

Supplementary Table S1: Study characteristics of tick-borne pathogens molecular surveys in cattle and buffaloes from Egypt.

Reference	Region	Host	Study Year	Sample size	No. positive (%)	Marker	Species	Molecular tools	Sequenced isolates	Accession numbers	
Mahmmod et al., 2010	Sharkeya, Dekhlia, Ismalia	Bovine	NS	30#	21 (70)	NS	<i>Th. annulata</i>	cPCR	-	-	
Abd Ellah and AL-Hosary, 2011	Assuit	cattle	NS	28	27 (96.42)	Tams-1	<i>Th. annulata</i>	cPCR	-	-	
Nayel et al., 2012	Menofia	cattle	NS	158	20 (12.66) 38 (24.05)	18S rRNA	<i>Babesia sp.</i> <i>Theileria sp.</i>	cPCR	-	-	
Ibrahim et al., 2013	Beheira and Faiyum	cattle	2011	151	8 (5.30)	RAP-1a	<i>B. bigemina</i>	nPCR	3	KF192810-KF192812	
		6 (3.97)			SBP-4	<i>B. bovis</i>	2	KF192806-KF192808			
		buffaloes		96	0 (0)	RAP-1a SBP-4	<i>B. bigemina</i>	2	KF192809		
					10 (10.42) 4 (4.17) 0 (0)		<i>B. bovis</i> Mixed sp.	1	KF192805		
Abdel Aziz et al., 2014	Sharkeya	cattle	NS	296	117 (39.5) 44 (14.8) 73 (24.7)	RRA RAP-1	<i>Babesia sp</i> <i>B. bovis</i> <i>B. bigemina</i>	nPCR	-	-	
Elhelw et al., 2014	NS	cattle	2008-2009	25	4 (16)	OspA	<i>B. burgdorferi</i>	cPCR	1	KC522030	
Ghoneim and El-Fayomy, 2014	Port Said	cattle	NS	64	44 (68.8)	Tams-1	<i>Th. annulata</i>	cPCR	2	KF765518 and KF765519	
AL-Hosary et al., 2015	Upper Egypt	cattle	2010-2013	210	97 (46.19)	Tams-1	<i>Th. annulata</i>	cPCR	4	KJ021626- KJ021629	
El-Ashker et al., 2015	Dakahlia	cattle	2012-2013	164	13	18S rRNA	<i>Babesia sp.</i>	cPCR DNA array cPCR	NS	Sequencing performed but, no GeneBank submitted accession numbers	
					12		<i>B. bovis</i>				
					2		<i>B. bigemina</i>				
Elsify et al., 2015	Menoufia, Behera, Giza, and Sohag	cattle	2013	439	35	16S rRNA	<i>A. marginale</i>	nPCR cPCR cPCR cPCR	11 10 14 3	AB917246-AB917257 AB917263-AB917274 AB917275-AB917302 AB917303 and AB917305	
					14 (3.18)		RAP-1				<i>B. bovis</i>
					35 (7.97)		AMA-1				<i>B. bigemina</i> , Mixed Babesia
					4 (0.9)		Tams-1				<i>T. annulata</i> ,
					42 (9.56) 3 (0.68)		MPSP				<i>T. orientalis</i>

		buffaloes		50	4 (0.9) 1 (2.00) 1 (2.00)	RAP-1 MPSP	Mixed Theleiria <i>B. bovis</i> <i>T. orientalis</i>	nPCR cPCR	1 1	AB917258 AB917306
Mahmoud et al., 2015	Kafr El-Sheikh, El-Beheira, Cairo	cattle	NS	253	38 (15.0) 82 (32.4) 22 (8.7)	rra rap-1c	<i>B. bovis</i> <i>B. bigemina</i> Mixed 2 sp.	nPCR	1 1	KM213000 KM212998
		buffaloes		81	3 (3.7) 0 (0.0)	rra rap-1c	<i>B. bovis</i> <i>B. bigemina</i>			
Elhaig et al., 2016	Ismailia, Sharkia and Qalubiya	cattle	2013-2014	500	55 (11)	18S rRNA	<i>B. bigemina</i>	cPCR	1	KM076937
AL-Hosary, 2017	Assuit	cattle	NS	76	13 (17.11) 20 (26.3) 20 (26.3)	18S rRNA	<i>B. bovis</i>	cPCR nPCR PCR-RLB	3	KM455548, KM455549 and KM455550
Abdel-Moein and Hamza, 2017	Giza	cattle buffaloes	NS	26 26	0 0	IS1111	<i>C. burnetii</i>	nPCR	-	-
ELHariri et al., 2017	Giza, Qalyoubia, El-Wadi El-Gadeed, Menofia	buffaloes	NS	150	104 (69.3)	msp1α	<i>A. marginale</i>	cPCR	-	-
Rizk et al., 2017	Menoufia, Behera, Giza, and Sohag	cattle	2013	439	49 (11.16) 45 (10.25)	RAP-1 AMA-1 Tams-1 MPSP	<i>Babesia</i> sp <i>B. bovis</i> <i>B. bigemina</i> <i>Theileria</i> sp. <i>T. annulata</i> <i>T. orientalis</i>	nPCR cPCR cPCR cPCR	5 2 5 2	AB917246, AB917251, AB917253, AB917255, and AB917257 AB917263 and AB917274 AB917275, AB917298, AB917299, AB917300 and AB917302 AB917303 and AB917304
AL-Hosary et al., 2018	EL-Wady EL-Geded	cattle	2015-2016	1068	679 (63.6) -----	Tams-1, 18Ss rRNA	<i>Th. annulata</i>	cPCR nPCR	13	KU550947- KU550959
Abdel-Baky and Allam, 2018	Variable	cattle	2014-2016	40	23 (17.83) 6 4 2 1 10	16S rRNA msp4 and hsp60	<i>Anaplasmataceae</i> <i>A. phagocytophilum</i> <i>A. marginale</i> <i>A. bovis</i> <i>A. centrale</i> <i>Anaplasma</i> spp.	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers

Allam et al., 2018	Variable	cattle	2014-2016	40	6 (5.88)	16S rDNA, OmpA and gltA	<i>Rickettsiae</i>	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers
El-Dakhly et al., 2018	El-Wadi El-Gadid	cattle	NS	376	43 (11.44)	Cytb1	<i>T. annulata</i>	cPCR	-	-
Anter et al., 2019¥	Sharkia	cattle buffaloes	2018	30# 29#	NS NS	Tams1	<i>T. annulata</i>	cPCR	1 1	MN251047 MN251046
AL-Hosary et al., 2020®	EL-Minia and Assiut, EL Fayoum, and New Valley	cattle	2018	309	211 (68.3) 155 (50.2) 49 (15.9) 18 (5.8) 2 (0.7) 1 (0.3%) 26 (8.4)	msp1β groEL 18S rRNA 18S rRNA 18S rRNA groEL	<i>A. marginale</i> <i>A. marginale</i> <i>T. annulata</i> <i>B. bovis</i> <i>B. bigemina</i> <i>B. occultans</i> <i>A. platys</i>	qPCR RLB RLB RLB RLB RLB		MN227687, MN227689-MN227692 MN223723-MN223737 MN227676-MN227679 MN227675
		buffaloes		85	25 (29.4) 36 (42.4) 1 (1.18) 2 (2.35) 4 (4.71)	msp1β groEL 18S rRNA 18S rRNA 16S rRNA	<i>A. marginale</i> <i>A. marginale</i> <i>T. annulata</i> <i>B. bigemina</i> <i>A. platys</i>	qPCR RLB RLB RLB RLB		MN202017-MN202023 and MN227688
Abbass et al., 2020	Assiut	cattle	2016-2017	38*	12 (31.6)	IS1111	<i>C. burnetii</i>	RT-qPCR	-	-
Abdel-Baky et al., 2020¥	NS	cattle	2014-2016	40	22.22%	OspA and flaB	<i>B. burgdorferi</i>	nPCR	-	-
El-Dakhly et al., 2020	Beni-Suef, El-Fayoum and El-Wadi El-Gadid	cattle	2015-2018	150	33 (22) 29 (19.33) 16 (10.6)	Tams1 SSrRNA msp1b	<i>T. annulata</i> <i>B. bigemina</i> <i>A. marginale</i>	cPCR cPCR cPCR	3 3 3	MH796632- MH796634 MH796638-MH796640 MH796635-MH796637
Nasreldin et al., 2020	New Valley	cattle	2017-2018	14#	12 14	msp1b VESA-1a	<i>A. marginale</i> <i>B. bovis</i>	cPCR cPCR	-	-
Tumwebaze et al., 2020	Menoufia	cattle	2017	92	5 (5.4) 6 (6.5) 14 (15.2) 13 (14.1) 9 (9.8)	SBP4 Rap1a groEL 16S rRNA	<i>B. bovis</i> <i>B. bigemina</i> <i>A. marginale</i> <i>Anaplasma</i> sp. (<i>A. platys</i> -like) Mixed <i>Anaplasma</i>	nPCR nPCR nPCR nPCR	4 3 4 6	MN870658-MN870661 MN870655-MN870657 MN870643-MN870646 MN861059-MN861064

		buffaloes		86	0 (0) 1(1.2) 0 (0.0) 1(1.2) 0 (0)	18S rRNA SBP4 Rap1a groEL 18S rRNA	<i>Theileria sp.</i> <i>B. bovis</i> <i>B. bigemina</i> <i>A. marginale</i> <i>Theileria sp.</i>	nPCR nPCR nPCR nPCR nPCR	1	MN870645
Parvizi et al., 2020a	variable	cattle	2015- 2016	758	40 (5.3)	-	<i>Anaplasma/Ehrlichia</i> <i>A. marginale</i>	qPCR	-	-
Yousef et al., 2020	Sharkia	cattle	2019	25#	25	Tams1	<i>T. annulata</i>	cPCR	-	-
Abdullah et al., 2021a	variable	cattle	2019- 2020	112	6 (5.36) 1 (0.89) 0 (0)	ITS 16S rRNA gltA	<i>Bartonella sp.</i> <i>Borrelia theileri</i> <i>Rickettsiae</i>	cPCR	1 1	MW596416 MW562684
		buffaloes		26	3 (11.54) 0 (0.0) 0 (0)	ITS 16S rRNA gltA	<i>Bartonella sp.</i> <i>Borrelia theileri</i> <i>Rickettsiae</i>		1	MW596417
Abdullah et al., 2021b	Beni-Suef, Qalyubia, El-Wady El-Geded, Qena, Beheira	cattle	2016- 2018	88	15 (17) 14 (15.9) 1 (1.1) 25 (28.4) 18 (20.4) 1 (1.1) 3 (3.4) 3 (3.4) 3 (3.4) 0 0 0 0	5.8S rRNA 18S rRNA 18S rRNA 23S rRNA Ana-rpoB Ana-rpoB Ana-rpoB Ana-rpoB 16S rRNA 16S RNA gltA IS1111 ITS3	<i>Piroplasmida</i> <i>T. annulata</i> <i>Ba. bigemina</i> <i>Anaplasmataceae</i> <i>An. marginale</i> <i>An. centrale</i> <i>An. ovis</i> <i>An. platys-like</i> <i>Borrelia sp.</i> <i>Bo. theileri</i> <i>Rickettsia sp.</i> <i>C. burnettii</i> <i>Bartonella sp</i>	qPCR nPCR nPCR qPCR cPCR cPCR cPCR cPCR qPCR cPCR qPCR qPCR		MN625888 and MN625889 MN625890 MN625935, MN626393, MN624134 MN626394 MN625933, MN624133 MN626397, MN626400, MN624137 MN621893
		buffaloes		26	2 (7.7) 2 (7.7) 2 (7.7) 2 (7.7) 0 0 0	5.8S rRNA 18S rRNA 23S rRNA Ana-rpoB gltA IS1111 ITS3	<i>Piroplasmida</i> <i>T. ovis</i> <i>Anaplasmataceae</i> <i>An. platys-like</i> <i>Rickettsia sp.</i> <i>C. burnettii</i> <i>Bartonella sp</i>	qPCR cPCR qPCR cPCR qPCR qPCR qPCR		MN625887 MN626399, MN624139
AL-Hosary et al. 2021b	Faiyum, Assiut and Kharja	cattle	2018	41	39 38 2	18S rRNA 16S rRNA 18S rRNA	<i>T. annulata</i> <i>An. marginale</i> <i>B. bovis</i>	RLB, cPCR		MN223728:MN223732 MN370071:MN370075

					2	18S rRNA	<i>B. bigemina</i>			MN227677 and MN227679
					1	18S rRNA	<i>B. occultans</i>			
El Damaty et al., 2021¥	El-Sharkia	cattle buffaloes	2019-2020	48/22	24/9	Tams-1, 18s rRNA	<i>T. annulata</i>	cPCR	-	-
Selim et al., 2021a	Kafr El-Sheikh, Menofia, and Al-Gharbia	cattle	2020	130*	130 (100) 0 0	MSP4	<i>A. marginale</i> <i>A. centrale</i> <i>A. bovis</i>	cPCR	2	MZ695054 and MZ695055
Barghash, 2022	Sinai	cattle	2020-2021	74	18 (24.32) 0 (0) 30 (40.54)	BbSBP-4 RAP-1a tams1	<i>B. bovis</i> <i>B. bigemina</i> <i>T. annulata</i>	cPCR	1 1	MZ197893 MZ197896
Selim et al., 2022b	Gharbia, Beheira, Kafr ElSheikh, Menofia	cattle	2020	500	44 (8.8)	MPSP	<i>T. orientalis</i>	cPCR	3	LC661355-LC661357
Selim et al., 2022c	Alexandria, Beheira, Kafr El Sheikh, Qalyubia, Menofia	cattle	2019-2020	570	94 (16.49)	Tams-1	<i>T. annulata</i>	cPCR	2	LC549653 and LC549654

*Seropositive samples

#Positive by microscopy

@Infections were detected using qPCR for *A. marginale* and PCR-RLB followed by sequencing for all detected pathogens as well as conventional and semi-nested PCRs/sequencing for confirmations of genotyping results.

¥ Studies not included in Meta-analysis.

Abbreviations: **AMA-1**; Apical Membrane Antigen-1, **BbSBP-4**; *B. bovis* Rhoptry Associated Protein-4, **cytb**; Cytochrome b, **gltA**; Citrate synthase, **groEL**; 'heatshock operon', **hspB**; Heat shock protein antigenic polypeptide, **IS1111**; *C. burnetii* transposon-like sequence, **ompA**; Outer membrane protein A, **MPSP**; Major Piroplasm Surface Protein gene, **mSP1b**; major surface protein-1b gene, **ospA**; Outer surface protein A. gene, **RAP-1**; Rhoptry Associated Protein-1, **RRA**; Rhoptry associated protein related antigen, **SSrRNA**; small subunit ribosomal RNA gene, **Tams-1**; *Theileria annulata* 30 KDa major merozoite surface antigen-1 gene

Supplementary Table S2: Study characteristics of tick-borne pathogens molecular surveys in sheep and goats from Egypt.

Reference	Region	Host	Study Year	Sample size	No. positive (%)	Marker	Species	Molecular tools	Sequenced isolates	Accession numbers
Elsify et al., 2015	Menoufia, Behera, Giza	sheep	2013	105	1 (0.95) 2 (1.90)	RAP-1 AMA-1	<i>B. bovis</i> <i>B. bigemina</i>	nPCR cPCR	1 2	AB917259 AB917260-AB917262
Khalifa et al., 2016	Qaluobia	sheep goats	2014- 2015	23* 27*	21 (91.3) 23 (85.2)	IS1111	<i>C. burnetii</i>	trans-PCR	-	-
Abdel-Moein and Hamza, 2017	Giza	goats sheep	NS	29# 27	1 (3.4) 0	IS1111	<i>C. burnetii</i>	nPCR	1	KU977532
Abdel-Baky and Allam, 2018	Variable	sheep	2014- 2016	120	41 (31.78) 12 2 5 2 20	16S rRNA msp4 and hsp60	<i>Anaplasmataceae</i> <i>A. phagocytophilum</i> <i>A. marginale</i> <i>A. ovis</i> <i>A. platys</i> <i>Anaplasma spp.</i>	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers
Allam et al., 2018	Variable	sheep	2014- 2016	110	30 (29.41)	16S rDNA, OmpA and gltA	<i>Rickettsiae</i>	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers
Selim et al., 2018	Menoufia, Qalubia, Alexandria and Gharbia	sheep goats	2015– 2016	110 80	37 (33.6) 13 (16.3)	icd	<i>C. burnetii</i>	qPCR	-	-
Selim et al., 2019	Alexandria	sheep	NS	21® 6 3	21 6 3	IS1111 - -	<i>C. burnetii</i>	qPCR MLVA MST	-	-
Abbass et al., 2020	Assiut	sheep goats	2016- 2017	30* 18*	14 (46.7) 8 (44.4)	IS1111	<i>C. burnetii</i>	RT-qPCR	-	-
Abdel-Baky et al., 2020¥	NS	sheep	2014- 2016	120	37.04%	OspA and flaB	<i>B. burgdorferi</i>	nPCR	-	-
Tumwebaze et al., 2020	Menoufia	sheep	2017	66	0 (0) 6 (9.1)	ssu rRNA msp4	<i>B. ovis</i> <i>A. ovis</i>	cPCR cPCR	4	MN882167- MN882170
Abdullah et al., 2021a	variable	sheep goats	2019- 2020	38 28	3 (7.89) 1 (3.57)	ITS	<i>Bartonella sp.</i>	cPCR	-	-

Abdullah et al., 2021b	Giza, Beni-Suef, Qalyubia, Sinai	sheep	2016-2018	58	5 (8.6)	5.8S rRNA	<i>Piroplasmida</i>	qPCR	MN625886	
					5 (8.6)	18S rRNA	<i>T. ovis</i>	nPCR		
					4 (6.9)	23S rRNA	<i>Anaplasmataceae</i>	qPCR		
					2 (3.4)	Ana-rpoB	<i>An. marginale</i>	cPCR		
					1 (1.7)	Ana-rpoB	<i>An. ovis</i>	cPCR		
					1 (1.7)	Ana-rpoB	<i>An. platys-like</i>	cPCR		
					2 (3.4)	16S rRNA	<i>Borrelia sp.</i>	qPCR		
					2 (3.4)	16S rRNA	<i>Bo. Theileri</i>	cPCR		
					1 (1.7)	IS1111	<i>Coxiella burnetii</i>	qPCR		
					0	gltA	<i>Rickettsia sp.</i>	qPCR		
					0	ITS3	<i>Bartonella sp</i>	qPCR		
		goats	33	1 (3)	IS1111	<i>Coxiella burnetii</i>	qPCR			
				0	5.8S rRNA	<i>Piroplasmida</i>	qPCR			
				0	23S rRNA	<i>Anaplasmataceae</i>	qPCR			
				0	16S rRNA	<i>Borrelia sp.</i>	qPCR			
				0	gltA	<i>Rickettsia sp.</i>	qPCR			
				0	ITS3	<i>Bartonella sp</i>	qPCR			
Al-Hosary et al., 2021a	Menoufia, Beheira, El-Wady El-Geded	sheep	2014	115	6 (5.22)	18S rRNA	<i>Theileria sp.</i>		AB986193 and AB986194	
					5 (4.37)		<i>T. ovis</i>	cPCR	5	KY494648- KY494650
					1 (0.87)		<i>T. lestoquardi</i>	nPCR	1	KY494651
Barghash, 2022	Sinai	sheep	2020-2021	108	11(10.19)	BbSBP-4	<i>B. bovis</i>	cPCR	1	MZ197895
					22(20.37)	tams1	<i>T. annulata</i>		1	MZ197898
		goats		48	8(16.67)	BbSBP-4	<i>B. bovis</i>		1	MZ197894
					24(50.00)	tams1	<i>T. annulata</i>		1	MZ197897
Ben Said et al., 2022	Gharbia, Kafr Elsheikh, Menofia, Alexandria	sheep	2020	355	55 (15.5)	msp4	<i>A. ovis</i>	cPCR	4	OL859531 to OL859534

*Seropositive samples

placental cotyledons and vaginal discharges were examined from aborted animals.

@Vaginal swabs from aborted sheep

¥ Studies not included in Meta-analysis.

Abbreviations: **ama-1**; Apical membrane antigen 1 genes, **Ana-rpoB**; Anaplasma gene encoding the β -subunit of RNA polymerase, **BbSBP-4**; B. bovis Rhoptry Associated Protein-4; **IS1111**; C. burnetii transposon-like sequence, **mSP4**; Merozoite surface protein 4, **icd**; iso citrate dehydrogenase gene, **MST**; Multi-spacer sequence typing, **MLVA**, Multiple-locus variable-number tandem repeat analysis, **rap-1**; Rhoptry-associated protein 1 gene, **SSU rRNA**; small subunit ribosomal RNA.

Supplementary Table S3: Study characteristics of tick-borne pathogens molecular surveys in equines from Egypt.

Reference	Region	Host	Study Year	Sample size	No. positive (%)	Marker	Species	Molecular tools	Sequenced isolates	Accession numbers
Mahdy et al., 2016	Giza and Cairo	horses donkeys	NS	168 133	104 (61.9) 67 (50.4)	EMA-1	<i>T. equi</i>	nPCR	1	KX262963
Mahmoud et al., 2016	Giza	horses donkeys	NS	88 51	32 (36.4) 17 (19.3) 22 (43.1) 8 (15.7)	ema-1 rap-1 ema-1 rap-1	<i>T. equi</i> <i>B. caballi</i> <i>T. equi</i> <i>B. caballi</i>	nPCR	3	KR811095- KR811097
Kuraa and Nageib, 2017	Assiut	donkeys	NS	50	19 (38)	B1	<i>T. equi</i>	cPCR	-	-
El-Seify et al., 2018	Giza and Cairo	horses donkeys mules	2015- 2016	45 50 5	11 (24.4) 18 (36) 1 (20)	18S rRNA	<i>T. equi</i>	cPCR	1 1 1	MF192854 MF192856 MF192855
El-Sayed et al., 2020	Menoufia, Mersa Matruh, Giza	donkeys	2017	149	9 (6.04)	EMA-1	<i>T. equi</i>	nPCR	1	LC269846
Al-Araby et al., 2021	Dakahlia	horses	NS	147	14 (9.52)	EMA-1	<i>T. equi</i>	nPCR	-	-
Abdullah et al., 2021a	variable	horses donkeys	2019- 2020	8 22	1 (12.5) 2 (9.09)	ITS	<i>Bartonella sp.</i>	cPCR	-	-
Elsawy et al., 2021	Cairo, Giza, Almonofia, Al fayoum, Beni Suef, Ismailia, and Alexandria	horses donkeys	NS	79 76	16 (20.3) 1 (1.2) 42 (53.1) 3 (4.5) 10 (13.1) 0 (0.0) 29 (38.1) 18 (26.8)	18S rRNA	<i>T. equi</i> <i>B. caballi</i> <i>T. haneyi</i> Mixed <i>Theleiria</i> <i>T. equi</i> <i>B. caballi</i> <i>T. haneyi</i> Mixed <i>Theleiria</i>	mPCR mPCR cPCR mPCR mPCR cPCR	5 1 2 4 1 3	MW659071- MW659075 MW678758 MW591694, MW591695 MW659076 -MW659079 MW678759 MW591692, MW591693, MW591697

Abdullah et al., 2022	Cairo, Beni Suef	horses	2009	320	13 (4.1)	5.8S rRNA	Piroplasmida	qPCR		
					4 (1.3)	18S rRNA	<i>Th. equi</i>	nPCR	2	MN625897 and MN625898
					9 (2.8)	18S rRNA	<i>Th. sp. Africa</i>	nPCR	4	MN625900- MN625903
					0	gltA	Rickettsia sp.	qPCR		
					0	16S rRNA	Borrelia sp.	qPCR		
					0	IS1111	<i>C. burnetii</i>	qPCR		
					0	ITS3	Bartonella sp.	qPCR		
					4 (26.6)	23S rRNA	Anaplasmataceae	qPCR		
		donkeys		15	2 (13.3)	23S rRNA	<i>A. marginale</i>	cPCR	1	MN614103
					2 (13.3)	23S rRNA	<i>A. ovis</i>	cPCR	1	MN614104
					2 (13.3)	5.8S rRNA	Piroplasmida	qPCR		
					2 (13.3)	18S rRNA	<i>Th. ovis</i>	nPCR	2	MN625886 and MN625887
					0	gltA	Rickettsia sp.	qPCR		
					0	16S rRNA	Borrelia sp.	qPCR		
					0	IS1111	<i>C. burnetii</i>	qPCR		
					0	ITS3	Bartonella sp.	qPCR		

Abbreviations: EMA-1; T. equi merozoite antigen-1, **gltA**; Citrate synthase, **IS1111**; C. burnetii transposon-like sequence, **rap-1**; Rhoptry-associated protein 1 gene

Supplementary Table S4: Study characteristics of tick-borne pathogens molecular surveys in dromedary camels (*Camelus dromedarius*) from Egypt.

Reference	Region	Study Year	Sample size	No. positive (%)	Marker	Species	Molecular tools	Sequenced isolates	Accession numbers
Youssef et al., 2015	Giza	2009	30	21 (70) 18 (60)	SSU rRNA 30-KDa	<i>Theileria spp.</i> <i>T. annulate</i>	cPCR	-	-

				3 (10)		<i>Theileria spp.</i>			
Abou El-Naga and Barghash, 2016	Matrouh	2012-2015	331	223 (67.37) 223 (67.37) 172 (51.96) 238 (71.9) 61 (18.43) 36 (10.87) 25 (7.55)	msp1β - SSU rRNA CPS II SSU rRNA	<i>Anaplasma sp.</i> <i>A. marginale</i> <i>A. centrale</i> <i>Th. Camelensis</i> <i>Babesia sp.</i> <i>B. bovis</i> <i>B. bigemina</i>	cPCR	-	-
Abdullah et al., 2018	Cairo, Giza, and Sinai	2017	113	52 (46)	IS30A	<i>C. burnetii</i>	cPCR	-	-
Abd El-Baky and Allam, 2018	Variable	2014-2016	110	65 (50.39) 20 10 6 5 6 5 13	16S rRNA msp4 and hsp60	<i>Anaplasmataceae</i> <i>A. phagocytophilum</i> <i>A. marginale</i> <i>A. ovis</i> <i>A. bovis</i> <i>A. centrale</i> <i>A. platys</i> <i>Anaplasma spp.</i>	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers
Allam et al., 2018	Variable	2014-2016	120	66 (64.71)	16S rDNA, OmpA and gltA	<i>Rickettsiae</i>	cPCR	-	Sequencing performed but, no GeneBank submitted accession numbers
Abdullah et al., 2019a	Giza and Cairo	NS	112	19 (16.9)	IS1111	<i>C. burnetii</i>	qPCR	-	-
Abdullah et al., 2019b	Cairo, Giza and Sinai	2013-2014	61	25 (41)	OmpA and gltA	<i>Rickettsiae</i> <i>R. africae</i>	cPCR		U83436.2
Abdel-Baky et al., 2020	NS	2014-2016	110	40.74%	OspA and flaB	<i>B. burgdorferi</i>	nPCR	-	-
Abdullah et al., 2021b	Cairo, Giza, Sinai	2016-2018	149	10 (6.7) 1 (0.7) 1 (0.7) 8 (5.4) 0 0 0 0 0	23S rRNA Ana-rpoB Ana-rpoB Ana-rpoB 5.8S rRNA 16S rRNA gltA IS1111 ITS3	<i>Anaplasmataceae</i> <i>An. marginale</i> <i>An. platys</i> <i>An. platys-like</i> <i>Piroplasmida</i> <i>Borrelia sp.</i> <i>Rickettsia sp.</i> <i>C. burnetii</i> <i>Bartonella sp.</i>	qPCR cPCR cPCR cPCR qPCR qPCR qPCR qPCR qPCR		MN625938 MN625937 MN626396, MN626401

El-Sayed et al. 2021	Halayeb and	2017	142	4 (2.81)	RAP-1	<i>B. bovis</i>	nPCR	1	MF737083
Rizk et al., 2021	Shalateen			17 (11.97)	SSU rRNA	<i>Babesia microti</i>	nPCR	1	MF737082
Mohamed et al., 2021	Abu Simbel	NS	100	29 (29)	16S rDNA	<i>Anaplasmataceae</i>	cPCR	28	LC592622-LC592650
					groEL	<i>Ca. An. camelii</i>		10	LC592667- LC592677
					gltA			10	LC592678-LC592688

Abbreviations: **Ana-rpoB**; Anaplasma gene encoding the β -subunit of RNA polymerase, **CPS II**; gene encoding the enzyme carbamoyl phosphate synthetase II, **gltA**; Citrate synthase, **groEL**; ‘heatshock operon’ **IS1111**; *C. burnetii* transposon-like sequence, **msp1 β** ; Major surface protein–1 β encoding gene, **msp4**; Merozoite surface protein 4, **ompA**; Outer membrane protein A, **rap-1**; Rhoptry-associated protein 1 gene, **SSU rRNA**; small subunit ribosomal RNA.

‡ Studies not included in Meta-analysis

Supplementary Table S5: Study characteristics of tick-borne pathogens molecular surveys in dogs from Egypt.

Reference	Region	Study Year	Sample size	No. positive (%)	Marker	Species	Molecular tools	Sequenced isolates	Accession numbers
Elhelw et al., 2014	NS	2008-2009	26	6 (23)	OspA	<i>B. burgdorferi</i>	cPCR	1	KC522030
Salem and Farag, 2014	Giza	2011-2012	13*	13	18S rRNA	<i>B. vogeli</i>	nPCR	-	-
El-Neshwy et al., 2020	Sharkia and Dakahlia	2018-2019	75	14 (18.67)	18s rRNA	<i>B. vogeli</i>	nPCR	-	-
Abdullah et al., 2021b	Cairo	2016-2018	203	1 (0.5) 1 (0.5)	5.8S rRNA 18S rRNA	<i>Piroplasmida</i> <i>Ba. canis</i>	qPCR nPCR		MN625891

				7 (3.4)	23S rRNA	<i>Anaplasmataceae</i>	qPCR		
				7 (3.4)	Ana-rpoB	<i>An. platys</i>	cPCR		MN625936, MN626395, MN624140
				3 (1.5)	gltA	<i>Rickettsia sp.</i>	qPCR		
				3 (1.5)	OmpB	<i>Rickettsia africae-like</i>	nPCR		MN629892, MN629893
				0	IS1111	<i>C. burnettii</i>	qPCR		
				0	ITS3	<i>Bartonella sp</i>	qPCR		
				0	16S rRNA	<i>Borrelia sp.</i>	qPCR		
Elhelw et al., 2021	Giza Cairo	2017	100	1 (1.67)	16S rRNA	<i>B. burgdorferi</i>	cPCR	1	MH685928
El-Dakhly et al., 2021 [‡]	Alexandria	NS	70	14 (20)	16sRNA	<i>Anaplasma/Ehrlichia</i>	cPCR	-	-
Selim et al., 2021b	Cairo, Giza, Qalyubia, Gharbia and Kafr El Sheikh	2019- 2020	500	32 (6.4)	16S rRNA	<i>A. platys</i>	cPCR	1	LC632659
Selim et al., 2021c	Cairo, Giza, and Qalyubia	NS	400	39 (9.7)	16S rRNA	<i>E. canis</i>	cPCR	1	LC490598
Zaki et al., 2021	Cairo	2017- 2019	242	62 (25.62)	18S rRNA	<i>B. vogeli</i>	cPCR	1	MT565474
Izenour et al., 2022	Cairo	2019	116	1	groEL	<i>Anaplasma sp.</i>	cPCR	1	MW557303
				1	18S rRNA	<i>Babesia sp.</i>		1	MW556745
				2	16S rRNA	<i>Ehrlichia sp.</i>			
				1	16S rRNA	<i>Borrelia sp.</i>			
				0	ssrA	<i>Bartonella sp.</i>			
Selim et al., 2022a	Giza, Kafr El Sheikh, Qalyubia and Gharbia	2019	275	14 (5.1)	18S rRNA	<i>B. vogeli</i>	cPCR	1	LC651125

*Samples from dogs with clinical signs of babesiosis and also were positive by microscopy.

[‡] Studies not included in Meta-analysis

Abbreviations: **Ana-rpoB**; Anaplasma gene encoding the β -subunit of RNA polymerase, **gltA**; Citrate synthase, **groEL**; ‘heatshock operon’ **ompB**; Outer membrane protein B, **ospA**; Outer surface protein A. gene.

Supplementary Table S6: Study characteristics of molecular surveys of pathogens in ticks infesting livestock animals from Egypt.

Reference #	Host	No. infested (%)	Tick species (N.) ®	Pathogens	Marker	No. positive (%)
Adham et al., 2009 ¹	NS	-	Boophilus annulatus	<i>B. bovis</i> <i>B. bigemina</i>	SSrRNA	55/100 (55) 66/100 (66)
Adham et al., 2010 ¹	NS	-	B. annulatus H. dromedarii H. excavatum R. sanguineus A. lepidum O. savignyi	<i>B. burgdorferi</i>	OspC	4/50 (8) 7/28 (25) 12/24 (50) 2/23 (8) 4/14 (28) 31/47 (66)
Allam et al., 2018 ¹	Camels Cattle Sheep	33.62% 59.03% 7.35%	A. gemma A. lepidum A. variegatum B. annulatus H. albiparmatum H. a. excavatum H. dromedarii H. impeltatum H. m. rufipes H. m. marginatum H. truncatum Rh. humeralis Rh. pulchellus Rh. sanguineus	<i>Rickettsiae</i> sp. R. aeschlimannii-like R. africae-like R. sibirica mongolitimonae-like	16S rDNA, OmpA and gltA	15/51 (4.78) 20/67 (6.37) 5/55 (1.59) 5/2922 (1.59) 6/25 (1.91) 24/127 (7.64) 112/1288 (35.67) 24/91 (7.64) 24/53 (7.64) 24/105 (7.64) 16/90 (5.10) 8/20 (2.55) 12/22 (3.82) 19/307 (6.05)
Chisholm et al., 2012 ^{1¶}	Cattle, buffalo, sheep, camels	NS	Hyalomma (138 pools) H. excavatum H. dromedarii	CCHFV	RT-PCR-S segment	6/138 (4.34) 1 5
Elhelw et al., 2014	cattle	NS	H. anatolicum excavatum	<i>B. burgdorferi</i>	OspA	3/14 (21.4)
ELHariri et al., 2017 [¶]	buffaloes	NS	Rhipicephalus (280), Boophilus (150), H. an. anatolicum (30), and H. a. excavatum (40).	<i>A. marginale</i>	msp1α	130/150 (86.6)

Hassan et al., 2017	cattle		R. annulatus	<i>B. theileri</i>	flab	10/172 (5.8)
				<i>B. bigemina</i>	18S rRNA	2/172 (1.16)
	camels		O. savignyi	<i>B. theileri</i>	flab	6/611 (1)
Abdel-Baky et al., 2020 ¹ ¥	camels,		A. variegatum	<i>B. burgdorferi</i>	OspA and	43.24%
	cattle,		A. lepidum		flaB	30.63%
	sheep		B. annulatus			26.13%
AL-Hosary et al. 2021b¥	cattle	NS	H. excavatum	<i>Theileria annulata</i>	RLB and	18.1 %
				<i>Babesia occultans</i>	variable	1.8 %
				<i>An. marginale</i>	targets	28.5 %
				<i>Anaplasma platys</i>		0.25 %
				<i>Midich. mitochondrii</i>		11.6 %
				<i>Ehrl. chaffeensis-like</i>		1.8 %
				<i>Ehrlichia minasensis</i>		1 %
			R. annulatus	<i>T. annulata</i>		2.3 %
				<i>B. bovis</i>		0.6 %
				<i>A. marginale</i>		18.0 %
				<i>A. platys</i>		1.2 %
				<i>M. mitochondrii</i>		2.9 %
				<i>E. minasensis</i>		0.6 %
Abdullah et al., 2022	equines	NS	R. annulatus (61)	Anaplasmataceae	23S rRNA	9 (14.7)
				<i>A. platys-like</i>	23S rRNA	1 (1.6)
				<i>A. marginale</i>	23S rRNA	1 (1.6)
				<i>Candidatus E. rustica</i>	23S rRNA	4 (6.6)
				<i>Ehrlichia sp.</i>	23S rRNA	3 (4.9)
				<i>Borrelia sp.</i>	16S rRNA	2 (3.3)
				<i>B. theileri</i>	16S rRNA	2 (3.3)
Abdel-Shafy et al., 2012	camels	10	H. dromedarii (42)	<i>R. africae</i> and <i>R. aeschlimannii</i>	gltA	8 (19.04)
			H. impeltatum (15)		ompA,	15 (100)
			H. marginatum (5)		ompB, Sca4	1 (20)
Abdullah et al., 2016	camels	NS	H. marginatum (5)	<i>Rickettsia sp.</i>	OmpA and gltA	1 (20)
Barghash et al., 2016¥	camels	212 (85.14)	H. dromedarii (73.65%), H. rufipes (12.03%), H. truncatum (6.62%), H. anatolicum excavatum (4.73%), H. impeltatum	<i>T. evansi</i> , <i>T. brucei</i> , <i>B. bovis</i> , <i>B. bigemina</i> and <i>Theileria sp.</i> , <i>A. marginale</i> , <i>Histophilus somni</i> , <i>Pasteurella multocida</i> and	Variable	NS

			(1.62%), and others (1.35%).	<i>Mycoplasma spp.</i>		
Abdullah et al., 2018	camels	NS	H. dromedarii (177)	<i>C. burnetii</i>	IS30A	10/190 (5.3)
Abdullah et al., 2019b	camels	NS	Hayalomma spp. (99) H. marginatum (5/99)	<i>Rickettsia spp. (R. africae)</i>	OmpA and gltA	1/99 (1.01) 1/5 (20)
Ghoneim et al., 2020	camels	181 (100)	H. dromedarii (259) A. variegatum (18) H. anatolicum anatolicum (19) R. pulchellus (28)	<i>C. burnetii</i>	IS1111	17 (6.6) 1 (5.6) 1 (5.3) 1 (3.6)
Bendary et al., 2022	camels	NS	H. dromedarii (837 pools) H. rufipes (411 pools)	CCHFV	RT-PCR-S segment	11 (1.3) 7 (1.7)
Ghaffar and Amer, 2012	dogs	NS	R. sanguineus (401)	A. phagocytophilum	16S rRNA	55/401 (13.7)
Elhelw et al., 2014	dogs	NS	R. sanguineus (12)	<i>B. burgdorferi</i>	OspA	7 (58.3)
Abdullah et al., 2016	dogs	NS	R. sanguineus (597)	<i>Rickettsia sp.</i>	OmpA and gltA	4/71 (5.6)
Nasr et al., 2020	dogs	156	R. sanguineus (156 pools)	<i>A. platys</i> <i>E. canis</i>	16S rRNA	2 (1.32) 3 (1.98)
Elhelw et al., 2021	dogs	69 (69)	R. sanguineus (60)	<i>B. burgdorferi</i>	16S rRNA	1 (1.67)

The collected ticks were morphologically identified using published identification keys and additionally some molecular markers were used.

® Tick species and genera examined for pathogens using molecular markers

¹ These articles identified pathogens in ticks' pools collected from various hosts

¥ Studies were not included in Meta-analysis

Abbreviated Tick genus: **A.**; Amblyomma, **D.**; Dermacentor, **H.**; Hyalomma, **R.**; Rhipicephalus, **O.**; Ornithodoros

Abbreviations: **flaB**; encoding flagellin B, **gltA**; Citrate synthase gene, **groEL**; 'heatshock operon', **IS1111**; *C. burnetii* transposon-like sequence, **ompA**; Outer membrane protein A, **ompB**; Outer membrane protein B, **ospA**; Outer surface protein A. gene, **Sca4**; Cell surface antigen-4 (gene D).

Supplementary Table S7: Haplotypes of *T. annulata* Tams-1 isolates from ruminant animals in Egypt.

Haplotype	Accession number	Host	Region
Ta-1	AB917277.1	Cattle	Menoufia
Ta-2	AB917296.1	Cattle	Menoufia
Ta-3	AB917298.1	Cattle	Menoufia
Ta-4	AB917284.1	Cattle	Behera
	AB917285.1	Cattle	Giza
	AB917293.1	Cattle	Menoufia
Ta-5	AB917287.1	Cattle	Giza
Ta-6	KJ021629.1	Cattle	El-Fayoum
Ta-7	MN251047.1	Cattle	Sharkia
	MN251046.1	Buffalo	Sharkia
	MZ197896.1	Cattle	Sinai
	MZ197898.1	Sheep	Sinai
Ta-8	AB917294.1	Cattle	Menoufia
	AB917295.1	Cattle	Menoufia
Ta-9	KJ021627.1	Cattle	Assiut
Ta-10	KF765518.1	Cattle	Port-Said
Ta-11	KF765519.1	Cattle	Port-Said
Ta-12	AB917281.1	Cattle	Behera
Ta-13	AB917286.1	Cattle	Giza
Ta-14	AB917289.1	Cattle	Giza
Ta-15	AB917278.1	Cattle	Menoufia
Ta-16	AB917280.1	Cattle	Behera
Ta-17	AB917283.1	Cattle	Behera
Ta-18	AB917300.1	Cattle	Menoufia
Ta-19	MZ197897.1	Goat	Sinai
Ta-20	AB917290.1	Cattle	Giza
Ta-21	AB917275.1	Cattle	Menoufia
Ta-22	AB917288.1	Cattle	Giza

Ta-23	AB917276.1	Cattle	Menoufia
Ta-24	AB917297.1	Cattle	Menoufia
Ta-25	AB917279.1	Cattle	Behera
	AB917282.1	Cattle	Behera
	AB917291.1	Cattle	Behera
	AB917292.1	Cattle	Behera
Ta-26	AB917301.1	Cattle	Menoufia
Ta-27	AB917302.1	Cattle	Menoufia
Ta-28	MH796634.1	Cattle	New Valley
	LC549654.1	Cattle	NS
Ta-29	KJ021628.1	Cattle	New Valley
Ta-30	MH796632.1	Cattle	New Valley
Ta-31	AB917299.1	Cattle	Menoufia
Ta-32	KJ021626.1	Cattle	El-Fayoum
Ta-33	MH796633.1	Cattle	New Valley
	LC549653.1	Cattle	NS