

Meta-Analysis

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Tick-borne pathogens in Iran: A meta-analysis

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ABSTRACT

Objective: Different studies have been performed on the prevalence of tick-borne pathogens in different areas of Iran; however, as far as our knowledge, there is no regional meta-analysis available for consideration and estimation of tick species infected with different pathogens in Iran.

Methods: In this review, among different databases, a total of 95 publications were included, and the infection of different tick species to different tick-borne pathogens was determined; furthermore, presence of pathogens (with 95% confidence intervals) in tick vectors was calculated separately for each province, using Comprehensive Meta-Analysis version 2 (Biostat, USA).

Results: Totally, among all 95 studies, 5673 out of 33521 investigated ticks were positive according to different detection methods. Overall estimated presence of pathogens in tick vectors in Iran was 8.6% (95% CI 7.0%-10.6%, P<0.001). Of all 46 species of ticks in 10 genera in Iran, 28 species in 9 genera, including Alveonasus, Argas, Boophilus, Dermacentor, Haemaphysalis, Hyalomma, Ixodes, Ornithodoros, and Rhipicephalus were infected with at least 20 pathogens in 10 genera including Aegyptianella, Anaplasma, Babesia, Borrelia, Brucella, Orthonairovirus [Crimean-Congo hemorrhagic fever virus (CCHFV)], Coxiella, Ehrlichia, Rickettsia and Theileria in 26 provinces of Iran. The presence of pathogens in ticks collected in western Iran was more than other regions. Hyalomma anatolicum (20.35%), Rhipicephalus sanguineus (15.00%), and Rhipicephalus bursa (14.08%) were the most prevalent infected ticks for different pathogens. In addition, most literatures were related to CCHFV and *Theileria/Babesia* spp.

Conclusions: Public health and veterinary professionals should be aware of diagnosing possible diseases or outbreaks in vertebrates.

KEYWORDS: Ticks; Tick-borne diseases; Vector-borne diseases; Iran

1. Introduction

Ticks are external obligatory blood-sucking parasites of vertebrates (phylum Arthropoda; class Arachnida) that fall into three families including Ixodidae (hard ticks), Argasidae (soft ticks), and Nuttalliellidae[1]. Ticks are the primary vectors and reservoirs for different pathogens including viruses, bacteria, and protozoa all over the world, which pose significant threats to human and animal health[2,3]. Tick-borne pathogens cause thousands of disease cases in human populations worldwide with the animal cases seeming to be more than humans[4]. Different species of ticks are able to transmit different diseases. And Crimean-Congo hemorrhagic fever (CCHF), Colorado tick fever, Q fever, borreliosis, relapsing fever, theileriosis, babesiosis, anaplasmosis, ehrlichiosis and Rocky Mountain spotted fever are

Significance

Several studies have shown the presence of tick-borne pathogens in ticks in Iran; however, as far as our knowledge, there is no meta-analysis available for estimation of ticks infected with tick-borne pathogens. Our analysis showed that the overall estimated presence of pathogens in tick vectors in Iran was 8.6% (95% CI 7.0%-10.6%, P<0.001). Furthermore, 28 tick species in 9 genera were found to be infected with at least 20 pathogens in 10 genera.

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among the most significant tick-borne diseases caused by these pathogens[5]. The spectrum of tick-borne diseases of both medical and veterinary importance has increased in recent years as a result of advances in molecular biology. New microorganisms are being detected in ticks collected in different countries, and the list of potential tick-transmissible pathogens is updating[6]. Problems caused by tick infestations are not limited only to transmission of pathogens. Bite stress, production loss, physical damage, anemia and poisoning are other aspects of tick bites[7]. Furthermore, the importance of animal productions in the economy and food industry around the world is undeniable[8]. Animal health can be altered by the direct and indirect effects caused by the bites of ticks and tick-borne diseases, leading to noteworthy production decrement of meat, milk, eggs, and leathers. In some severe cases, tick-borne pathogens lead to the death of humans and animals. Indirect effects are related to the costs associated to the treatment and control[8]. From past to present, ticks and tick-borne diseases have been recognized as a threat for human and animal health. Ticks are responsible for the majority of vector-borne diseases in Asia, America and Europe[9].

Iran, covering an area of 1648195 km², with a population of 83 million, is located in the Middle East. This country is located in Palearctic and Oriental zoogeographic regions, with different types of climate: mild and quite wet on the coast of the Caspian Sea, continental and arid in the plateau, cold in high mountains, desert and hot on the southern coast and in the southeast, resulting in diversity of tick species[10,11]. Ecology of ticks, their interactions with environment and risk of infection by tick-borne pathogens are directly related to the spatial and temporal variations. As a result, diversity of climate, as well as the vast geographical area, increases the diversity of tick populations which leads to the risk of transmission of different tick-borne pathogens[12]. To date, it has been reported that 46 species of ticks (10 Argasidae and 36 Ixodidae) in 10 genera occur in the country[13].

Tick species can be considered as sentinels to track the circulation of tick-borne pathogens before an outbreak breaks out in humans and animals. Although many studies revealed data about prevalence of different tick-borne pathogens in different areas of Iran, as far as our knowledge, there is no comprehensive data available for consideration and estimation of the damages caused by pathogens transmitted by ticks, on the economy and public health in Iran. For this reason, performing an updated regional review and meta-analysis on the studies conducted on the prevalence of tick-borne pathogens in different provinces of this country is highly necessary. Considering the damages caused by tick-borne diseases on the public health, animal husbandry, and Iran tourism industry, the current study attempted to determine and highlight the presence of pathogens in tick vectors and epidemiological aspects of tick-borne diseases in Iran.

2. Materials and methods

2.1. Searching approach

The present meta-analysis was performed according to the guidelines of preferred reporting items for systematic reviews and meta-analyses statement. In this regional meta-analysis study, nine English and Persian language databases including PubMed, Google Scholar, Science Direct, Scopus, Web of Science, Magiran, Civilica, Iranian Research Institute for Information Science and Technology (IranDoc), and Scientific Information Database (SID) were selected to explore the articles and data with no time limitation (last updated: 7 March, 2021). Duplicate articles, case series, animal-based studies, human-based studies and studies carried out in other countries were excluded. All studies, representing the prevalence of tick-borne pathogens in ticks as hosts/reservoirs were concerned and all PRISMA criteria have been met (Figure 1).

Totally, 95 articles and data fit into the criteria. Then, author(s) names, year of publication, province of study, tick vectors, pathogens, the number of examined ticks and the number of positive ticks were extracted from the collected data. The search was conducted using English and Persian language keywords with different patterns (e.g.: Tick, Iran, Anaplasma, Babesia, Theileria, Crimean-Congo hemorrhagic fever virus, CCHFV, Ehrlichia, Agyptinella, Francisella, Brucella, Borrelia, Coxiella, and Rickettsia). Advanced search options and Boolean operators 'AND' and 'OR' were also used to find more relevant records.

2.2. Paper selection

PICO process or framework (Population, Intervention, Comparator and Outcome) is a common method for formulating a systematic review queries. However, this format is not suitable for prevalence studies. Quality assessment for the included studies of the present research were setup and developed according to CoCoPop structure [Co (Condition)=infection by pathogens; Co (Context)=provinces of Iran; Pop (Population)=ticks]. Studies and the selected data were independently analyzed and the eligibility was determined by HB and ASJ. Disagreements were resolved by MK.

2.3. Meta-analysis

Initially, the prevalence of each genus of pathogen (with 95% confidence intervals) was calculated separately for each province (at least two studies were needed for calculation of each pathogen in separate provinces). Then, an overall prevalence was calculated for all pathogens in respect to each province. Furthermore, the total

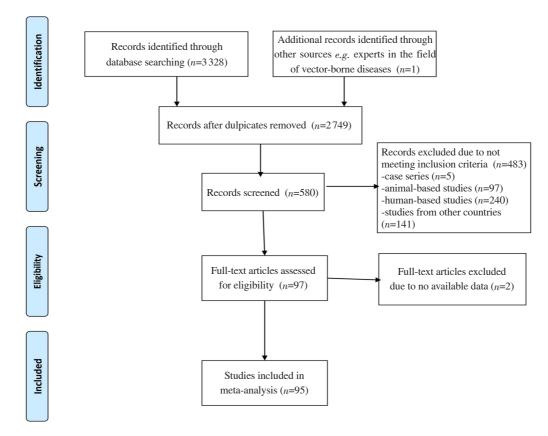


Figure 1. Fowchart of studies selection in terms of tick-borne pathogens in Iran.

prevalence for each pathogen in Iran was estimated. Cochran Q test (P<0.05 shows statistically significant heterogeneity) and I^2 test [25% (low), 50% (moderate), and 75% (high) heterogeneity] were used to evaluate heterogeneity among studies. To compute overall size effect (Q<0.05), random model was used; otherwise (Q>0.05), fixed model was assessed. For determination of publication bias, Egger's and Begg's tests were applied (P>0.05 indicates) a reasonable publication bias. Also, a funnel plot was used to visualize the publication bias. P<0.05 was considered statistically significant for statistical analysis of prevalence. All statistical analyses were performed using Comprehensive Meta-Analysis version 2 (Biostat, USA).

3. Results

Among all databases screened, 3328 records were identified through database searching; then, a total of 95 publications were selected and included in this review. Among these 95 publications, 33 521 ticks were surveyed and 5 673 were positive according to different detection methods in all provinces of Iran. Of all 46 species of ticks (in 10 genera) which occur in Iran[13], 28 species (in 9 genera) including *Alveonasus* (1 species: *Al. canestrinii*), *Argas* (2 species: *Ar. persicus*, *Ar. reflexus*), *Boophilus* (*Boophilus* spp.), *Dermacentor* (2 species: *D. marginatus*, *D. niveus*), *Haemaphysalis*

(4 species: Ha. concinna, Ha. inermis, Ha. punctata, Ha. sulcata), Hyalomma (10 species: H. aegyptium, H. anatolicum, H. asiaticum, H. detritum, H. dromedarii, H. excavatum, H. marginatum, H. rufipes, H. schulzei, H. scupense, H. sp.), Ixodes (1 species: I. ricinus), Ornithodoros (3 species: O. erraticus, O. lahorensis, O. tholozani), and Rhipicephalus (5 species: R. annulatus, R. appendiculatus, R. bursa, R. sanguineus, R. turanicus, R. spp.) were found to be infected with at least 20 pathogens (in 10 genera) including Aegyptianella (1 species: Ae. pullorum), Anaplasma (4 species: An. ovis, An. bovis, An. phagocytophilum, An. marginale, An. spp.), Babesia (3 species: Ba. ovis, Ba. bigemina, Ba. occultans, Ba. spp.), Borrelia (3 species: Bo. microti, Bo. anserina, Bo. persica, Bo. sp.), Brucella (Brucella sp.), Orthonairovirus (1 virus: CCHFV), Coxiella (1 species: Cx. burnetii), Ehrlichia (2 species: Eh. canis, Eh. ovina, Eh. spp.), Rickettsia (1 species: Ri. hoogstraalii, Ri. sp.), Theileria (4 species: Th. annulata, Th. lestoquardi, Th. ovis, Th. equi, Th. spp.), as well as unspecified An. centrale/An. bovis (Table 1). In this review, D. marginatus, D. niveus, H. detritum and H. scupense were considered as separate species.

Among the provinces where ticks were found to be infected with different genera of pathogens (including CCHFV), Lorestan (7 genera), Ardabil (6 genera), Golestan (5 genera), and Sistan and Baluchestan (5 genera) provinces had the most number of ticks infected with different genera of pathogens (Table 2).

Among 31 provinces of Iran, 26 provinces were surveyed in

Ref. [14] [15] [16] [17] [26] [27] [28] [21] [22] [23] [21] [24] [21] [25] [18] [19] [20] [15] [29] [30] [31] R. turanicus R. sp. k. sanguineus 30 38 12 20 20 113 12 30 5 18 4 113 R. bursa 81 R. appendiculatus R. annulatus 22 22 22 in solo for income in the control of the controlO. lahorensis 6 119 119 O. erraticus snuinii I .qs .H 9 H. scupense iszluńse. H sədifur .H mutanigram .H 15 15 Tick vectors шпұрарэхә Ж ∞ ∞ н. дготедагіі mutirish .H H. asiaticum 13 13 22 5 H. anatolicum 47 47 75 16 3 19 19 H. aegyptiumHa. sulcata Ha. punctata ғишыш ъң Ha. concinna D. niveusD. marginatus 11 10 = = = dds snjiydoog enxəlfər .1A Ar. persicus Al. canestrinii Total tested/ positive tick specimens 17/7 1421/NA 1062/226 168/37 215/122 30/10 413/169 182/0 93/4 275/4 133/20 133/20 177/9 998/202 530/52 848/94 146/64 146/64 289/69 289/69 211/9 1589/155 2017 2016 2014 2002 2002 2 studies 2010 1 study 2020 1 study 2030 2013 3 studies 2017 1 study 4 studies study Pathogens screened" Th. lestoquardi Th. annulata Total An./Eh. sp.^{b,##} Ba./Th. sp. c,## Cx. burnetii Total 7 pathogens 4 pathogens 5 pathogens An./Ri. sp.^b Br. sp. ##,*** Ba/Th. sp. Eh. canis Total CCHFV CCHFV Total Azerbaijan, East Azerbaijan, Provinces Ardabil

 Table 1. Summary of tick-borne pathogens in tick species in different provinces of Iran.

[32]

[30] [31] [33]

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Ref.

R. turanicus

[34] [35] [37] [37] [37] [39] [40] [41] [42]

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Table 1. Continued.	Provinces Pathc			ī	C4 Ø	T	[Total 5	Gilan	7		7 [. 1		Total 4	Golestan	,-	7	7	,	~ [[-	F		Total 6	Hamadan	7		J	<u> </u>	•		Total 2
	Pathogens screened	CCHFV	Total	Th. lestoquardi	Th. lestoquardilTh. sp.°	Th. ovis	Total	5 pathogens	An. marginale	An. ovis	Iotal	<i>bo.</i> sp. Total	Br spn °	Total	4 pathogens	An./ Eh. sp. ^b	Total	Ba. occultans	Ba. ovis	Total	Bo. sp.	CCHEV	Total	Th. ovis	Total	6 pathogens	Bo. persica	Bo. persica	Total	CCHFV	CCHFV	CCHFV	Total	2 pathogens
	Year of study	2016	1 study	2013	2005	2013	3 studies	4 studies	2020	2016	z studies	2020 1 stridy	2017	1 study	4 studies	2017	1 study	2017	2017	1 study	2020	1 suddy 2017	1 study	2017	1 study	3 studies	2003	1998	2 studies	2016	2010	2008	3 studies	5 studies
	Total tested/ positive tick specimens	200/9	200/9	171/5	89/53	5/06	350/63	550/110	30/1	53/25	02/20	507/2	1/1	1/1	591/29	48/12	48/12	48/1	48/2	48/3	507/42	130/7	130/7	48/14	48/14	82/18	82/3	1157/0	1 239/3	100/7	328/63	88/10	516/80	1 755/83
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				,					Tick	Tick vectors						
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Hormozgan		An. sp.	2020	30/1					l						[34]	<u> </u>
	Total		1 study	30/1					1							
Ilam		CCHFV	2015	137/9											4	<u> </u>
	Total	1 pathogen	1 study	137/9												
Isfahan		CCHFV	2016	210/11							2			8	[45]	<u></u>
	Total	1 pathogen	1 study	210/11			-	3 2			2			3		
Kerman		An. sp.	2020	96/23						11				6	[46]	[
		Total	1 study	96/23				2 1		11				6		
		Ba. sp.	2016	211/0											[47]	7
		Total	1 study	211/0												
		CCHFV	2020	258/0											[48]	~
		CCHFV	2018	203/0											[49]	-
		Total	2 studies	461/0												
		Cx. burnetii	2018	375/47										47	[20]	\subseteq
		Cx. burnetii	2011	245/18				15						ю	[51]	
		Total	2 studies	620/65				15						50		
		Eh. sp.	2016	408/25										25	[52]	27
		Total	1 study	408/25										25		
	Total	5 pathogens	7 studies	1796/113				17 1		11				8		
Kermanshah		CCHFV	2016	131/5				3 1						1	[53]	3
		Total	1 study	131/5				3 1						1		
		Th. annulata	2019	420/20				20							[54]	—
		Th. lestoquardi	2019	420/50				10							40 [54]	-
		Th. ovis	2019	420/60						20						∓
		Total	1 study	420/130				30		20					80	
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Khorasan,		Ba. caballi	2014	37/0											[55]	
North		Ba. ovis	2014	44/2						-					1 [56]	$\overline{\mathcal{L}}$
		Ba. motasi	2014	44/0											[56]	<u></u>
		Total	2 studies	81/2						1					1	
		CCHFV	2019	62/5				3						2	[57]	_
		CCHFV	2016	134/0											[58]	~
		Total	2 studies	196/5				3						2		
		Th. equi	2014	37/3				2							[55]	<u></u>
		Th. lestoquardi	2012	220/5						5					[65]	_
		Th. ovis	2012	220/10						5					5 [59]	_

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Final Fina		Th. lestoquardi/ Th. ovis°	2012	220/5		S			[65]
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Pick sp. 2013 4290 120	Khorasan,	Ba. sp.	2015	246/0					[09]
Total	Razavi	Ba. sp.	2013	429/0					[61]
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CCHFV 2015 1064 1 <th< td=""><td></td><td>CCHFV</td><td>2016</td><td>152/0</td><td></td><td></td><td></td><td></td><td>[58]</td></th<>		CCHFV	2016	152/0					[58]
Total 3 studies 33710 1		CCHFV	2015	105/4	1	1	1	1	[64]
Th. annulates 2012 510231 1902 190		Total	3 studies	357/10	1	7	1	1	
The Insequential 2013 429/10 The Insequential 2013 429/10 The Insequential 2013 429/10 The Insequential 2013 429/12 The orisis 2013 429/12 The orisis 2013 429/12 The orisis 2013 429/12 The Insequential 2013 429/12 The Insequential 2013 246/11 The Insequential 2013 246/11 The Insequential 2013 2107/244 The Insequential 2013 2107/244 The Insequential 2013 2014/26 The Insequential 2014/26 The Ins		$Th.\ annulata$	2002	510/231	1	230			[65]
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Total		Th. sp.	2015	246/1		1			[09]
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An. ouisi## 2020 100/20 1 4 4 4 4 4 4 1 9 3 1 4 4 4 1 1 9 3 1 4 4 4 1 2 1	Ţ		8 studies	2707/344	2		52 1	51	
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Total 3 pathogens 3 studies 553/101 1 16 6 4 46 4 1 2 20 Th. spp. 2018 655/67 54 10 2 1 2 1 Total 1 pathogen 1 study 469/1 1 1 1 Total 1 pathogen 1 study 469/1 1 1 1		Total	1 study	100/0					
Th. spp. 2018 655/67 54 10 2 1 Total 1 pathogen 1 study 655/67 54 10 2 1 A CCHFV 2019 469/1 1 1 Total 1 pathogen 1 study 469/1 1	Ĕ		3 studies	553/101	9	46	1		
Total 1 pathogen 1 study 655/67 54 10 2 1 d CCHFV 2019 469/1 1 Total 1 pathogen 1 study 469/1 1			2018	655/67	10	1			[89]
d CCHFV 2019 469/1 1 Total 1 pathogen 1 study 469/1 1			1 study	655/67	10	1			
Total 1 pathogen 1 study	p		2019	469/1			_		[69]
			1 study	469/1			1		

Table 1. Continued.	į.										-										
											lick vectors	tors									
Provinces	Pathogens screened	Year of study	Total tested/ positive tick specimens	Al. canestrinii Ar. persicus	Ar. reflexus Boophilus spp.	entanigram .A B. niveus	Ha. concinna Ha. inermis Ha. punctata	Ha. sulcata H. aegyptium	musiloisna H	musitaisa .H mutirtəb .H	і: Аготедагіі тильэтогь Н	H. marginatum	eəqilur .H iəzluhəs .H	H. scupense H. sp.	l. ricinus O. erraticus	sisnərohal .0 inazoloht .0	R. annulatus R. appendiculatus	R. bursa	R. sanguineus R. sp.	R. turanicus	Ref.
Kurdistan	Ba. sp.	2018	3107/1303				113			Cl	31						283		١.		[02]
	Total	1 study	3107/1303				15				31						283	385	327		
	Bo. persica	2009	96/19													19					[71]
	CCHFV	2012	5/06						1		_	3									[73]
	Total	1 study	90/2						1			3									
	Th. sp.	2018	3 107/939					7		101 41	78						77	113	86		[70]
	Total	1 study	3 107/939					7	431 10	101 41	78						11	113	86		
T	Total 4 pathogens	4 studies	3393/2269				13		653 11	119 66	1 109	3				19	360	498 4	425		
Lorestan	Ae. pullorum	2018	20/5		2																[74]
	Total	1 study	20/5	•	5																
	An. ovis	2020	70/14							11									33		[34]
	Total	1 study	70/14						1	11									ϵ		
	Bo. anserina	2017	212/140	140	0																[75]
	Total	1 study	212/140	140	0																
	Cx. burnetii	2020	160/80	60 20	0																[92]
	Total	1 study	160/80	60 20	0																
	CCHFV	2015	434/29						12	7		_							6		[77]
	Total	1 study	434/29						12	7		П							6		
	Ri. hoogstraalii	2020	9/49		9																[78]
	Total	1 study	64/6		2																
	Th. lestoquardi***	2015	54/5						5												[62]
	Th. lestoquardi	2015	171/1							1											[30]
	Th. lestoquardi"	2013	54/5						5												[80]
	Total	3 studies	279/11						10	-											
	Th. ovis***	2014	152/37																37		[62]
	Th. ovis#	2015	152/37																37		[80]
	Total	2 studies	304/74																74		
T	Total 8 pathogens	9 studies	1543/359	60 171	_				22 1	18 1		1							98		
Mazandaran	An. bovis	2013	618/364			4 22	2 6 105	2							5			119	8	95	[81]
	An. bovis/ An. centrale ^b	2014	101/50					1							4		1		34		[83]
	An.	2004	5/86												5						[83]
	Tetal	:	0177710			,	7								2		-	110	ć	90	
	Iotal	s studies	81 //419			4	001 0 7	0							t ,		ī	,	1 1 1		1
	Bo. sp.	2020	501/27												9			_ ,	- 1	n ([35]
	Total	1 study	507/27												91			_	_	30	
	Cx. burnetii	2005	605/0																		[84]

Table 1. Continued.

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Table 1. Condition								,								
								Tick vectors	r.S							1
Provinces	Pathogens screened"	Year of study	Total tested/ positive tick specimens	Al. canestrinii Ar. persicus Ar. reflexus Boophilus spp. D. marginatus	D. niveus Ha. concinna Ha. inermis Ha. sulcata	muitqtgəv.H muəilətənn .H	musitaises. H musirtseb. H	ітарьтоть .H тихалагит	mutanigram .H esqrfur .H	H. schulzei H. scupense H. sp.	r. op. 1. ricinus 0. erraticus	o. lahorensis inpsolodi .0	R. annulatus R. appendiculatus	R. bursa	R. sanguineus R. sp.	R. turanicus R A
	Total	1 study	0/209													
	CCHFV	2017	130/7			3		2	1						_	[38
	CCHFV	2016	58/1												_	[85]
	Total	2 studies	188/8			3		2	1					(1	6)	
	Th. ovis	2012	20/1												_	<u>×</u>
	$Th./Ba. {\rm sp.}^{\circ}$	2012	20/10											10		[98]
	Total	1 study	20/11											11	_	
	Total 7 pathogens	8 studies	2137/465	4	22 6 106	3		2	1		40		_	120 62		86
Qazvin	Bo. microti	2007	24/12								12					<u>\&</u>
	Bo. persica	2010	344/16									16				[88]
	Bo. Persica ##	2007	231/20									20				<u>∞</u>
	Bo. sp.	2010	344/3									3				<u>×</u>
	Total	2 studies	599/51									3 36				
	Total 3 pathogens	2 studies	599/51								12 3					
Qom	CCHFV	2012	9/88						9							[68]
,	Total 1 Pathogen	1 study	9/88						9							
Semnan	Bo. persica	1999	5 938/243									243				[06]
	Total	1 study	5 938/243									243				
	CCHFV	2018	93/4			1		2								[91]
	Total	1 study	93/4			П		2							_	
	Total 2 pathogens	2 studies	6031/247			-						243			_	
Sistan and	An. / Eh. sp. b,**	2019	256/175			79 24	7		36	2						[92]
Baluchestan	An. marginale	2021	248/12													12 [9:
	An. ovis	2020	100/20													[94]
	An. ovis / Eh. sp. ^b	2014	53/14			ε į								7		[65]
	Total	4 studies	657/221			10/ 2	7	32 3	36	2 1				. 1		12
	$Cx. burnetii^{""}$	2020	100/0					,								[94]
	Cx. burnetii	2017	583/18			7		9						4,	S	<u>ŏ</u>
	$Cx.\ burnetii^a$	2016	1305/105													[6]
	Total	3 studies	1988/123			7		9						S	16	
	Eh. sp.	2017	50/5											4,	5	[86]
	Total	1 study	50/5											4,	16	
	CCHFV##	2020	100/0													[94]
	CCHFV	2017	49/3						1						1	6
	CCHFV	2013	140/6		1					5						[10
	Total	3 studies	289/9		1				1	S					_	
	Th. sp.	2019	110/18				6							7		5 [101]

Table 1. Continued.

	Ref.	[102]	[24]			[103]		[104]			[105]		[106]	[106]			[28]	[107]	[108]		NA
	R. turanicus			5	17													8		∞	303
	R. sp.		_					••												_	851 23
	R. sanguineus		10	20	33			18	18	18							8	9		14	851
	R. bursa																_	20		21	799
	R. appendiculatus																				1 1
	R. annulatus																				12 132 360 384 1
	innzolodi .0																				2 36
	o. lahorensis																				2 13;
	o. erraticus																				43 1
	.qs .H sunisin .I				9																15 4
	9sn9quəs .H																				5
	iəzludəs .H				2																3
	sədifini .H																				_
SJO	тильпізльт .Н				37						1	-				-					146
Tick vectors	шпұрарэхә Н				9																94 363 146
Tick	іїлььэтоль .Н				32						\mathcal{C}	\mathfrak{C}				\mathfrak{C}					94
	тийлдэр .Н				7						7	7				7					125
	muəitaisa .H			6	36						1	_				_			10	10	238
	musilotana .H	30		30	144						1	Т	15		15	16					1155 238 125
	muitqv3əv .H																				_
	Ha. sulcata																		2	2	
	Ha. punctata																				120 10
	eimnəni .pH				_														_	_	∞
	риигоиог ъН																				22
	D. niveus																				6
	eutanigram .a		2	7	7																79
	.qqs sulinqood																				-
	Ar. reflexus																		20	20	32 2
	Ar. persicus																		(1	(4	0 15
	> ∺ ∞ iinirtsənəə AA																				3 ^h 6
	Total tested/ positive tick specimens	346/36	93/12	549/66	3 533/424	0/68	0/68	27/18	27/18	116/18	140/8	140/8	250/15	250/0	250/15	390/23	211/9	269/34	61/36	541/79	/567
	lotal positi spec	34	6	54	3533	80	<u></u>	7	7	1	4	4	25(25(25(39	21	26	[9	54	3521
					s																s 3.
	Year of study	2003	2018	3 studies	12 studies	2017	1 study	2020	1 study	2 studies	2011	1 study	2015	2015	1 study	2 studies	2013	2007	2020	3 studies	95 studies 33521/5673 ^h 60 192 2
	Ye	2	2	3 SI	12 s	2	1.8	2	-	2 st	2	1.8	2	2	-	2 st	2	2	2	3 SI	95 s
	<u>*</u>																				
	senec		sp.		sus			ata		sus			ata	^r h. lestoquardi		sus				sus	22 pathogens ^g
	s scre	يَ ا	Th. I Ba. sp.b	_	hoge	ΙŁΛ	_	Th. annulata	_	hoge	ŀΥ	_	Th. annulata	estog	_	hoge	.ds	.ds	ъ.	hoge	athog
	Pathogens screened*	Th. sp.	Th. /	Total	7 pathogens	CCHFV	Total	Th. a	Total	2 pathogens	CCHFV	Total	Th. a	Th. l	Total	Total 3 pathogens	Ba. sp.	Ba. sp.	Ri. sp.	2 pathogens	22 p
	Path				Total					Total						tal				Total	
					Tc					Tc						Tc				Tc	
																	ed	S.F.			Total
	Provinces					an.					7						Unspecified	Locations ^f			
	Prov					Tehran					Yazd						Uns	Loca			

Abbreviations: Ba: Babesia; Bo: Borrelia; Cx: Coxiella; Eh: Ehrlichia; Ri: Rickettsia; Th: Theileria; An: Anaplasma; Ae: Aegyptianella; Br: Brucella, Brucellaceae; Al: Alveonasus; Ar: Argas; D: Dermacentor; Ha: Haemaphysalis; H: Totally, 95 studies were included; of 31 provinces, the infection of different ticks by different pathogens were recorded in 26 provinces; at least 20 pathogens (in 10 genera) were detected in 28 species of tick vectors (in 9 genera); Hyalomma; I: Ixodes; O: Ornithodoros; R: Rhipicephalus; NA: not applicable.

In this review, total positive ticks have been reported as 175 in its source; however, the addition of individual positive ticks is reported as 174. For this reason, we changed the positive number of H. anatolicum from 78 to 79. : In this table, all unidentified species of pathogens (e.g.: Ba. sp.) have been considered as separate pathogens in the meta-analysis; in Ilam province, the species of CCHFV vector(s) have not been mentioned in the source.

In this study, the total number of positive (infected to pathogen) ticks as well as their species has not been reported. As a result, the number related to this research has not been concluded in our table. ": In these studies, the total number of tested ticks has been reported in terms of each specific pathogen. As a result, total sample size of the study may be different from each pathogen's sample size.

^{***} Abdoli et al., have reported Brucellaceae in this research. We considered this finding as Brucella in our analysis.

[.] In these investigations, only the exact number of positive ticks were reported and the number of positive species were not specified

In these investigations, further to insufficient data regarding genus of pathogen, we considered the pathogen of these studies as Anaplasma sp. in the meta-analysis. In these investigations, further to insufficient data regarding genus of pathogen, we considered the pathogen of these studies as Theileria sp. in the meta-analysis.

^{1.} In this study, due to insufficient data regarding the number of positive ticks, the percentage of infection was used as the number of positive samples.

[:] This study was not included in the meta-analysis due to sample size less than 2.

In some investigations, the province of the infected tick(s) was not specified. We have grouped these studies as "unspecified location".

². Of 22 pathogens investigated, the infection of ticks to Ba. caballi and Ba. onis was not confirmed; ticks were found to be infected with 20 pathogens.

[:] In some investigations, the species or genera of positive ticks have not been stated. In such cases, we have included the studies as well. So, the sum of the total positive ticks differs with the total number of the ticks morphologically identified at the genus/species level.

Province	Total tested/positive tick(s)	detected in tick vectors in different provinces of Iran. Positive tick vector(s)	Pathogen(s)
Trovince	Total tested/positive tiek(s)	D. marginatus; D. niveus; H. aegyptium; H. anatolicum; H.	
Ardabil	1 062/226	asiaticum; H. excavatum; H. marginatum; H. schulzei; H. sp.; O. lahorensis; O. tholozani; R. bursa; R. sanguineus	Rabesia: Rorrelia: CCHEV:
Azerbaijan, East	998/202	D. marginatus; Ha. sulcata; H. anatolicum; H. asiaticum; H. marginatum; I. ricinus; O. lahorensis; R. bursa; R. sanguineus	Anaplasma; Babesia; Brucella; CCHFV
Azerbaijan, West	1 904/192	D. marginatus; H. marginatum; R. annulatus; R. bursa; R. sanguineus; R. turanicus	Babesia; Theileria
Fars	550/110	H. anatolicum; H. marginatum; H. sp.; R. sanguineus; R. sp.; R. turanicus	Babesia; Ehrlichia; CCHFV; Theileria
Gilan	591/29	Boophilus spp.; D. marginatus; I. ricinus; R. annulatus; R. sanguineus; R. sp.	Anaplasma; Borrelia; Brucella
Golestan	685/78	H. anatolicum; H. dromedarii; H. excavatum; H. marginatum; H. rufipes; H. scupense; I. ricinus; R. bursa; R. sanguineus; R. turanicus	Ananlasma: Babesia: Borrelia:
Hamadan	1 755/83	Ar. reflexus; Ha. punctata; H. anatolicum; H. asiaticum; H. detritum; H. dromedarii; H. marginatum; O. tholozani; R. bursa; R. sanguineus	
Hormozgan	30/1	H. dromedarii	Anaplasma
Ilam	137/9	NA	CCHFV
Isfahan	210/11	Ha. sulcata; H. anatolicum; H. asiaticum; H. sp.; R. sanguineus	CCHFV
Kerman	1796/113	H. anatolicum; H. asiaticum; H. marginatum; R. sanguineus	Anaplasma; Coxiella; Ehrlichia
Kermanshah	551/135	H. anatolicum; H. asiaticum; H. marginatum; R. sanguineus; R. turanicus	CCHFV; Theileria
Khorasan, North	497/30	H. anatolicum; H. marginatum; R. bursa; R. sanguineus; R. turanicus	Babesia; CCHFV; Theileria
Khorasan, Razavi	2707/344	H. asiaticum; H. excavatum; H. marginatum; O. tholozani; R. appendiculatus; R. turanicus	Borrelia; CCHFV; Theileria
Khorasan, South	553/101	Ar. persicus; D. niveus; H. anatolicum; H. asiaticum; H. detritum; H. dromedarii; H. marginatum; O. lahorensis; R. sanguineus; R. sp.	
Khuzestan	655/67	H. anatolicum; H. asiaticum; H. detritum; H. dromedarii	Theileria
Kohgiluye and Boyer- Ahmad	469/1	R. bursa	CCHFV
Kurdistan	3 393/2 269	Ha. punctata; H. anatolicum; H. asiaticum; H. detritum; H. dromedarii; H. excavatum; H. marginatum; O. tholozani; R. annulatus; R. bursa; R. sanguineus	Rabesia: Rorrelia: (HEV:
Lorestan	1 543/359	Al. canestrinii; Ar. persicus; H. anatolicum; H. asiaticum; H. detritum; H. marginatum; R. sanguineus	Aegyptianella; Anaplasma; Borrelia; Coxiella; CCHFV; Rickettsia; Theileria
Mazandaran	2137/465	D. marginatus; Ha. concinna; Ha. inermis; Ha. punctata; H. anatolicum; H. dromedarii; H. marginatum; I. ricinus; R. annulatus; R. bursa; R. sanguineus; R. turanicus	Anaplasma; Borrelia; CCHFV; Theileria
Qazvin	599/51	O. erraticus; O. lahorensis; O. tholozani	Borrelia
Qom	88/6	H. marginatum	CCHFV
Semnan	6 0 3 1 / 2 4 7	H. anatolicum; H. dromedarii; O. tholozani; R. sanguineus	Borrelia; CCHFV
Sistan and Baluchestan	3 533/424	D. marginatus; Ha. inermis; H. anatolicum; H. asiaticum; H. detritum; H. dromedarii; H. excavatum; H. marginatum; H. schulzei; H. sp.; R. sanguineus; R. sp.; R. turanicus	Ananlasma' Coxiella'
Tehran	116/18	R. sanguineus	Theileria
Yazd	390/23	H. anatolicum; H. asiaticum; H. detritum; H. dromedarii; H. marginatum	CCHFV; Theileria

Babesia (7 provinces), Borrelia (10 provinces), CCHFV (19 provinces), Coxiella (4 provinces), Ehrlichia (4 provinces), Theileria (14 provinces), Anaplasma (9 provinces), Brucella (2 provinces), Aegyptianella (1 province), Rickettsia (1 province); Positive tick species in different provinces are as follows: Al. canestrinii (1 province), Ar. persicus (2 provinces), Ar. reflexus (1 province), D. marginatus (6 provinces), D. niveus (2 provinces), H. aegyptium (1 province), H. anatolicum (17 provinces), H. asiaticum (13 provinces), H. detritum (7 provinces), H. dromedarii (10 provinces), H. excavatum (5 provinces), H. marginatum (17 provinces), H. rufipes (1 province), H. schulzei (2 provinces), H. scupense (1 province), Ha. concinna (1 province), Ha. inermis (2 provinces), Ha. punctata (3 provinces), Ha. sulcata (2 provinces), I. ricinus (4 provinces), O. erraticus (1 province), O. lahorensis (4 provinces), O. tholozani (6 provinces), R. annulatus (4 provinces), R. appendiculatus (1 province), R. bursa (9 provinces), R. sanguineus (18 provinces), R. turanicus (8 provinces), Boophilus spp. (1 province), Hyalomma spp. (4 provinces), Rhipicephalus sp. (4 provinces), NA (1 province).

terms of detection of infection of different pathogens in ticks; meanwhile, the status of tick infection with different pathogens remained unclear in Alborz, Bushehr, Chaharmahal and Bakhtiari, Markazi, and Zanjan provinces. The provinces in which the most studies have been carried out are Sistan and Baluchestan (12 studies), Lorestan (9 studies), Razavi Khorasan (8 studies), Mazandaran (8 studies), Kerman (7 studies), and Ardabil (7 studies). On the other hand, Hormozgan, Ilam, Isfahan, Khuzestan, Kohgiluyeh and Boyer-Ahmad, and Qom were among the least studied provinces (only one study in each province). More than 60 literatures were related to CCHFV and Theileria/Babesia spp., while Aegyptianella, Brucella and Rickettsia were limited to less than 10 publications (Table 1). According to a random effect model, the total prevalence of tick-borne pathogens in Iran was calculated as 8.6% (95% CI 7.0%-10.6%, P<0.001). The highest and lowest prevalence rate occurred in Kurdistan (20.5%; 95% CI 14.0%-29.1%, P<0.001), and Khorasan, Razavi (2.4%; 95% CI 0.8%-6.7%, P=0.008), respectively. In addition, Anaplasma sp. was the pathogen with the highest statistically significant prevalence (23.5%; 95% CI 15.1%-34.7%, P<0.001), while the lowest infection rate belonged to Babesia sp. (4.0%; 95% CI 1.9%-8.1%, *P*<0.001) (Table 3).

Statistical analysis revealed that the highest prevalence of Anaplasma sp., Babesia sp., Borrelia sp., CCHFV, Coxiella sp., and Theileria sp. occurred in East-Azerbaijan (36.5%; 95% CI 15%-63.9%, P=0.335), West-Azerbaijan (8.8%; 95% CI 6.1%-12.5%, P<0.001), Kurdistan (8.5%; 95% CI 1.2%-41.6%, P=0.022), South-Khorasan (14.3%; 95% CI 3.7%-42.0%, P=0.017), Kerman (9.9%; 95% CI 5.8%-16.4%, P<0.001), and Mazandaran (21.0%; 95% CI 1.5%-82.4%, P=0.009), respectively. Brucella sp., Ehrlichia sp., Rickettsia sp., and Aegyptianella sp. did not meet the criteria for entering province-specific meta-analysis (less than 2 publications in each province). A forest plot was used to show the prevalence of tick-borne pathogens across the country (Supplementary Figure 1). In addition, funnel plot revealed an asymmetry in the funnel which might indicate that some studies were missed on the right side of the plot (Figure 2). In line with funnel plot, the results of Egger's test (P<0.001) showed a publication bias among studies. Based on the funnel plot, most of the studies with low prevalence of tickborne pathogens were included in this meta-analysis (Figure 2).

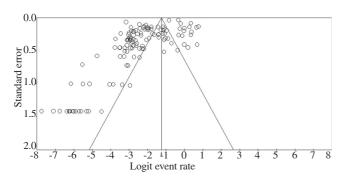


Figure 2. Funnel plot of standard error by logit event rate.

4. Discussion

As far as we know, the present meta-analysis is the first largescale study that examined the prevalence of tick-borne pathogens in tick vectors in Iran. Overall estimated prevalence of tick-borne pathogens in Iran was 8.6% (95% CI 7.0%-10.6%, P<0.001). The greatest infection rates among tick vectors were dedicated to Rickettsia sp. (P>0.05), and Anaplasma sp., respectively. Anaplasma species are Gram-negative obligate intraerythrocytic bacteria (Rickettsiales; Anaplasmataceae) which are of great veterinary concern. An. marginale, the most probable causative agent of bovine anaplasmosis, has been reported worldwide. This pathogen mainly affects ruminants resulting in mild to severe febrile hemolytic anemia that leads to significant economic losses[109]. Other species are as follows An. ovis and An. mesaeterum (in sheep and goat), An. phagocytophilum (in horse, dogs and cats), An. platys (in dogs) and An. centrale in cattle[110,111]. Although medically important pathogens such as Borrelia sp., Coxiella sp., and CCHFV were less prevalent in ticks according to the pooled results of literature review, it should be noted that to determine the epidemiological status of a pathogen, all factors affecting pathogen's life cycle must be taken into consideration. For example, CCHF is endemic in Iran and its neighboring countries and a significant number of human cases are reported each year. In a recent review on distribution of ticks and their infection to CCHFV, the main vectors of CCHF, H. marginatum and H. anatolicum, have been reported in more than 38.7% of provinces of Iran[112]. In our review, among all pathogens, CCHFV positive ticks were reported in 19 provinces. The point may be that in Iran, the main way of CCHFV transmission is not tick bite. CCHFV infection in human mostly occurs due to direct contact with infected livestock (blood, tissues, secretions), which have been infected by ticks[113,114].

Q fever is a zoonosis caused by the bacterium Cx. burnetii. Human infection mainly occurs through inhalation of contaminated animal products, direct contact with infected animals and consumption of unpasteurized milk or other dairy products contaminated with this pathogen. Ticks play a key role in transmitting bacteria between animals, and are considered as reservoirs of Cx. burnetii bacteria and guarantee the long-term presence of this microorganism in nature[84]. Borrelia spp. is the causative agent of Lyme disease and relapsing fever which are zoonotic vectorborne diseases transmitted primarily by ticks[115]. In a descriptive and retrospective study during 1997-2006, Masoumi et al. reported that the disease is detected in humans in 18 provinces of the 31 provinces in Iran[116]. Other reports also revealed that Borrelia spp. is present in ticks and other vertebrates[35,117]. According to reports of Cx. burnetii and Borrelia spp. in ticks, humans, and animals in Iran, Q-fever, Lyme disease and relapsing fever can be considered as emerging diseases in the country[118-120].

The most infected provinces in terms of tick-borne pathogens

Table 3. Meta-analysis result of different genera of pathogens (including CCHFV), detected in each province as well as in the country.

		No. of		Prevalence	95%	CI	Hetero	geneity	- P values of		tion bias
Provinces	Pathogens	No. of studies	Sample size	(pooled effect size)	Lower	Upper	<i>I</i> ² (%)	Q test	prevalence	Begg's test (2 tailed <i>P</i> value)	Egger's tes (2 tailed P value)
Ardabil	Babesia sp.	2	489	0.012	0.000	0.255	81.938	5.537	0.009	NA	NA
	Tick borne pathogens	7	1 351	0.186	0.104	0.310	93.410	91.046	< 0.001	0.763	0.357
Azerbaijan, East	Anaplasma sp. Theileria sp.	3 2	413 275	0.365 0.032	0.158 0.013	0.639 0.077	95.564 71.037	45.088 3.45	0.335 <0.001	1.000 NA	0.678 NA
	Tick borne pathogens	7	998	0.133	0.051	0.305	96.091	153.502	< 0.001	0.367	0.051
Azerbaijan, West		3	1 589	0.088	0.061	0.125	75.961	8.320	< 0.001	0.296	0.032
	Tick borne pathogens	4	1904	0.097	0.074	0.125	67.142	9.130	< 0.001	0.308	0.176
Fars	Theileria sp.	3	350	0.123	0.009	0.682	97.645	84.928	0.158	1.000	0.081
	Tick borne pathogens	6	810	0.115	0.035	0.316	96.359	137.321	< 0.001	0.259	0.045
Gilan	Anaplasma sp.	2	83	0.169	0.008	0.830	89.515	9.537	0.326	NA	NA
	Tick borne pathogens	3	590	0.049	0.001	0.699	96.472	56.697	0.127	1.000	0.334
Golestan	Babesia sp.	2	96	0.033	0.011	0.097	0.000	0.331	< 0.001	NA	NA
	Tick borne pathogens	6	829	0.066	0.030	0.139	87.992	41.639	< 0.001	0.707	0.683
Hamedan	Borrelia sp. CCHFV	2 3	1 239 516	0.005 0.124	0.000 0.066	0.278 0.221	88.288 78.850	8.538 9.456	0.017 <0.001	NA 0.296	NA 0.126
	Tick borne pathogens	5	1755	0.060	0.023	0.149	88.583	35.034	< 0.001	0.027	0.001
Hormozgan							NA				
Ilam Isfahan							NA NA				
Kerman	Coxiella sp. CCHFV	2 2	620 461	0.099 0.002	0.058 0.000	0.164 0.015	75.927 0.000	4.154 0.014	<0.001 <0.001	NA NA	NA NA
	Tick borne pathogens	7	1796	0.060	0.029	0.119	88.637	88.637	< 0.001	0.763	0.110
Kermanshah	Theileria sp.	3	1 260	0.096	0.055	0.164	90.249	20.511	< 0.001	0.296	0.042
	Tick borne pathogens	4	1391	0.082	0.047	0.139	88.747	26.659	< 0.001	0.308	0.164
Khorasan, North	Babesia sp. CCHFV	3 2	125 196	0.029 0.023	0.009 0.001	0.087 0.319	0.000 77.002	1.209 4.348	<0.001 0.014	1.000 NA	0.050 NA
	Theileria sp. Tick borne	4	697	0.036	0.024	0.054	37.422	4.794	< 0.001	1.000	0.938
	pathogens	9	1018	0.038	0.027	0.054	31.263	11.639	< 0.001	0.676	0.219
Khorasan, Razavi	Babesia sp. CCHFV Theileria sp.	2 3 7	675 357 2381	0.002 0.044 0.033	0.000 0.024 0.007	0.014 0.078 0.139	0.000 52.013 98.126	0.000 4.168 327.182	<0.001 <0.001 <0.001	NA 0.269 0.367	NA 0.102 0.014
	Tick borne pathogens	13	4409	0.024	0.007	0.067	97.677	516/536	<0.001	0.076	0.014
Khorasan, South	Anaplasma sp. CCHFV	2 2	159 294	0.299 0.143	0.129 0.037	0.552 0.420	88.666 12.466	8.823 91.978	0.115 0.017	NA NA	NA NA
	Tick borne pathogens	5	553	0.176	0.089	0.317	87.984	33.288	< 0.001	0.426	0.243
Khuzestan Kohgiluyeh and							NA				
Boyer-Ahmad							NA				
Kurdistan	Borrelia sp.	2	196	0.085	0.012	0.416	90.511	10.538	0.022	NA	NA
	Tick borne pathogens	5	6500	0.205	0.140	0.291	97.348	150.833	< 0.001	0.462	0.240
Lorestan	Theileria sp. Tick borne	5 11	583 1543	0.125 0.172	0.064 0.087	0.228 0.314	83.837 96.425	24.748 279.715	<0.001 <0.001	0.086 0.061	0.000 0.064
Mazandaran	pathogens <i>Anaplasma</i> sp.	3	817	0.323	0.131	0.601	96.098	51.254	0.207	0.296	0.231
	CCHFV Theileria sp.	2 2	188 40	0.047 0.210	0.023	0.090 0.824	15.618 85.552	1.185	<0.001	NA NA	NA NA
	Tick borne pathogens	9	2157	0.100	0.013	0.324	97.765	357.961	0.001	0.754	0.049

Table 3. Continued.

		NI C		Prevalence	95%	c CI	Heter	ogeneity	- P values of		tion bias
Provinces	Pathogens	No. of studies	Sample size	(pooled effect size)	Lower	Upper	I ² (%)	Q test	prevalence		Egger's test (2 tailed P value)
Qazvin	Borrelia sp. = Tick borne pathogens	4	943	0.077	0.020	0.253	94.702	56.624	0.001	0.734	0.993
Qom							NA				
Semnan	Tick borne pathogens	2	6031	0.041	0.036	0.046	0.000	0.010	< 0.001	NA	NA
Sistan and	Anaplasma sp.	4	657	0.241	0.054	0.641	98.232	169.554	0.193	0.734	0.083
Baluchestan	Coxiella sp.	3	1988	0.041	0.015	0.103	89.324	18.734	< 0.001	1.000	0.374
	CCHFV	3	289	0.040	0.018	0.090	28.217	2.786	< 0.001	1.000	0.430
	Theileria sp.	3	549	0.122	0.097	0.152	29.684	2.844	< 0.001	1.000	0.471
	Tick borne pathogens	14	3 5 3 3	0.093	0.043	0.188	97.420	503.959	< 0.001	1.000	0.392
Tehran	Tick borne pathogens	2	116	0.110	0.000	0.975	93.702	15.878	0.477	NA	NA
Yazd	Theileria sp.	2	500	0.015	0.001	0.299	82.719	5.787	0.014	NA	NA
	Tick borne pathogens	3	640	0.055	0.037	0.081	65.569	5.809	< 0.001	0.296	0.142
Unspecified	Babesia sp.	2	480	0.077	0.026	0.208	89.207	9.265	< 0.001	NA	NA
location	Tick borne pathogens	3	541	0.175	0.033	0.565	97.476	79.225	0.093	1.000	0.982
Iran (all collected	Anaplasma sp.	18	2373	0.235	0.151	0.347	96.596	498.733	< 0.001	0.080	0.000
data)	Babesia sp.	17	6943	0.040	0.019	0.081	97.737	706.904	< 0.001	0.010	0.000
	Borrelia sp.	15	5 1 2 4	0.068	0.029	0.150	97.567	534.363	< 0.001	1.000	0.289
	Brucella sp.						NA				
	CCHFV	31	4819	0.056	0.039	0.081	86.951	199.253	0.001	0.091	0.000
	Coxiella sp.	9	3753	0.065	0.030	0. 138	96.738	245.246	< 0.001	1.000	0.450
	Ehrlichia sp.	4	693	0.177	0.056	0.437	96.744	92.137	0.019	0.734	0.594
	Rickettsia sp.	2	125	0.283	0.029	0.839	96.370	27.552	0.480	NA	NA
	Theileria sp.	36	11076	0.093	0.067	0.129	96.157	910.777	< 0.001	0.827	0.000
	Tick borne pathogens	135	35 184	0.086	0.070	0.106	97.429	5211.303	< 0.001	0.933	0.000

Note: In this analysis, each row of Table 1 was considered as an individual data. Furthermore, the sample size of each row of Table 1 was considered a separate sample size, and all pathogens were included. Provinces with less than two data were not included in meta-analysis. However, the pathogens detected in these provinces were calculated in Iran's total prevalence of pathogens section.

were Kurdistan (20.5%), Ardabil (18.6%), South Khorasan (17.6%), Lorestan (17.2%), East Azerbaijan (13.3%) and Fars (11.5%), respectively. Geographically, these provinces (except South Khorasan) are located in the western parts of Iran. Therefore, it can be concluded that although tick-borne pathogens have been reported from different regions of Iran, the western part of the country is more infected than other regions. This high prevalence can be justified due to high livestock population, common border with neighboring countries and traditional livestock holding methods with low hygiene.

In this analysis, 26 out of 31 provinces were surveyed regarding tick-borne pathogen detection in ticks; meanwhile, the status of infection of ticks to different pathogens remained unclear in five provinces: Alborz, Bushehr, Chaharmahal and Bakhtiari, Markazi, and Zanjan. Due to the importance of ticks and their impact on human and animal health, it is highly advisable to conduct studies concerning tick-borne diseases to clarify the status of these provinces. Vector surveillance seems to be vital for observing the

presence or occurrence of emerging and reemerging tick borne diseases in Iran and provides a preliminary warning for predicting probable epidemics.

In our analysis, *H. anatolicum* (20.35%), *R. sanguineus* (15.00%), and *R. bursa* (14.08%), were the most prevalent infected ticks in Iran. Genera of *Hyalomma* species have received much attention due to the role in the transmission of *Theileria* spp., *Babesia* spp., *Rickettsia* spp., and CCHFV. *R. sanguineus* (brown dog tick, kennel tick) is found worldwide with an interest toward warmer climates (tropics and sub-tropics)[121]. Dogs are specific host for *R. sanguineus*, however, it can be found on domestic ruminants and other vertebrates. Several pathogens such as *Ba. canis*, *Cx. burnetii*, *Eh. canis*, *Ri. conorii*, *Ri. rickettsii*, *Theileria* sp., *Anaplasma* sp., and CCHFV have been isolated from *R. sanguineus*[122–124]. *R. bursa* is common among livestock transmitting the protozoans *Ba. bigemina*, *Ba. caballi*, *Th. equi* and *Ba. bovis*[125]. Following these highly infected vectors, much lower prevalence levels were detected in *R. appendiculatus*, *H. schulzei*, *H. rufipes*, *H. aegyptium*

and *Boophilus* sp. These vectors should not be underestimated, as future investigations may reveal a high tendency of these species to transmit pathogens.

Controlling strategies against ticks and tick-borne diseases for prevention of significant losses due to both economic and public health problems are also seem to be important and helpful. Many attempts have been carried out for the control of ticks and tickborne diseases[126]. Some other additional methods have been suggested: (1) livestock sheds should be checked regularly in terms of tick infestation; (2) different species of livestock should be held separately to avoid interspecies tick infection; (3) quarantine of newly purchased animals decreases the chance of tick transmission to existing animals; (4) periodic application of acaricide and chemotherapy according to regional and national guidelines is sometimes suggested; (5) clearance of vegetation cut off the connection between different stages of tick's life and disrupts their life cycle is also suggested; (6) some novel methods including application of vaccines against tick-borne pathogens, biological control, and genetically resistant livestock breeds are in the spotlight[127].

This investigation had some limitations: In the old classification of Iran provinces, some provinces are currently divided in two or more provinces, resulting in the less accuracy of the old literature, as they cover a larger area. In addition, access to the full text of some dissertations required a visit to the relevant center, which was very difficult due to the COVID-19 pandemic. In such cases, we missed some dissertations. Furthermore, the scientific name of some of tick species had changed since the publication of the associated papers, so we had to search with the old names as well.

In conclusion, the occurrence of at least 20 different pathogens (in 10 genera) in 28 species (in 9 genera) of ticks in 26 provinces of Iran, sheds light on the current status of the country in terms of tick-borne pathogens. Rate of infection to different pathogens in different regions, especially western parts of Iran, is a warning for public and animal health. Further investigations and persistent surveillance of vectors as well as vertebrate hosts will expand the chance of controlling tick-borne pathogens. In most parts of the meta-analysis concerning total pathogens of Iran, the results showed high heterogeneity ($I^2 > 75\%$). Similarly, meta-analysis of separate provinces revealed high heterogeneity. This is not unexpected due to the variations associated with the different detection methods, sample size, geographical traits, location, time of the study, and population of interest. While the significance of a meta-analysis in regarding to the prevalence of tick-borne pathogens is undeniable, it is suggested that meta-analysis should not be an adequate alternative for large-scaled epidemiological studies due to heterogeneous approaches, regions and times of different studies.

Conflict of interest statement

The authors declare that there is no conflict of interest.

Authors' contributions

HB, MK, and ASJ planned for the study. HB, ASJ, MK, and MMS performed the literature search and data extraction. MK and ZT critically evaluated the manuscript. ASJ performed the meta-analysis. The final manuscript approved by all the authors.

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