	1	-	-
6.	Truck Road	20	-	-	-	20	4	-	-	-
7.	Al-Wagan	30	-	-	-	30	5	1	-	-
8.	Dubai Road	70	0 (15)	-	-	70	4	1	-	-
9.	Bukriya	15	-	-	-	15	5	2	-	-
10.	Al-Saad	53	-	-	-	53	4	-	-	-
11.	Al-Hayer	5	-	-	-	5	-	-	-	-
12.	Swehan	24	-	-	-	24	-	-	-	-
13.	Nabagh	15	-	-	-	15	-	-	-	-
14.	Al-Dahra	50	-	-	0 (30)	50	-	-	-	-
15.	Al-Yahar	6	-	-	-	6	-	-	-	-
16.	Malaket	12	-	-	-	12	-	-	-	-
17.	Remah	5	-	-	-	5	-	-	-	-
18.	Beda Fares	17	-	-	-	17	-	-	-	-
19.	Seh Saba	3	-	-	-	3	-	-	-	-
20.	Bilayat	2	-	-	-	2	-	-	-	-
21.	Al-Arad	44	-	-	-	44	-	-	-	-
Sub-total		498 (498)	0	4 (36)	0	502 (534)	30	7		
Dubai										
22.	Dubai Camel Hospital	17 (17)	-	-	-	17	-	-	-	-
23.	Al-Qusais Market, Dubai	-	20 (20)	9 (9)	9 (9)	38	-	-	-	-
Sub-total		17 (17)	20 (20)	9 (9)	9 (9)	55 (55)				
Sharjah										
24.	Kalba, Sharjah	1 (3)	2 (6)	1 (25)	1 (25)	5	-	-	1	1
Sub-total		1 (3)	2 (6)	1 (25)	1 (25)	5 (59)	-	-	1 (detected in ticks from cows)	1 (detected in ticks from goats)
Total		516 (518)	22 (26)	14 (70)	10 (34)	562 (648)	30	7	1	1

Numbers in parenthesis represent the number of animals.