

Exploring the microbiomes of camel ticks to infer vector competence: insights from tissue-level symbiont-pathogen relationships

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Supplementary results

Supp. table 1: Relative abundance (%) of bacterial genera communities in the four tick species collected from camels in North Kenya based on 16S rRNA sequencing of the V1-V2 segment.

Genus	Percentage relative abundance %			
	<i>Am. gemma</i>	<i>Rh. pulchellus</i>	<i>Hy. dromedarii</i>	<i>Hy. rufipes</i>
<i>Acinetobacter</i>	19.70%	27.00%	3.60%	3.10%
<i>Candidatus Midichloria</i>	0.00%	0.50%	0.90%	5.30%
<i>Corynebacterium</i>	0.80%	4.30%	5.50%	3.90%
<i>Coxiella</i>	11.60%	16.30%	0.10%	0.00%
<i>Cutibacterium</i>	1.90%	3.40%	1.60%	1.00%
<i>Francisella</i>	4.00%	5.90%	33.50%	42.50%
Others	13.90%	18.20%	10.80%	13.30%
<i>Proteus</i>	4.40%	0.40%	37.50%	24.20%
<i>Pseudomonas</i>	4.90%	21.00%	5.00%	2.60%
<i>Rickettsia</i>	36.60%	0.60%	0.30%	3.30%
<i>Staphylococcus</i>	2.30%	2.30%	1.40%	0.90%
Total	100.00%	100.00%	100.00%	100.00%

Supp. table 2: Relative abundance (%) of bacterial genera communities in different tick tissues of the four tick species collected from camels in North Kenya.

<i>Amblyomma gemma</i>										
Genus	Percentage relative abundance									
	HL1	HL2	HL3	HL4	HL5	MG1	MG2	MG3	MG4	SG1
<i>Acinetobacter</i>	25.30%	4.70%	19.30%	60.30%	5.30%	0.10%	3.40%	6.30%	36.60%	0.20%
<i>Corynebacterium</i>	0.30%	3.00%	2.30%	2.10%	2.90%	0.00%	0.00%	0.30%	0.00%	0.00%
<i>Coxiella</i>	0.00%	0.00%	0.50%	17.80%	0.00%	8.70%	0.60%	3.90%	6.50%	0.40%
<i>Cutibacterium</i>	0.30%	1.90%	14.70%	1.90%	11.90%	0.00%	0.10%	0.90%	0.70%	0.00%
<i>Ehrlichia</i>	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	32.80%	0.00%	0.00%
<i>Francisella</i>	0.10%	0.10%	1.00%	0.00%	0.00%	0.00%	0.30%	0.80%	8.80%	0.10%
<i>Others</i>	22.20%	13.30%	41.90%	12.30%	43.80%	0.00%	0.60%	2.60%	6.10%	0.10%
<i>Pseudomonas</i>	3.30%	0.80%	3.70%	3.00%	15.70%	0.60%	1.00%	0.80%	40.70%	0.20%
<i>Rickettsia</i>	41.60%	74.40%	11.40%	0.20%	0.00%	90.60%	93.80%	50.80%	0.10%	99.00%
<i>Sphingobacterium</i>	6.80%	0.10%	1.20%	0.00%	0.30%	0.00%	0.20%	0.30%	0.00%	0.10%
<i>Staphylococcus</i>	0.20%	1.60%	4.00%	2.50%	20.00%	0.00%	0.00%	0.50%	0.50%	0.00%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
Genus	SG2	SG3	SG4	SG5	SG6	SL1	SL2	SL3	SL4	SL5
	<i>Acinetobacter</i>	0.10%	2.60%	1.40%	0.00%	10.80%	35.10%	15.90%	6.00%	92.70%
<i>Corynebacterium</i>	0.00%	0.00%	0.30%	0.00%	0.30%	6.80%	0.20%	1.00%	1.20%	33.80%
<i>Coxiella</i>	2.90%	24.30%	77.00%	92.00%	9.80%	0.00%	0.00%	0.70%	0.00%	0.00%
<i>Cutibacterium</i>	0.00%	0.10%	1.20%	0.40%	0.20%	0.10%	0.10%	7.50%	0.20%	1.40%
<i>Ehrlichia</i>	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Francisella</i>	0.50%	0.20%	3.40%	0.00%	64.20%	0.10%	0.10%	0.10%	0.00%	0.70%
<i>Others</i>	1.70%	0.40%	9.70%	2.50%	2.60%	11.90%	69.50%	16.70%	4.80%	34.50%
<i>Pseudomonas</i>	0.40%	2.70%	5.40%	4.80%	11.30%	2.20%	5.80%	2.90%	0.30%	4.30%
<i>Rickettsia</i>	94.10%	69.40%	0.20%	0.00%	0.10%	29.10%	0.50%	52.40%	0.00%	0.70%
<i>Sphingobacterium</i>	0.00%	0.30%	0.00%	0.00%	0.00%	3.10%	7.70%	0.40%	0.00%	0.10%
<i>Staphylococcus</i>	0.20%	0.00%	1.40%	0.30%	0.70%	11.80%	0.20%	12.30%	0.90%	22.90%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
<i>Rhipicephalus pulchellus</i>										
Genus	HL1	HL2	HL3	HL4	MG1	MG2	MG3	MG4	MG5	SG1
	<i>Acidovorax</i>	0.00%	0.10%	0.00%	0.00%	3.00%	1.60%	1.10%	3.40%	1.10%
<i>Acinetobacter</i>	66.80%	17.20%	87.00%	83.30%	5.40%	47.10%	15.70%	1.60%	18.20%	3.80%
<i>Corynebacterium</i>	1.80%	0.10%	1.40%	1.30%	0.70%	1.60%	0.60%	0.30%	18.60%	0.00%
<i>Coxiella</i>	0.00%	0.70%	1.20%	0.00%	4.30%	4.60%	25.20%	3.70%	16.90%	78.00%
<i>Cutibacterium</i>	3.10%	0.80%	0.30%	0.70%	4.80%	1.20%	4.70%	2.20%	0.90%	0.30%
<i>Delftia</i>	7.10%	0.40%	0.10%	0.30%	0.80%	1.70%	1.70%	1.20%	0.00%	0.30%
<i>Francisella</i>	0.60%	61.50%	0.00%	0.10%	1.50%	11.70%	2.30%	0.60%	0.00%	12.50%
<i>Others</i>	10.90%	16.10%	8.40%	11.40%	25.90%	12.20%	20.30%	14.50%	13.80%	2.90%
<i>Peptoniphilus</i>	0.00%	0.50%	0.20%	1.10%	0.00%	0.20%	0.80%	0.00%	3.30%	0.00%
<i>Pseudomonas</i>	8.50%	1.90%	0.30%	1.50%	51.60%	18.10%	26.30%	71.80%	26.00%	2.20%
<i>Staphylococcus</i>	1.30%	0.80%	1.00%	0.30%	2.00%	0.00%	1.50%	0.60%	1.40%	0.00%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
Genus	SG1	SG2	SG3	SG4	SG5	SL1	SL2	SL3	SL4	
	<i>Acinetobacter</i>	0.10%	2.60%	1.40%	0.00%	10.80%	35.10%	15.90%	6.00%	92.70%

<i>Acidovorax</i>	0.50%	1.50%	0.80%	2.20%	0.30%	0.00%	0.00%	0.00%	0.10%
<i>Acinetobacter</i>	10.20%	0.90%	0.20%	6.90%	11.10%	34.70%	89.80%	4.40%	23.30%
<i>Corynebacterium</i>	0.10%	0.10%	0.00%	0.30%	8.60%	20.40%	2.50%	2.60%	25.20%
<i>Coxiella</i>	17.60%	45.70%	52.30%	8.70%	55.90%	0.00%	0.00%	0.00%	0.10%
<i>Cutibacterium</i>	6.90%	0.20%	0.80%	2.00%	0.20%	0.70%	0.10%	22.10%	7.20%
<i>Delftia</i>	0.70%	1.50%	1.90%	0.50%	0.00%	1.10%	0.00%	1.00%	0.30%
<i>Francisella</i>	17.40%	1.00%	1.00%	3.80%	0.10%	1.30%	0.10%	0.00%	0.00%
Others	20.10%	9.70%	7.70%	13.40%	4.90%	18.40%	6.10%	61.70%	28.90%
<i>Peptoniphilus</i>	0.10%	0.00%	0.00%	0.60%	0.60%	0.70%	0.30%	0.30%	11.00%
<i>Pseudomonas</i>	20.40%	39.30%	34.20%	60.20%	17.60%	4.40%	0.20%	1.40%	1.00%
<i>Staphylococcus</i>	5.80%	0.20%	1.10%	1.30%	0.60%	18.40%	0.80%	6.50%	3.10%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%

Hyalomma dromedarii

Genus	HL1	HL2	HL3	HL4	HL5	MG1	MG2	MG3	MG4
<i>Acinetobacter</i>	11.80%	16.30%	0.50%	2.70%	0.10%	0.00%	0.00%	0.00%	0.10%
<i>Anaerococcus</i>	3.10%	0.20%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Corynebacterium</i>	3.10%	4.10%	0.10%	0.30%	0.20%	0.00%	0.00%	0.00%	0.10%
<i>Cutibacterium</i>	0.20%	24.50%	0.50%	0.10%	0.10%	0.00%	0.00%	0.00%	0.00%
<i>Francisella</i>	0.10%	1.30%	9.60%	0.00%	1.00%	0.30%	2.00%	3.90%	99.30%
Others	6.90%	36.30%	1.70%	0.40%	0.60%	0.00%	0.00%	0.00%	0.00%
<i>Peptoniphilus</i>	4.00%	0.70%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Proteus</i>	3.20%	1.00%	86.60%	96.00%	97.40%	99.60%	97.90%	95.50%	0.30%
<i>Pseudomonas</i>	67.30%	2.30%	0.70%	0.40%	0.10%	0.10%	0.00%	0.60%	0.20%
<i>Sediminibacterium</i>	0.20%	4.50%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Staphylococcus</i>	0.20%	8.70%	0.20%	0.10%	0.40%	0.00%	0.00%	0.00%	0.00%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%

Genus	SG1	SG2	SG3	SG4	SG5	SL1	SL2	SL3	SL4
<i>Acinetobacter</i>	0.00%	0.00%	1.00%	2.40%	0.00%	4.30%	0.40%	1.10%	26.50%
<i>Anaerococcus</i>	0.00%	0.00%	0.00%	0.00%	0.00%	17.20%	0.60%	0.60%	0.20%
<i>Corynebacterium</i>	0.00%	0.00%	0.00%	0.00%	0.00%	33.20%	57.80%	3.30%	0.40%
<i>Cutibacterium</i>	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.10%	1.00%	3.10%
<i>Francisella</i>	88.00%	79.30%	60.50%	95.90%	100.00%	0.30%	0.10%	0.00%	35.10%
Others	0.10%	0.00%	3.90%	0.20%	0.00%	17.30%	18.10%	14.50%	22.70%
<i>Peptoniphilus</i>	0.00%	0.00%	0.00%	0.00%	0.00%	11.10%	0.40%	0.30%	0.40%
<i>Proteus</i>	11.50%	20.50%	33.00%	0.00%	0.00%	1.10%	20.00%	68.40%	1.30%
<i>Pseudomonas</i>	0.20%	0.20%	1.50%	1.50%	0.00%	12.80%	0.00%	2.70%	1.20%
<i>Sediminibacterium</i>	0.00%	0.00%	0.00%	0.00%	0.00%	0.80%	0.00%	0.00%	2.20%
<i>Staphylococcus</i>	0.10%	0.00%	0.10%	0.00%	0.00%	1.70%	2.50%	8.10%	6.90%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%

Hyalomma rufipes

Genus	HL1	HL2	HL3	MG1	MG2	MG3	SG1	SG2	SG3	SG4
<i>Acinetobacter</i>	5.50%	4.30%	16.80%	0.00%	0.30%	0.80%	0.00%	0.00%	1.00%	0.00%
<i>Anaerococcus</i>	0.40%	0.00%	10.50%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Candidatus Midichloria</i>	0.00%	0.00%	0.00%	2.80%	0.00%	27.00%	9.20%	8.10%	0.00%	9.00%
<i>Corynebacterium</i>	0.70%	2.90%	6.20%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%
<i>Francisella</i>	61.20%	1.40%	0.00%	29.00%	0.40%	49.40%	88.70%	81.70%	83.00%	90.30%

Others	13.80%	7.60%	16.30%	0.00%	1.60%	1.30%	0.10%	0.10%	0.00%	0.00%
<i>Peptoniphilus</i>	0.70%	0.00%	20.20%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Proteus</i>	2.30%	79.60%	3.00%	68.00%	93.10%	0.00%	1.90%	6.30%	14.10%	0.00%
<i>Pseudomonas</i>	4.40%	0.70%	15.50%	0.10%	0.00%	1.90%	0.10%	0.80%	0.40%	0.00%
<i>Pusillimonas</i>	0.00%	0.00%	11.60%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Rickettsia</i>	11.10%	3.30%	0.00%	0.00%	4.60%	19.40%	0.00%	3.00%	1.40%	0.70%
Total	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%
	SL1	SL2	SL3							
<i>Acinetobacter</i>	6.00%	2.20%	14.80%							
<i>Anaerococcus</i>	1.00%	0.10%	12.10%							
<i>Candidatus Midichloria</i>	0.00%	0.00%	0.00%							
<i>Corynebacterium</i>	27.20%	3.20%	7.80%							
<i>Francisella</i>	0.00%	22.40%	0.00%							
Others	50.10%	8.80%	19.00%							
<i>Peptoniphilus</i>	1.10%	0.30%	19.60%							
<i>Proteus</i>	11.20%	59.80%	3.10%							
<i>Pseudomonas</i>	3.40%	0.10%	16.00%							
<i>Pusillimonas</i>	0.00%	0.00%	7.70%							
<i>Rickettsia</i>	0.00%	3.10%	0.00%							
Total	100.00%	100.00%	100.00%							

HL, hemolymph; MG, midgut; SGs, salivary glands; SL, saliva

Supp. table 3: Alpha diversity of bacterial species communities P-values based on different tick species.

Samples name	Chao1	Shannon	Pielou
Ag vs Hd	0.20	0.60	0.65
Ag vs Hr	0.36	0.78	0.22
Ag vs Rp	0.15	0.61	0.61
Hd vs Hr	0.94	0.29	0.43
Hd vs Rp	0.01**	0.01**	0.16
Hr vs Rp	0.01**	0.07	0.49

Ag, *Am. gemma*; **Rp**, *Rh. pulchellus*; **Hd**, *Hy. dromedarii*; **Hr**, *Hy. rufipes*.
P-value (*P < 0.05, **P < 0.01, ***P < 0.001)

Supp. table 4: Alpha diversity of bacterial species communities P-values based on tissues in different tick species.

Tick species	Samples name	<i>Chao1</i>	<i>Shannon</i>	<i>Pielou</i>
<i>Amblyomma gemma</i>	HL vs MG	0.01**	0.82	0.18
	HL vs SGs	0.01**	0.01**	0.03*
	HL vs SL	0.59	0.94	1.0
	MG vs SGs	0.88	0.88	0.88
	MG vs SL	0.017	0.082	0.18
	SGs vs SL	0.01**	0.01**	0.07
<i>Rhipicephalus pulchellus</i>	HL vs MG	0.11	0.03	0.06
	HL vs SGs	0.61	0.91	0.61
	HL vs SL	0.2	0.34	0.34
	MG vs SGs	0.54	0.18	0.33
	MG vs SL	0.41	0.41	0.56
	SGs vs SL	0.26	0.35	0.35
<i>Hyalomma dromedarii</i>	HL vs MG	0.27	0.18	0.18
	HL vs SGs	0.39	0.48	0.82
	HL vs SL	0.25	0.13	0.13
	MG vs SGs	0.85	0.33	0.13
	MG vs SL	0.01**	0.01**	0.01**
	SGs vs SL	0.01**	0.01**	0.03*
<i>Hyalomma rufipes</i>	HL vs MG	0.27	0.18	0.18
	HL vs SGs	0.39	0.48	0.82
	HL vs SL	0.25	0.13	0.13
	MG vs SGs	0.85	0.33	0.13
	MG vs SL	0.01**	0.01**	0.01**
	SGs vs SL	0.01**	0.01**	0.03*

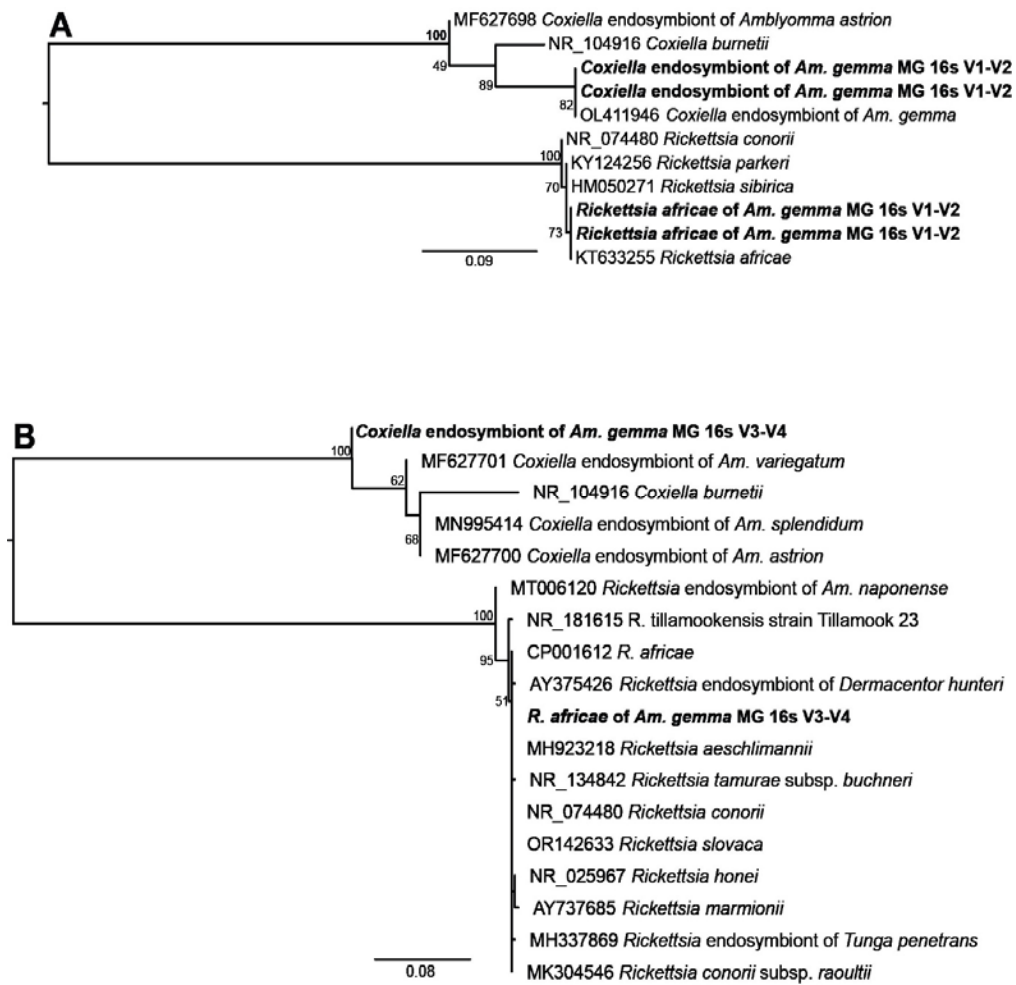
HL, hemolymph; MG, midgut; SGs, salivary glands; SL, saliva.
P-value (*P < 0.05, **P < 0.01, ***P < 0.001)

Supp. table 5: Alpha diversity of bacterial species communities P-values based on tissues in different tick species.

Tick tissue	Samples name	Chao1	Shannon	Pielou
<i>Hemolymph</i>	Ag vs Hd	1.00	0.10	0.93
	Ag vs Hr	0.43	0.34	0.34
	Ag vs Rp	0.41	0.53	0.41
	Hd vs Hr	0.56	0.29	0.56
	Hd vs Rp	0.49	0.34	0.49
	Hr vs Rp	0.73	0.56	1.00
<i>Midgut</i>	Ag vs Hd	0.67	0.84	0.10
	Ag vs Hr	0.73	0.56	0.29
	Ag vs Rp	0.01**	0.02*	0.09
	Hd vs Hr	0.11	0.11	0.73
	Hd vs Rp	0.01**	0.01**	0.09
	Hr vs Rp	0.02*	0.02*	0.06
<i>Salivary glands</i>	Ag vs Hd	0.27	0.84	0.23
	Ag vs Hr	0.37	0.64	0.27
	Ag vs Rp	0.14	0.09	0.10
	Hd vs Hr	0.85	0.79	1.00
	Hd vs Rp	0.02*	0.09	0.94
	Hr vs Rp	0.03*	0.03*	0.93
<i>Saliva</i>	Ag vs Hd	0.66	0.93	0.66
	Ag vs Hr	0.26	0.76	0.61
	Ag vs Rp	0.48	0.76	1.00
	Hd vs Hr	0.73	0.73	0.90
	Hd vs Rp	0.09	0.90	0.90
	Hr vs Rp	0.69	0.69	0.69

Ag, *Amblyomma gemma*; **Rp**, *Rhipicephalus pulchellus*; **Hd**, *Hyalomma dromedarii*; **Hr**, *Hyalomma rufipes*.

P-value (*P < 0.05, **P < 0.01, ***P < 0.001)



Supp. Figure 1: Maximum likelihood phylogenies of representative V1-V2 and V3-V4 16S rRNA gene sequences amplified from *Coxiella* and *Rickettsia* in tick tissues of camel ticks collected in Marasbit County. **A)** V1-V2 16S rRNA alignment **B)** V3-V4 16S rRNA sequences. The study sequences are highlighted in bold. The bootstrap values at the nodes are the indicating percentage agreement from 1000 replicates. The branch length scale represents the substitution per site.