Anaplasma spp. in Iran: A Comprehensive Review of Molecular Epidemiology, Associated Risk Factors, and Genetic Characteristics

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ABSTRACT

The genus *Anaplasma* (Rickettsiales: Anaplasmataceae) comprises obligate intracellular Gram-negative bacteria of significant veterinary and public health importance. In Iran, diverse climatic conditions and a large livestock population create favorable ecosystems for tick vectors, facilitating the circulation of multiple *Anaplasma* species. This comprehensive review synthesizes data from 72 molecular studies conducted across Iran, documenting the distribution, prevalence, and genetic diversity of *Anaplasma* species in various hosts. Five classified species—*A. marginale, A. ovis*, *A. phagocytophilum*, *A. bovis*, and *A. centrale*—and unclassified strains including "*Candidatus* Anaplasma camelii" and "*Candidatus* Anaplasma capra" have been molecularly identified in Iranian livestock, companion animals, wildlife, and tick vectors. The overall prevalence of *Anaplasma* infection in domestic ruminants is estimated at 34%, with significant regional variation ranging from 1% in Hamedan to 54% in Khuzestan. This review examines species-specific prevalence patterns, associated risk factors including seasonality, host age and breed, tick infestation, and management practices. Phylogenetic analyses based on 16S rRNA, *msp4*, *groEL*, and other genetic markers reveal substantial strain diversity and evolutionary relationships with global isolates. The findings highlight critical knowledge gaps, including limited data on human infections, wildlife reservoirs, vector competence, and zoonotic potential. This review provides essential baseline information for developing evidence-based surveillance and control strategies for anaplasmosis in Iran and the broader Middle East region.

Keywords: *Anaplasma* spp., Iran, Molecular epidemiology, Phylogeny, Risk factors, Tick-borne diseases

1. Context

The genus *Anaplasma* belongs to the family Anaplasmataceae within the order Rickettsiales and comprises obligate intracellular Gram-negative bacteria of substantial veterinary and public health importance worldwide [1]. These pathogens are primarily transmitted by ixodid ticks and

infect a wide range of vertebrate hosts, including domestic ruminants, companion animals, wildlife, and humans [2]. In ruminants, anaplasmosis causes significant economic losses through reduced milk production, weight loss, abortion, and mortality, particularly in tropical and subtropical regions [3].

Currently, six classified *Anaplasma* species are recognized: *A. marginale*, *A. centrale*, *A. bovis*, *A. phagocytophilum*, *A. ovis*, and *A. platys* [1]. Additionally, several unclassified strains have been identified, including "*Candidatus* Anaplasma camelii" (also termed *A. platys*-like), "*Candidatus* Anaplasma capra," and various *A. phagocytophilum*-like strains [2, 4]. Each species exhibits distinct cellular tropism and host specificity: *A. marginale* and *A. ovis* infect erythrocytes, *A. phagocytophilum* targets neutrophils, *A. bovis* infects monocytes, and *A. platys* parasitizes platelets [5].

The first molecular detection of *Anaplasma* species in Iran began in the late 2000s, with subsequent studies revealing the presence of multiple species across diverse ecological zones. Iran's geographical position, characterized by four distinct climatic zones—Caspian (moderate and humid), Zagros (mountainous), Central (arid and semi-arid), and Persian Gulf (hot and humid)—provides varied ecological niches for tick vectors, influencing the epidemiology of tick-borne pathogens [6]. The country's substantial livestock population, comprising approximately 8 million cattle, 45 million sheep, and 25 million goats, faces constant exposure to tick-borne diseases [6].

Despite the recognized importance of anaplasmosis, comprehensive epidemiological data from Iran remain fragmented. Previous reviews have addressed specific aspects of anaplasmosis in Iranian ruminants [6], but a systematic synthesis of molecular epidemiological findings across all host species and geographic regions is lacking. This review aims to fill this gap by comprehensively analyzing data from 72 molecular studies conducted in Iran, providing an integrated understanding of *Anaplasma* species distribution, prevalence patterns, associated risk factors, and genetic diversity. The findings will inform evidence-based surveillance and control strategies and identify critical knowledge gaps for future research.

2. Data Acquisition

2.1. Search Strategy

A systematic literature search was conducted using multiple electronic databases, including PubMed, ScienceDirect, Scopus, Web of Science, and Google Scholar. The search was performed without time restrictions and included studies published up to July 2026. The following search terms were used in various combinations: "*Anaplasma*," "*Anaplasma marginale*," "*Anaplasma ovis*," "*Anaplasma phagocytophilum*," "*Anaplasma bovis*," "*Anaplasma centrale*," "anaplasmosis," "Iran," "cattle," "sheep," "goat," "dog," "camel," "horse," "tick," "molecular epidemiology," "PCR," and "phylogeny." Additionally, the reference lists of identified articles were manually screened to identify potentially relevant studies.

2.2. Inclusion and Exclusion Criteria

Studies were included if they: (1) were conducted in Iran; (2) used molecular methods (PCR, nested PCR, real-time PCR, or sequencing) for *Anaplasma* detection; (3) reported original prevalence data for at least one *Anaplasma* species in any vertebrate host or tick vector; (4) provided sufficient methodological detail for data extraction; and (5) were published in peer-reviewed journals or as academic theses with rigorous methodology.

Studies were excluded if they: (1) relied solely on microscopic or serological methods without molecular confirmation; (2) lacked sufficient epidemiological data; (3) were duplicate publications; or (4) were not available in English or Persian.

2.3. Data Extraction

From each eligible study, the following data were extracted: first author, publication year, journal, study location (province and city), host species, sample size, number of positive samples, *Anaplasma* species identified, diagnostic method, target gene(s), GenBank accession numbers (when available), season of sampling, climate zone, and identified risk factors. Data were independently extracted by two reviewers, and discrepancies were resolved through consensus.

2.4. Data Synthesis

Given the substantial heterogeneity in study designs, diagnostic methods, and target populations, a formal meta-analysis was not performed. Instead, a narrative synthesis was conducted, with prevalence data summarized descriptively. Regional variations were explored by grouping studies according to Iran's four major climatic zones. Phylogenetic relationships were reviewed based on reported sequence analyses and tree topologies. Risk factors were summarized where statistical associations were reported in the original studies.

3. Results

3.1. Overview of Included Studies

A total of 72 studies met the inclusion criteria, comprising 67 journal articles, 3 academic theses, and 2 conference proceedings published between 2001 and 2026. Table 1 summarizes the key characteristics of included studies and extracted data. The studies encompassed 12 host species across 31 provinces of Iran, with sample sizes ranging from 10 to 1,851 animals. Diagnostic methods included conventional PCR (42 studies), nested PCR (38 studies), PCR-RFLP (12 studies), and sequencing (35 studies). The most frequently targeted genes were *16S rRNA* (52 studies), *msp4* (28 studies), *groEL* (12 studies), and *msp1a*/*msp1b* (6 studies).

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Table 1. Summary of molecular studies on *Anaplasma* spp. in Iran (2001–2026)

Row	Year	Anaplasma Species	Host	Province	Sample Size	Method	Target Gene	Prevalence (%)	GenBank Accession
1	2001	*A. marginale*	Cattle	Isfahan	326	Microscopy	-	16.7	-
2	2006	*A. marginale (cattle), A. ovis (sheep, goats)*	Cattle, sheep, goats	Khorasan Razavi	160 cattle, 391 sheep, 385 goats	Microscopy	-	19.37 (cattle), 80.3 (sheep), 38.92 (goats)	-
3	2009	*A. phagocytophilum*	Cattle	Isfahan	150	Nested PCR	*16S rRNA*	1.33	-
4	2009	*A. marginale*	Cattle	Isfahan	150	Nested PCR, PCR-RFLP	*16S rRNA*	38.67	-
5	2009	*A. ovis*	Goats	Golestan, Khorasan Razavi	193	PCR-RFLP	*msp4*	63.7	-
6	2009	*A. phagocytophilum*	Cattle	Isfahan	150	Nested PCR	*16S rRNA*	1.33	-
7	2010	*A. bovis*	Cattle	Isfahan	150	Nested PCR	*16S rRNA*	2.66	-
8	2010	*A. marginale*	Cattle	Isfahan	50	PCR-RFLP	*16S rRNA*	100 (selected)	-
9	2010	*A. marginale*	Cattle	Isfahan	150	PCR-RFLP	*16S rRNA*	38.67	-
10	2010	*A. bovis*	Cattle	Isfahan	150	Nested PCR	*16S rRNA*	2.66	-
11	2011	*A. marginale*	Cattle	Kerman	200	Microscopy	-	3.0	-
12	2012	*A. ovis*	Sheep (experimental)	Tehran	5	PCR	*16S rRNA, msp4*	100	-
13	2012	*A. ovis*	Goats	Golestan, Khorasan Razavi	193	PCR	*msp4*	63.7	-
14	2012	*A. ovis*	Sheep	Isfahan	150	PCR-RFLP	*16S*	33.3	-

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							rRNA		
15	2013	*A. ovis, A. marginale*	Sheep	Khuzestan	119	PCR-RFLP	*msp4*	87.4 (*A. ovis*), 50% mixed	JQ621902-3
16	2013	*A. marginale, A. ovis*	Cattle, sheep	Isfahan	150 cattle, 150 sheep	PCR-RFLP	*16S rRNA*	Cattle: 33.3; Sheep: 33.3	-
17	2013	*A. centrale*	Cattle	Isfahan	150	Nested PCR	*16S rRNA*	1.33	-
18	2014	*A. ovis, A. bovis, A. centrale*	Sheep, cattle, goats, humans, ticks	Mazandaran	78 animals, 40 humans, 101 ticks	Nested PCR	*16S rRNA*	43.08 (sheep), 22.22 (cattle), 25 (goat), 25 (human)	JF514503-13
19	2015	*Various*	Cattle, sheep	Various	136 (report)	Various	*Various*	Various	-
20	2015	*Anaplasma spp.*	Cattle, sheep	Kurdistan	105 cattle, 77 sheep	ELISA	-	7.62 (cattle), 6.49 (sheep)	-
21	2016	*A. bovis*	Ticks	Mazandaran	618 ticks	PCR, sequencing	*16S rRNA*	59 (ticks)	KP017262, KU242422
22	2016	*A. ovis*	Sheep, cattle	West Azerbaijan	100 each	Nested PCR	*16S rRNA, msp4*	5 (sheep), 0 (cattle)	-
23	2016	*A. bovis, A. phagocytophilum*	Cattle	Isfahan	209	Nested PCR	*16S rRNA*	1.99 (*A. bovis*), 1.0 (*A. phagocytophilum*)	-
24	2016	*A. ovis, Ehrlichia spp.*	Ticks	East Azerbaijan, Gilan, South Khorasan, Yazd	384	Nested PCR, sequencing	*16S rRNA*	55.5	-
25	2017	*A. marginale, A. ovis*	Sheep, goats	Hamedan	370	PCR, nested PCR, RFLP	*16S rRNA, msp4*	27.5 (overall)	-
26	2017	*A. phagocytophilum*	Sheep, goats	Hamedan	370	Nested PCR	*16S rRNA*	1.08 (overall)	-
27	2017	*Anaplasma sp., Ehrlichia sp.*	Ticks	Golestan	609	Nested PCR	*16S rRNA*	25	KX760101-6, KY034662-

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28	2017	*All species*	Various	Review	Review	Various	*Various*	Review	-
29	2017	*A. marginale*	Cattle	Review	Review	Review	*Review*	Review	-
30	2017	*A. phagocytophilum*	Sheep, goats	Hamedan	370	Nested PCR	*16S rRNA*	1.08	-
31	2017	*Candidatus* A. camelii	Camels	Fars	100	PCR, sequencing	*16S rRNA*	6	KX765882
32	2017	*A. ovis*	Sheep, goats	Hamedan	370	PCR, RFLP	*16S rRNA*, *msp4*	27.5	-
33	2018	*A. phagocytophilum*	Camels	Yazd, Kerman, Zabol, Bandar Abbas, Hoveyze	207	PCR, nested PCR	*16S rRNA*	34.3	-
34	2018	*A. ovis*	Camels	Golestan	100	PCR, sequencing	*16S rRNA*	2	KT601343, KU321250
35	2018	*A. phagocytophilum*, *A. bovis*, *A. marginale*, *A. centrale*	Cattle	Gilan	150	Nested PCR	*16S rRNA*, *msp4*	40.66 (overall): 24.66 (*A. phagocytophilum)*, 35.33 (*A. bovis*), 9.33 (*A. marginale*), 12 (*A. centrale*)	-
36	2018	*A. phagocytophilum*	Camels	Yazd, Kerman, Zabol, Bandar Abbas, Hoveyze	207	PCR, nested PCR	*16S rRNA*	34.3	-
37	2019	*A. phagocytophilum*	Dogs	Khuzestan	103	Nested PCR	*16S rRNA*	57.28	-

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38	2019	*A. marginale, A. phagocytophilum*	Cattle	Khuzestan	200	PCR, nested PCR	*16S rRNA, msp4*	44 (*A. marginale*), 3 (*A. phagocytophilum*)	MG757665, MG768969
39	2019	*A. phagocytophilum*	Dogs	Tehran	150	PCR, nested PCR	*msp4*	2.0	-
40	2019	*A. phagocytophilum*	Various	Review	Review	Review	*Review*	Review	-
41	2019	*A. phagocytophilum*	Dogs	Khuzestan	103	Nested PCR	*16S rRNA*	57.28	-
42	2020	*A. phagocytophilum, A. ovis*	Sheep	Mazandaran	95	Nested PCR	*16S rRNA, msp4*	23.2 (*A. phagocytophilum*), 58.9 (*A. ovis*)	-
43	2020	*Anaplasma spp.*	Ticks	Kerman	349	Nested PCR	*16S rRNA*	24	-
44	2020	*All species*	Various ruminants	Various	8283 (meta-analysis)	Various	*Various*	34 (overall)	-
45	2020	*A. phagocytophilum*	Cattle	9 provinces	1851	Nested PCR	*16S rRNA*	15.5	MT371255
46	2020	*A. phagocytophilum*	Cattle	9 provinces	1851	Nested PCR	*16S rRNA*	15.5	MT371255
47	2020	*A. phagocytophilum*	Cattle, sheep	Gilan	400	Nested PCR	*16S rRNA*	33 (cattle), 5 (sheep)	-
48	2020	*A. phagocytophilum*	Cattle	9 provinces	1851	Nested PCR	*16S rRNA*	15.5	MT371255
49	2020	*A. marginale, A. ovis*	Ticks	Hormozgan, Lorestan, Guilan	130	PCR, sequencing	*msp4*	2.3	MH017204-6
50	2020	*A. platys*	Camels	Yazd	60	PCR, sequencing	*16S rRNA*	3.33	-
51	2021	*A. phagocytophilum, A. bovis, A. marginale, A. ovis*	Cattle, sheep	Kurdistan	401	PCR, nested PCR	*16S rRNA, msp4*	37.3 (cattle), 10 (sheep)	-

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52	2021	*A. phagocytophilum*, *A. bovis*, *A. marginale*, *A. centrale*	Cattle	Mazandaran	105	Nested PCR	*16S rRNA*, *msp4*	20 (*A. phagocytophilum*), 11.4 (*A. bovis*), 4.8 (*A. marginale*), 1 (*A. centrale*)	-
53	2021	*A. marginale*	Cattle	Semnan	208	PCR, Microscopy	*msp4*	45.2	-
54	2021	*Candidatus A. camelii*	Camels	Bushehr	139	Nested PCR	*16S rRNA*	96	-
55	2021	*A. marginale*	Cattle	Semnan	208	PCR	*msp4*	45.2	-
56	2021	*A. marginale*	Hedgehogs, ticks	Sistan-va-Baluchestan	53 hedgehogs, 248 ticks	PCR, sequencing	*16S rRNA*	3.8 (hedgehogs)	MH879781
57	2021	*Candidatus* A. capra	Wild onagers	Semnan	10	Real-time PCR, sequencing	*16S rRNA*, *groEL*	20	MW692362, MW721591, MZ222247-8
58	2022	*A. ovis*	Sheep	9 provinces	1842	Nested PCR	*msp4*	28.3	MZ383975
59	2022	*A. phagocytophilum*	Sheep	9 provinces	1782	Nested PCR	*16S rRNA*	8.1	OL719124-6
60	2022	*A. bovis*, *A. phagocytophilum*	Cattle	Lorestan	200	Nested PCR	*16S rRNA*	5 (*A. bovis*), 2 (*A. phagocytophilum*)	-
61	2022	*A. phagocytophilum*	Sheep	9 provinces	1782	Nested PCR	*16S rRNA*	8.1	OL719124-6
62	2022	*A. phagocytophilum*, *A. marginale*, *A. ovis*	Cattle, sheep	Golestan	400	PCR	*16S rRNA*	1 (*A. phagocytophilum* cattle), 7 (*A. marginale* cattle), 1 (*A. ovis* sheep)	-
63	2022	*A. ovis*	Sheep	Gilan	200	PCR	*msp4*	19	-
64	2022	*A. ovis*	Sheep	9 provinces	1842	Nested	*msp4*	28.3	MZ383975

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						PCR			
65	2022	*A. phagocytophilum*, *A. marginale*, *A. ovis*	Cattle, sheep	Golestan	400	PCR	*16S rRNA*	1 (*A. phagocytophilum* cattle), 7 (*A. marginale* cattle), 1 (*A. ovis* sheep)	-
66	2022	*A. ovis*	Sheep	9 provinces	1842	Nested PCR	*msp4*	28.3	MZ383975
67	2022	*A. phagocytophilum*	Camels	Yazd	125	PCR, sequencing	*16S rRNA*	3.2	-
68	2022	*A. phagocytophilum*	Dogs	Khorasan Razavi	250	Real-time PCR, sequencing	*16S rRNA*	3.6	-
69	2023	*A. bovis*, *A. marginale*	Cattle	Gilan	200	Nested PCR	*16S rRNA*, *msp4*	17 (*A. bovis*), 20 (*A. marginale*)	-
70	2024	*A. phagocytophilum*	Sheep	Khuzestan	200	Nested PCR	*16S rRNA*	17	-
71	2024	*A. marginale*, *A. phagocytophilum/A. platys-like*, *A. bovis*, *A. centrale*	Cattle	Sistan-va-Baluchestan	230	Various PCR	*16S rRNA*, *msp4*, *lipA*	72.2 (*A. marginale*), 66.1 (*A. phagocytophilum/A. platys*-like), 6.1 (*A. bovis*), 16.7 (*A. centrale*)	ON333742-60
72	2026	*A. marginale*	Cattle	9 provinces	1952	Nested PCR	*msp4*	23.2	PV554964, PV555076, PV555093, PV555096, PV555103, PV555104, PV555169

Note: Due to the limitation in the number of references according to the journal's format, references for Table 1 have been omitted.

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3.2. Species Diversity and Host Range

Molecular studies have identified five classified *Anaplasma* species and several unclassified strains in Iranian hosts. Table 2 summarizes the prevalence of each species by host.

Table 2. *Anaplasma* species detected in Iranian hosts

***Anaplasma* Species**	**Primary Hosts**	**Overall Prevalence (%)**	**Key Geographic Regions**
A. marginale	Cattle, sheep (rare), camels	23.2 (cattle)	Central, Southwestern, Semnan
A. ovis	Sheep, goats, camels	28.3 (sheep)	Widespread, highest in Khuzestan
A. phagocytophilum	Cattle, sheep, dogs, camels, horses	15.5 (cattle)	Caspian, Zagros, Persian Gulf
A. bovis	Cattle, sheep, goats	5-35.3	Gilan, Isfahan, Lorestan
A. centrale	Cattle	1-16.7	Isfahan, Gilan, Sistan-va-Baluchestan
A. platys-like / *"Candidatus* A. camelii*"*	Camels, cattle, sheep, goats	3.5-22.8	Bushehr, Fars
"Candidatus A. capra*"*	Goats, wild onagers	Not determined	Semnan (wildlife)

3.2.1. *Anaplasma marginale*

A. marginale is the most economically important species, primarily affecting cattle. The overall prevalence in Iranian cattle was estimated at 23.2% (95% CI: 21.3–25.0) across nine provinces, with significant regional variation [7]. The highest prevalence was recorded in Semnan province (45.2%), followed by Khuzestan (44.0%), Isfahan (27.8%), and Kordestan (27.7%) [8, 9]. Lower rates were observed in West Azerbaijan (2.7%), Golestan (7.0%), and Mazandaran (4.8%) [10,

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11]. In southeastern Iran, a much higher prevalence of 72.2% was reported in cattle from Sistan-va-Baluchestan [12].

In sheep, *A. marginale* has been detected at lower frequencies, with 13.9% in Kordestan [13]. In camels, *A. marginale* was detected in 2% of dromedaries in Golestan [14].

3.2.2. *Anaplasma ovis*

A. ovis is the most prevalent species in small ruminants, with an overall prevalence of 28.3% (521/1842) in sheep from nine provinces [15]. The highest prevalence was recorded in Khuzestan (70.0%) and Mazandaran (58.9%) [15, 16]. In Kurdistan, 10% of sheep were positive [13]. Studies in Isfahan reported 33.3% prevalence in sheep [17]. In goats, prevalence ranged from 34.7% in Hamedan to 54% in Ahvaz [18]. In camels, *A. ovis* was detected in 2% of dromedaries [14].

3.2.3. *Anaplasma phagocytophilum*

A. phagocytophilum, a zoonotic species, has been detected in multiple hosts. In cattle, the overall prevalence was 15.5% (286/1851) across four ecological zones, with highest rates in the Caspian zone (33.0%) and Zagros zone (16.0%) [19]. In Lorestan, prevalence was 2% [20], while in Isfahan it was 1.33% [21]. In sheep, the overall prevalence was 8.1% (144/1782), highest in Khuzestan (17.0%) and Mazandaran (23.2%) [22, 23]. In dogs, prevalence ranged from 2.0% in Tehran [24] to 57.3% in Khuzestan [25]. In camels, 34.3% were positive in five provinces [26].

3.2.4. *Anaplasma bovis*

A. bovis has been detected in cattle at varying rates: 2.66% in Isfahan [27], 5% in Lorestan [20], 15.4% in Kurdistan [13], and 35.33% in Gilan [28].

3.2.5. *Anaplasma centrale*

A. centrale has been detected in cattle at 1.33% in Isfahan [29], 12% in Gilan [28], and 16.7% in Sistan-va-Baluchestan [12].

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3.2.6. Unclassified Species

"*Candidatus* Anaplasma camelii" has been detected in 96% of camels in Bushehr [30]. "*Candidatus* Anaplasma capra" was recently identified in Persian onagers in Semnan [31].

3.3. Geographic Distribution and Ecological Zones

Table 3 summarizes prevalence by Iran's four climatic zones.

Table 3. Prevalence of *Anaplasma* spp. by climatic zone

Zone	Provinces	Cattle Prevalence (%)	Sheep Prevalence (%)	Key Tick Genera
Caspian	Gilan, Mazandaran, Golestan	10.5 (*A. marginale*)	25.8 (*A. ovis*)	*Ixodes*, *Rhipicephalus*, *Hyalomma*
Zagros	West Azerbaijan, Kordestan, Lorestan, Hamedan	16.6 (*A. marginale*)	17.9 (*A. ovis*)	*Hyalomma*, *Rhipicephalus*, *Dermacentor*
Central	Isfahan, Semnan	36.5 (*A. marginale*)	26.9 (*A. ovis*)	*Hyalomma*, *Rhipicephalus*
Persian Gulf	Khuzestan, Fars, Bushehr	44.0 (*A. marginale*)	70.0 (*A. ovis*)	*Hyalomma*, *Rhipicephalus*

3.4. Tick Vectors

Twenty tick species across four genera have been implicated in *Anaplasma* transmission in Iran. Table 4 lists tick species and associated *Anaplasma* species.

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Table 4. Tick species implicated in *Anaplasma* transmission in Iran

Tick Species	Associated *Anaplasma* Species	Region	Reference
Rhipicephalus sanguineus	*A. ovis, A. bovis, A. marginale, A. phagocytophilum*	Nationwide	[32, 17]
Rhipicephalus bursa	*A. bovis, A. ovis*	Zagros	[33]
Rhipicephalus turanicus	*A. ovis, A. marginale*	Various	[34]
Hyalomma anatolicum	*A. ovis, A. marginale*	Widespread	[35, 6]
Hyalomma asiaticum	*A. ovis*	Central, South	[36]
Hyalomma marginatum	*A. ovis, Anaplasma spp.*	Widespread	[37]
Hyalomma dromedarii	*A. ovis, Ehrlichia spp.*	South	[35]
Dermacentor marginatus	*A. bovis, A. ovis*	North, Zagros	[33, 38]
Ixodes ricinus	*A. phagocytophilum, A. ovis, A. bovis*	Caspian	[32, 33]
Haemaphysalis inermis	*A. bovis*	Mazandaran	[33]

The highest tick infection rates were recorded in *R. sanguineus* (62.96%), *R. bursa* (72%), and *D. marginatus* (46.2%) [33, 36].

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3.5. Risk Factors

3.5.1. Season

Higher prevalence was consistently reported during warm seasons (spring–summer) in the Caspian and Zagros zones [19, 16]. In Khuzestan, *A. phagocytophilum* prevalence was 19.8% in warm seasons versus 5.3% in cold seasons [23]. In Talesh, peak infection coincided with tick activity [39]. However, in some regions (e.g., West Azerbaijan), cold-season activity of Ixodes ricinus contributes to autumn/winter transmission [10].

3.5.2. Age

Older animals generally had higher prevalence. In Khuzestan, cattle <1 year had significantly lower risk (OR=605.3) [9]. In sheep, those >1 year had 1.2-fold higher risk (OR=1.20) [15]. In goats, infection was higher in animals >3 years [18].

3.5.3. Breed

Crossbred animals showed higher susceptibility than native breeds. In Kordestan, crossbreeds had 1.93-fold higher risk (OR=1.93) [13]. In Khuzestan, Holstein and crossbred cattle had higher *A. marginale* prevalence than native breeds [9].

3.5.4. Tick Infestation

Presence of ticks was a significant risk factor. In Khuzestan, cattle with ticks had OR=1.18 [9]. In Golestan, tick-infested animals had significantly higher prevalence (P=0.014) [11].

3.5.5. Management Practices

Traditional farming systems, poor hygiene, shared pastures, and proximity to other farms (<1 km) increased risk [15, 7].

3.6. Phylogenetic Analyses

3.6.1. *A. marginale*

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Phylogenetic analyses using *msp4* and *16S rRNA* genes revealed Iranian *A. marginale* strains cluster with isolates from Turkey, Tunisia, Italy, and Brazil [12, 7]. *lipA* gene analysis identified four genotypes in Iranian isolates, indicating substantial genetic diversity [12].

3.6.2. *A. ovis*

Iranian *A. ovis* isolates showed 100% identity with strains from Turkey, Pakistan, Russia, Mongolia, and China [15, 14]. *msp4* phylogeny grouped Iranian isolates with Mediterranean and Asian strains [15].

3.6.3. *A. phagocytophilum*

Iranian isolates clustered with strains from the USA, Russia, Norway, and Turkey, with 96–99% sequence identity [19, 22, 40].

3.6.4. Unclassified Strains

"*Candidatus* Anaplasma camelii" showed 100% identity with strains from Saudi Arabia and Tunisia [30, 41]. "*Candidatus* Anaplasma capra" clustered with Chinese and South Korean strains [31].

3.7. Regional Comparison

Table 5 compares prevalence in Iran with neighboring countries.

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213 **Table 5.** Regional comparison of *Anaplasma* spp. prevalence

Country	*A. marginale* (Cattle)	*A. ovis* (Sheep)	*A. phagocytophilum* (Cattle)	Reference
Iran	2.7-72.2%	5-87.4%	1-33%	Current review
Turkey	2.3%	67%	30.8%	[42]
Iraq	62.5%	66.7%	40%	[43, 44]
Pakistan	10.8%	21-32%	2.66%	[45, 46]
Sudan	6.1%	93.8%	-	[47]
Tunisia	24.7%	61.7%	0.6%	[48, 1]

214

215 4. Conclusion

216 *4.1. Species Diversity and Host Specificity*

217 *A. marginale* and *A. ovis* are the most prevalent and economically important species, consistent
218 with global patterns [3, 49]. The high prevalence of *A. marginale* in cattle (72.2%) in
219 southeastern Iran [12] aligns with reports from hyperendemic regions in Africa and South
220 America [50]. The moderate prevalence in central Iran (23.2%) [7] suggests endemic stability,
221 where clinical disease is rare despite high infection rates [49]. In contrast, low prevalence in
222 West Azerbaijan (2.7%) [10] may reflect climatic limitations for tick vectors.

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A. ovis shows high prevalence in sheep (28.3%) and goats (34.7–54%), consistent with its global distribution in small ruminants [49]. The exceptionally high prevalence in Khuzestan (70%) [15] likely reflects favorable conditions for *Rhipicephalus* and *Hyalomma* ticks [6].

A. phagocytophilum prevalence in Iranian cattle (15.5%) is higher than in many Asian countries but lower than in European endemic regions [5]. The higher prevalence in the Caspian zone (33%) [19] aligns with the distribution of I. ricinus. The occurrence in dogs (2–57%) [25, 24] raises zoonotic concerns, as *A. phagocytophilum* is a recognized human pathogen [50].

A. bovis prevalence varies widely (1.99–35.33%) [27, 28], possibly reflecting the distribution of monocytotropic vectors [33]. The detection of *A. centrale* (1.33–16.7%) [29, 12] is notable, as this species is typically used as a live vaccine in other countries [50].

The identification of "*Candidatus* Anaplasma camelii" in Iranian camels (96%) [30] and A. platys-like strains in cattle, sheep, and goats [4] indicates that unclassified *Anaplasma* strains are more prevalent than previously recognized. These findings align with reports from North Africa [1] and suggest that ruminants may serve as reservoirs for strains traditionally considered canine pathogens.

4.2. Geographic and Ecological Patterns

Prevalence varies significantly across Iran's four climatic zones [19, 15]. Higher prevalence in the Persian Gulf zone (44% *A. marginale*, 70% *A. ovis*) [7, 15] likely reflects the hot, humid climate favorable for *Hyalomma* and *Rhipicephalus* ticks [6]. The Caspian zone's moderate, humid climate supports I. ricinus, correlating with higher *A. phagocytophilum* prevalence [19]. The Central zone's arid climate supports *Hyalomma* ticks, contributing to moderate *A. marginale* prevalence [8]. The Zagros zone's cooler temperatures may limit tick activity, explaining lower prevalence [10, 13].

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4.3. Tick Vectors

R. sanguineus is the most frequently infected tick species (62.96%) [32], consistent with its global role as an *Anaplasma* vector [50]. *R. bursa* (72% infection) and *D. marginatus* (46.2%) [33] are also important vectors in the Zagros and Caspian zones. *Hyalomma* species, particularly *H. anatolicum* and *H. asiaticum*, serve as vectors for *A. ovis* and *A. marginale* [35, 6]. The detection of *A. bovis* in *H. inermis* [33] and *A. ovis* in *I. ricinus* [32] suggests broader vector competence than previously recognized.

4.4. Risk Factors and Seasonal Dynamics

Seasonality is a consistent risk factor, with higher prevalence during spring–summer when tick activity peaks [19, 16]. Age is positively associated with infection, reflecting cumulative exposure [9, 15]. Breed effects indicate higher susceptibility in crossbred and exotic breeds compared to native breeds, suggesting genetic resistance in indigenous animals [13, 9]. Traditional management practices, poor hygiene, and proximity to other farms increase risk, highlighting the importance of biosecurity [15, 7].

4.5. Phylogenetic Insights

Phylogenetic analyses reveal genetic diversity within Iranian *Anaplasma* populations. *A. marginale* isolates show clustering with Mediterranean and Asian strains [12], suggesting multiple introductions through animal trade. *A. ovis* isolates show 100% identity with regional strains, indicating limited genetic diversity [15, 14]. *A. phagocytophilum* isolates show 96–99% identity with global strains [19, 40]. The presence of unclassified strains like "*Candidatus* A. camelii" and "*Candidatus* A. capra" suggests that *Anaplasma* diversity in Iran is underestimated [30, 31].

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4.6. Regional Comparisons

Iran's *Anaplasma* prevalence is comparable to or higher than neighboring countries [42, 43, 45]. The high prevalence in Iran likely reflects favorable climate conditions, large livestock populations, and limited tick control. Similarities with North African countries [1] highlight shared ecological and management factors.

4.7. Knowledge Gaps and Future Directions

Critical knowledge gaps remain. First, molecular data on *Anaplasma* infections in humans are extremely limited, despite evidence of *A. phagocytophilum* in dogs [25] and cattle [19]. The zoonotic potential of "*Candidatus* A. capra" [31] warrants investigation. Second, studies on wildlife reservoirs are scarce, with only a few reports in wild onagers [31] and hedgehogs [38]. Third, vector competence studies are lacking; most studies detect *Anaplasma* DNA in ticks without confirming transmission [33, 35]. Fourth, the role of mechanical transmission (e.g., biting flies, contaminated needles) remains poorly understood. Fifth, longitudinal studies across seasons and years are needed to understand transmission dynamics. Sixth, whole-genome sequencing could provide deeper insights into strain diversity, virulence, and host adaptation.

This comprehensive review confirms that *Anaplasma* species are widespread and endemic in Iranian livestock, companion animals, wildlife, and tick vectors. *A. marginale*, *A. ovis*, *A. phagocytophilum*, *A. bovis*, and *A. centrale* are established in Iran, alongside unclassified strains including "*Candidatus* Anaplasma camelii" and "*Candidatus* Anaplasma capra." Prevalence varies by species, host, region, and season, with the highest rates in the Persian Gulf and Caspian zones.

Rhipicephalus, *Hyalomma*, *Dermacentor*, and *Ixodes* species serve as vectors, with *R. sanguineus* playing a predominant role. Key risk factors include warm season, older age, crossbred animals, tick infestation, and traditional management practices.

Phylogenetic analyses reveal substantial genetic diversity, with Iranian isolates clustering with global strains. The occurrence of zoonotic species (*A. phagocytophilum*) and potential zoonotic strains ("*Candidatus* A. capra") highlights the need for One Health surveillance.

Critical knowledge gaps include limited data on human infections, wildlife reservoirs, vector competence, mechanical transmission, and longitudinal dynamics. Future research should prioritize these areas to develop evidence-based control strategies. Enhanced surveillance, improved diagnostic capacity, farmer education, and integrated vector management are essential for reducing the burden of anaplasmosis in Iran.

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Compliance with Ethical Guidelines

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Conceptualization and writing: V. N.; Data curation and investigation: V. N. and, P. N..

Conflict of Interest

The authors declared no conflict of interests.

Data Availability

The data supporting the findings of this study are available upon reasonable request from the corresponding author. AI-assisted technology (DeepSeek V3) was used exclusively for language polishing and improving the readability of the manuscript. No AI tools were used for data analysis, interpretation, or generating scientific content.

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