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RESEARCH

Occurrence of *Rickettsia* spp. and *Coxiella burnetii* in ixodid ticks in Kassena-Nankana, Ghana

Seth Offei Addo[1,2] · Ronald Essah Bentil[1] · Bernice Olivia Ama Baako[3] · Kevin Nii Yartey[1] · Eric Behene[1] · Benjamin Asiamah[1] · Abena Akyeamaa Nyarko[1] · Victor Asoala[3] · Mohamed Sallam[4] · Suzanne Mate[5] · James C. Dunford[6,7] · John Asiedu Larbi[2] · Philip Kweku Baidoo[2] · Michael David Wilson[1] · Joseph W. Diclaro II[8] · Samuel K. Dadzie[1]

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Abstract
Ticks are arthropods of veterinary and medical importance which spread zoonotic pathogens that link animal and human health. In this study, ticks were collected from 448 livestock between February and December 2020 in the Kassena-Nankana Districts of Ghana and screened for the presence of zoonotic pathogens DNA using PCR and sequencing approaches. In total, 1550 ticks were collected and morphologically identified. Three tick genera were identified with *Amblyomma variegatum* (63%) as the predominant tick species collected. DNA was extracted from 491 tick pools and screened for the presence of DNA of *Rickettsia* spp. based on the 115 bp fragment of the 17 kDa surface protein and 639 bp of the Outer membrane protein A (*ompA*) gene and the 295 bp fragment of the transposase gene of *Coxiella burnetii IS1111a* element. From the 491 pools screened, the DNA of *Rickettsia* spp. and *C. burnetii* was detected in 56.8 and 3.7%, respectively. Coinfections were identified in 2.4% of the tick pools. Characterization of the *Rickettsia* spp. in this study based on the *ompA* gene showed that the DNA of *Rickettsia africae* and *Rickettsia aeschlimannii* accounted for 39.7 and 14.7%, respectively, and were 100% similar to sequences in GenBank. Most *R. africae* and *C. burnetii* infections occurred in ticks collected in the wet season, whereas *R. aeschlimannii* occurred mostly in the dry season. These pathogens are potential public health threats, thus there is a need to implement control measures to reduce the risk of infections in vulnerable populations.

Keywords Ixodidae · *Rickettsia africae* · *Rickettsia aeschlimannii* · *Coxiella burnetii* · PCR · Ghana

Introduction

The distribution of tick species and the associated risk of tick-borne infections are influenced by their preference for peculiar ecological environments (Parola and Raoult 2001). By adapting to the movement of animals and bird migration, ticks proliferate and colonize a region

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(Madder et al. 2011). Worldwide, and especially in Sub-Saharan Africa, tick-borne pathogens are the cause of many emerging infectious diseases (Dunster et al. 2002; Parola et al. 2005). Ticks are efficient in the transmission of various pathogens that affect both man and animals (Casati et al. 2006; AL-Hosary et al. 2018). Moreover, tick-borne diseases constitute a serious animal disease problem in Africa (Young et al. 1988), particularly among small-scale farmers in Central, East and Southern Africa (Jongejan and Uilenberg 2004). West Africa is no exception as tick-borne pathogens of medical and veterinary importance have been detected in Nigeria (Lorusso et al. 2016), Ghana (Bell-Sakyi et al. 1996; Akuffo et al. 2016; Paintsil et al. 2022), Burkina Faso (Moumouni et al. 2022), Benin (Ouedraogo et al. 2021) d te d'Ivoire (Ehounoud et al. 2016; Adjogoua et al. 2021).

Rickettsial infections continue to spread to non-endemic regions with tick bites as the primary route of transmission (Parola et al. 2013). Reports from countries including Burkina Faso and Côte d'Ivoire indicate that human exposure occurs at a seroprevalence rate of 17–36% (Mediannikov et al. 2010a; Parola et al. 2001). It is common to find rickettsial infections in travelers returning from endemic zones (Leshem et al. 2011). *Rickettsia africae*, the agent of African tick-bite fever, is transmitted by *Amblyomma hebraeum* or *Amblyomma variegatum* depending on geographical location (Parola et al. 2005). However, *Rickettsia aeschlimannii* has been isolated from *Hyalomma marginatum* in Algeria (Bitam et al. 2006), Egypt (Abdel-Shafy et al. 2012; Kernif et al. 2012) and Morocco (Sarih et al. 2008). Various tick species have been reported to harbor *Rickettsia* due to co-feeding (Mediannikov et al. 2012).

Coxiella burnetii is a bacterium that causes Q fever in humans (Gangoliya et al. 2019; Gondard et al. 2017). Apart from ruminants serving as the primary source of infection for man, wild animals, dogs and cats can be potential sources of infection (Dalton et al. 2014). *Coxiella burnetii* is transmitted through inhaling contaminated aerosol (Hogerwerf et al. 2012; Leski et al. 2011), consuming contaminated milk (Bell and Beck 1950; Hermans et al. 2011) and contact with infected tissues or tick faeces (Delsing et al. 2010). Although ticks harbour and transmit *C. burnetii* to animals, there is scarce information to support their role in transmission to humans (Eklund et al. 1947; Loukaides et al. 2006; Nett et al. 2012; Rolain et al. 2005). Even though animals such as goats and sheep are asymptomatic when infected with *C. burnetii* (De Cremoux et al. 2012), abortions can occur in pregnant animals as well as low birth weight in offspring (Stoker and Marmion 1955).

In Ghana, ticks have been identified to harbor pathogens including *Rickettsia* spp. and *C. burnetii* (Paintsil et al. 2022). This indicates the importance of ticks in the country and their significant influence on animal and human health. In the Upper East Region of Ghana, most inhabitants rear livestock for food and income. However, these animals may be amplifying hosts for infectious zoonotic pathogens, putting owners at a considerable risk of infection (Al-Tayib 2019). Movement of livestock from countries, including Burkina Faso, into Ghana could facilitate the introduction of exotic tick species as well as tick-borne pathogens. It is crucial to adopt effective control measures to reduce the burden and spread of tick-borne infections. This study sought to assess the prevalence of *Rickettsia* species and *C. burnetii* in ixodid ticks infesting livestock in Kassena-Nankana of Northern Ghana. The findings from this study will be an addition to the limited information on tick-borne pathogens in Ghana and the veterinary and public health implications.

Methods

Study site and tick collection

The study area included sites within Kassena-Nankana of the Upper East Region (Fig. 1). Kassena-Nankana has been divided into Kassena-Nankana Municipal (formerly Kassena-Nankana East) and Kassena-Nankana West District. The vegetation of the study area is Guinea Savannah with two seasons; a dry season that occurs from November to April and a wet season that spans from May to October. Residents of the district are largely into agriculture (Mensah and Fosu-Mensah 2020). Between February and December 2020, ticks were collected from randomly selected livestock (cattle, sheep and goats) in the dry and wet seasons. Each animal was restrained and ticks were removed using blunt forceps. The collected ticks were sorted out based on the host, kept in well-labelled 15-mL Eppendorf tubes containing RNALater and transported to Noguchi Memorial Institute for Medical Research. In the laboratory, the ticks were identified using morphological keys (Walker et al. 2003).

Nucleic acid extraction and detection of pathogens

The tick samples were pooled (1–10), with each pool made up of ticks of the same sex, and species and from the same animal host. Total nucleic acid was extracted from each pool using QIAamp Mini Kit (Qiagen, Valencia, CA, USA) according to the manufacturer's instructions (Crowder et al. 2010).

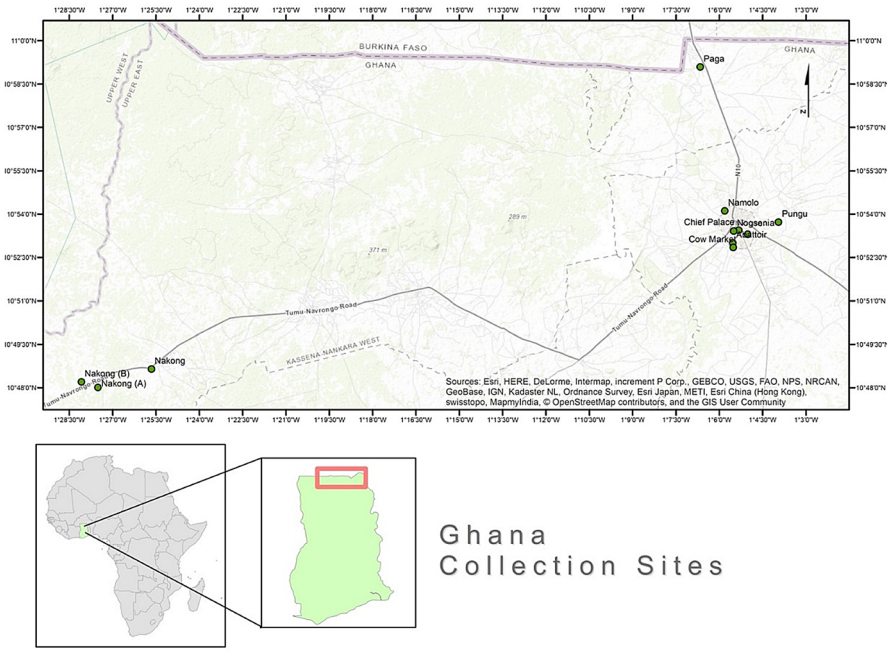

Fig. 1 Map indicating the study sites in Kassena-Nankana Districts, Ghana

The tick pools were screened for the presence of *C. burnetii* DNA using a real-time polymerase chain reaction (RT-PCR) assay that targets the 295-bp fragment of the transposase gene of *C. burnetii IS1111a* element (Klee et al. 2006). The primers used were Cox-F (CCCCGAATCTCATTGATCAGC), Cox-R (CCCCGAATCTCATTGATCAGC) and probe Cox-TM (FAM-AGCGAACCATTGGTATCGGACGTT-TAMRA-TATGG). The PCR run was performed in a 7300 RT-PCR System (Applied Biosystems, Waltham, MA, USA) per the cycling conditions: initial hold at 50 °C for 2 min, a second hold at 95 °C for 10 min and a third hold at 40 cycles for 95 °C for 15 s and 60 °C for 30 s.

Furthermore, *Rickettsia* DNA was detected in tick pools using primers R17k128F (GGGCGGTATGAAYAAACAAG), R17k238R (CCTACACCTACTCCVACAAG) and probe R17k202TaqP (FAM-CCGAATTGAGAACCAAGTAATGC-TAMRA) in a quantitative PCR (qPCR) which targets the 115 bp fragment of the 17 kDa surface protein of *Rickettsia* species (Jiang et al. 2004). The PCR was run using a 7300 RT-PCR System (Applied Biosystems) based on the cycling conditions: 1 cycle at 95 °C for 2 min, followed by 45 cycles at 95 °C for 5 s and 60 °C for 30 s (fluorescence read and data acquisition) and finally 1 cycle at 40 °C for 30 s.

The samples that were *Rickettsia* genus positive were subsequently characterized using primers 190-70 F (ATGGCGAATATTTCTCCAAAA) and 190-701R (GTTCCG TTAATGGCAGCATCT) that target the rOmpA gene (ompA) of *Rickettsia* amplifying at 632 bp (Jiang et al. 2005). Amplification was performed in a Mastercycler X50-PCR thermocycler (Eppendorf, Germany) according to the cycling conditions: initial hold at 95 °C for 5 min, followed by a second hold at 34 cycles at 95 °C for 30 s, 51.5 °C for 30 s and 72 °C for 1 min and finally a third hold at 72 °C for 5 min, followed by a hold at 4 °C. The PCR product was run on a 2% agarose gel for about 1 h and 30 min.

The positive PCR products were subsequently shipped to a commercial facility (Macrogen Europe, Amsterdam, The Netherlands) for sequencing.

Phylogenetic analysis

Nucleotide sequences obtained in this study were cleaned, edited and compared to other sequences included in the NCBI database as well as reference sequences (https://blast.ncbi.nlm.nih.gov/Blast.cgi). The Clustal Omega tool in MEGA X was used to align the sequences and phylogenetic trees constructed using the neighbor-joining method (Kumar et al. 2018). The countries of origin and accession numbers of all the GenBank sequences used in the analysis are shown in the phylogenetic tree.

Statistical analysis

STATA v.13 was used to analyze the data. The χ^2 test was used to determine the association between pooled tick infection status and livestock characteristics. A univariate generalized negative binomial mixed effect model was used to determine the association between the tick burden with animal characteristics and season. Pool Screen software was used to estimate the infection rates in the various tick species (Katholi and Unnasch 2006). The significance level was set at $\alpha = 0.05$.

Results

From the 448 livestock screened, tick infestations were 54.2% in cattle, 26.8% in sheep and 19.0% in goats (Table 1). In total, 1550 ticks, made up of 1247 adults and 303 nymphs, were collected from the examined livestock. More adult ticks were collected in the wet season than in the dry season. There was no significant association between adult ticks and characteristics such as animal host, sex, age and body part. Furthermore, more nymphs were collected from the male animals and most were attached to the scrotum (Table 1).

Tick species composition

Ticks of the genera *Amblyomma* (n = 976), *Hyalomma* (n = 290) and *Rhipicephalus* (n = 284) were identified in this study. The predominant species was *A. variegatum* (63.0%) with the least occurring tick species being *Rhipicephalus sanguineus* (s.l.) (0.06%) (Fig. 2). Adult *A. variegatum* occurred mostly in the wet season compared to the dry season (Table 2).

Table 1 Prevalence and distribution of tick life stages sampled from livestock

	No. examined (% infested)	Adult ticks (total n = 1247)				Nymph ticks (total n = 303)			
		No. collected	χ^{2a}	df	*P*	No. collected	χ^{2a}	df	*P*
Animal host									
Cattle	243 (54.24)	1052	2.87	1	0.090	303			–
Goat	85 (18.97)	13				–			
Sheep	120 (26.79)	182				–			
Animal sex									
Male	135 (30.13)	444	0.84	1	0.36	244	20.65	1	< 0.001
Female	313 (69.87)	803				59			
Age									
≤ 3 years	299 (66.74)	644	3.55	1	0.060	152	1.31	1	0.25
> 3 years	149 (33.26)	603				151			
Season									
Wet	172 (38.39)	837	44.02	1	< 0.001	–			–
Dry	276 (61.61)	410				303			
Body part									
Anal region	448	441	3.75	1	0.053	48	4.95	1	0.0261
Chest	448	258				77			
Head	448	3				1			
Limbs	448	18				–			
Udder/Scrotum	448	527				177			

[a]Wald chi-square; univariate generalized negative binomial mixed effect model was used to determine the association between the tick burden with animal characteristics and season

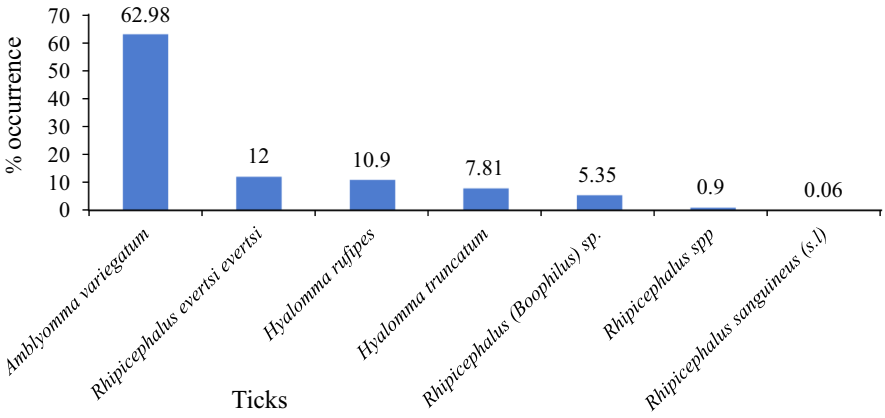

Fig. 2 Tick species sampled in Kassena-Nankana Districts, Ghana

Table 2 Seasonal abundance of tick species in Kassena-Nankana Districts, Ghana

Tick species	Adults					Nymphs	
	Wet season	Dry season	χ^{2a}	df	P	Wet season	Dry season
Amblyomma variegatum	741	34	30.64	1	< 0.001	–	201
Hyalomma rufipes	16	153	0.21	1	0.65	–	–
Hyalomma truncatum	6	110	1.72	1	0.19	–	5
Rhipicephalus evertsi evertsi	74	112	0.61	1	0.43	–	–
Rhipicephalus (*Boophilus*) sp.	–	–				–	83
Rhipicephalus spp.	–	–				–	14
Rhipicephalus sanguineus (s.l.)	–	1				–	–

[a]Wald chi-square; univariate generalized negative binomial mixed effect model was used to determine the association between the burden of tick species with season

Tick-borne pathogens DNA detected

Out of the 491 tick pools screened, an overall *Rickettsia* species positive rate of 56.8% was recorded (Table 3). *Amblyomma variegatum* had the highest positive pools for *Rickettsia* spp. DNA with an infection rate of 28.3% [95% confidence interval (95% CI) 24.38–32.51]. *Coxiella burnetii* DNA was detected in 3.7% of the tick pools examined (Table 3). Additionally, *Rhipicephalus evertsi evertsi* recorded the highest *C. burnetii* infection rate of 3.9% (95% CI 1.48–8.09). An overall coinfection of 2.4% was observed in the tick pools (Table 3).

The screened tick pools indicated a significant association between *Rickettsia*, *Coxiella* and season of tick collection with most *R. africae* and *C. burnetii* DNA detected in the wet season samples whereas *R. aeschlimannii* occurred mostly in the dry season samples (Table 4). All the above-mentioned pathogens were identified mostly in ticks collected from cattle. The DNA of *C. burnetii* was identified mostly in ticks collected from female animals whereas the DNA of *R. aeschlimannii* was detected in ticks collected from animals

Table 3 Prevalence of *Rickettsia* spp. and *Coxiella burnetii* in sampled tick species from Kassena-Nankana Districts, Ghana

Tick species	No. pools tested	*Rickettsia* spp.		*C. burnetii*		Coinfection	
		No. positive	Infection rate (95% CI)	No. positive	Infection rate (95% CI)	No. positive	Infection rate (95% CI)
Amblyomma variegatum	258	195	28.31 (24.38–32.51)	7	0.72 (0.27–1.51)	7	0.72 (0.27–1.51)
Hyalomma rufipes	85	56	47.87 (36.99–59.15)	2	1.18 (0.14–4.09)	1	0.59 (0.02–3.01)
Hyalomma truncatum	58	17	16.12 (9.17–25.28)	2	1.70 (0.20–5.83)	2	1.70 (0.20–5.83)
Rhipicephalus evertsi evertsi	52	9	5.12 (2.21–9.74)	7	3.93 (1.48–8.09)	2	1.11 (0.13–3.83)
Rhipicephalus (*Boophilus*) sp.	31	2	2.57 (0.31–8.77)	–	–	–	–
Rhipicephalus spp.	6	–	–	–	–	–	–
Rhipicephalus sanguineus (s.l.)	1	–	–	–	–	–	–
Total	491	279 (56.82%)		18 (3.67%)		12 (2.44%)	

Table 4 Association of tick-borne pathogens in the sampled ticks

	No. tick pools	*Rickettsia africae*	χ^2	df	P	*Rickettsia aeschlimanni*	χ^{2a}	df	P	*Coxiella burnetii*	χ^{2a}	df	P
Season													
Dry	283	62 (21.91)	88.4729	1	<0.001	67 (23.67)	43.3474	1	<0.001	6 (2.12)	4.5203	1	0.033
Wet	208	133 (63.94)				5 (2.40)				12 (5.77)			
Animal host													
Cattle	437	186 (42.56)	14.7149	2	0.001	72 (16.48)	10.4259	2	0.005	11 (2.52)	15.6220	2	<0.001
Goat	5	2 (40.00)				0				1 (20.0)			
Sheep	49	7 (14.29)				0				6 (12.24)			
Sex													
Female	287	106 (36.93)	2.2315	1	0.14	49 (17.07)	3.2041	1	0.073	16 (5.57)	7.1276	1	0.008
Male	204	89 (43.63)				23 (11.27)				2 (0.98)			
Age													
≤3 years	206	86 (41.75)	0.6125	1	0.43	18 (8.74)	9.9599	1	0.002	11 (5.34)	2.8155	1	0.093
>3 years	285	109 (38.25)				54 (18.95)				7 (2.46)			
Tick stage													
Adult	399	161 (40.35)	0.3598	1	0.55	68 (17.04)	9.6282	1	0.002	18 (4.51)	4.3083	1	0.038
Nymph	92	34 (36.96)				4 (4.35)				0			

[a]Pearson chi-square

older than 3 years. A significant association was also observed for *R. aeschlimannii*, *C. burnetii* and the tick developmental stage with DNA of the latter detected only in adult ticks (Table 4).

Characterization of *Rickettsia* species

Two *Rickettsia* species were identified, *R. africae* (39.7%) and *R. aeschlimannii* (14.7%). The *Rickettsia* sequences in this study were 100% similar to sequences from Benin (acc. nrs. KT633262 and KT633264), Spain (MW398876) and China (MH932058). *Rickettsia africae* was identified in *A. variegatum* (38.7%) and *R. evertsi evertsi* (1.0%). *Rickettsia aeschlimannii* was identified in *A. variegatum* (1.0%), *H. rufipes* (11.4%) and *H. truncatum* (2.2%).

With bootstrap support of 85%, it was observed from the phylogenetic analysis that the *R. africae* samples from this study clustered with *R. africae* from Burkina Faso (acc. nr. KX063619) (Fig. 3). Furthermore, *R. aeschlimannii* from this study clustered with *R. aeschlimannii* from Ethiopia (acc. nr. KX063618) and Burkina Faso (acc. nr. KX063617) with bootstrap support of 99%.

The sequences obtained in this study have been deposited in GenBank: *R africae* (acc. nrs. OQ331037 and OQ331038) and *R. aeschlimannii* (OQ331039 and OQ331040).

Discussion

Ticks and tick-borne pathogens have recently emerged as one of the major public health concerns globally. *Amblyomma variegatum*, the most common type of tick identified in this study, infested predominantly cattle in both the wet and dry seasons. Furthermore, adult *A. variegatum* was more common during the wet season with nymphs of the same species occurring only during the dry season. This finding collaborates with other studies which reported that adult *A. variegatum* feeds largely in the rainy season as opposed to the nymphs which feed mostly in the dry season (Spickler 2009).

In this study, *Rickettsia* spp. and *C. burnetii* were identified in all three genera of ticks examined. Furthermore, coinfections were observed in tick pools. It is common to find coinfections in ticks that feed on a co-infected host (Levin and Fish 2000, 2001). The finding in this study can be compared to previous studies that found mixed infections of *Rickettsia* spp. and *C. burnetii* in ticks in Nigeria (Reye et al. 2012) and Ghana (Paintsil et al. 2022).

Rickettsia species are considered to be among the oldest known cause of zoonotic vector-borne diseases (Parola et al. 2013). In Africa, *R. africae* which causes African tick-borne fever is the most predominant *Rickettsia* species (Kelly et al. 1996). In Sub-Saharan African countries like Senegal and Cameroon, studies have revealed a significant seroprevalence of *R. africae* in humans (Ndip et al. 2004; Mediannikov et al. 2010a). Apart from the principal vectors *A. variegatum* and *A. hebraeum* (Parola 2006; Parola et al. 2013), R. *africae* has been reported in tick species of the genera *Rhipicephalus* and *Hyalomma* from Nigeria, Liberia, Guinea, and Senegal (Mediannikov et al. 2010a, 2012; Ogo et al. 2012; Reye et al. 2012).

The high occurrence of *Rickettsia* DNA in *A. variegatum* is similar to a previous study in Ghana (Paintsil et al. 2022). Further characterization of the *Rickettsia* spp. revealed a high occurrence of *R. africae* DNA in *A. variegatum* similar to the report

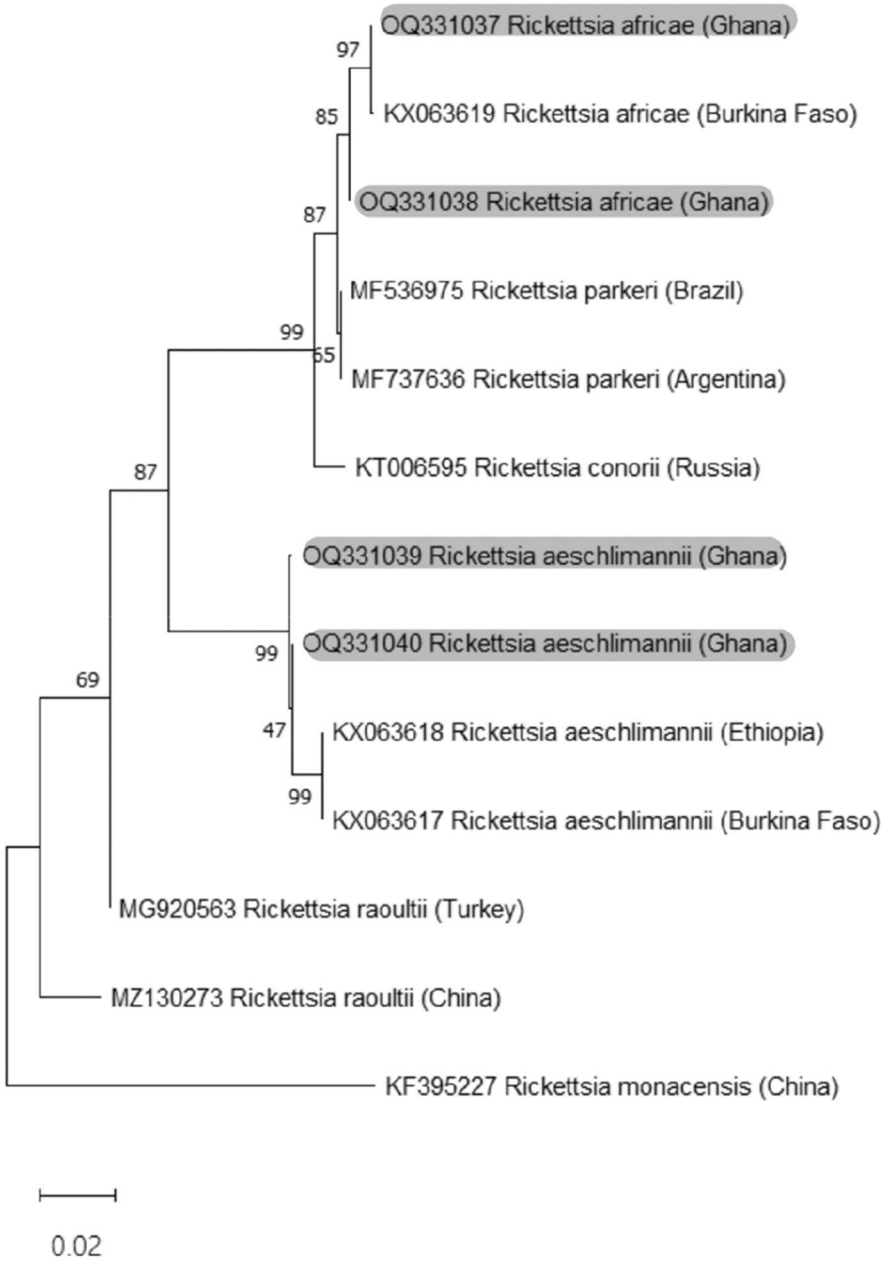

Fig. 3 Phylogenetic analysis of *Rickettsia* species based on the rOmpA gene. The sequences from this study have been highlighted. The sequences were aligned in MEGA X and phylogenetic trees were built using the neighbor-joining method with 1000 bootstrap replications

of studies conducted in Côte d'Ivoire, Guinea and Liberia (Mediannikov et al. 2012). This finding could be due to the transstadial and transovarial transmission of *R. africae* in *A. variegatum* (Socolovschi et al. 2009). Other African countries that reported DNA of *R. africae* in *A. variegatum* include Nigeria, Uganda (Lorusso et al. 2013), Burkina Faso (Tomassone et al. 2016) and Benin (Moumouni et al. 2016). With the difficulties associated with the accurate diagnosis of most febrile illnesses, there is the possibility of unreported cases of tick-bite fever within the country (Ahorlu et al. 1997; Dalrymple et al. 2017). Furthermore, African tick bite fever (ATBF) infections within the Kassena-Nankana Districts are more likely to occur in the wet season when the principal vector *A. variegatum* is abundant and there are high chances of contact with humans that are engaged in agricultural activities.

Rickettsia aeschlimannii DNA was also found in the ticks examined in this study. This bacterium has been reported in ticks collected from Burkina Faso (Tomassone et al. 2016), Nigeria (Kamani et al. 2015), Senegal (Mediannikov et al. 2010a)d te d'Ivoire (Ehounoud et al. 2016). The first case of *R. aeschlimannii* infection was reported in a patient who had visited from Morocco (Raoult et al. 2002). The pathogen has since been discovered in *H. marginatum*, *H. rufipes* and *H. truncatum* from Tunisia, Mali, Nigeria, Niger, Algeria, Senegal, Sudan and Egypt (Parola et al. 2001, 2005; Kernif et al. 2012; Mediannikov et al. 2010a; Kamani et al. 2015). Similarly, this study identified *R. aeschlimannii* in pools of *H. rufipes*, *H. truncatum* and *A. variegatum*. The results from this study suggest that several *Rickettsia* spp. are present in ticks in Ghana. Thus, necessitating the need for their proper identification to assess their veterinary and public health implications and to develop effective management methods. This is especially important because the DNA of *Rickettsia* spp. was detected in ticks that were collected from cattle imported from Burkina Faso to be marketed in the Kassena-Nankana Districts.

Coxiella burnetii causes severe infections that can lead to abortion and chronic endocarditis (Kazar 2005; Maurin and Raoult 1999). Domestic animals such as sheep, cattle, goats, and dogs can be a source of infection to humans through direct contact (Cooper et al. 2011). *Coxiella burnetii* has been detected in ticks belonging to the genera *Dermacentor*, *Amblyomma* and *Rhipicephalus* (Parola and Raoult 2001). Infections in ticks have been reported in West Africa at rates ranging from 0.7 to 6.8%. (Mediannikov et al. 2010b). This is in line with the findings of this study, which found 2.4% of ticks to harbor the DNA of *C. burnetii*.

Infections of *C. burnetii* were found in *A. variegatum*, *Hyalomma* spp. and *Rhipicephalus* spp. in Senegal, suggesting that they may play a role in Q fever epidemiology (Mediannikov et al. 2010b). In the Kassena-Nankana Districts, these tick species were also found to harbor the DNA of *C. burnetii*. Thus, these tick species may play a role in the epidemiology of *C. burnetii* in the study area. The DNA of *C. burnetii* was most prevalent in *R. evertsi evertsi* collected from sheep and screened in this study. Although small ruminant infections are normally asymptomatic, abortions and stillbirths can occur, particularly in late pregnancy (Van den Brom et al. 2015).

Infected animals can spread *C. burnetii* through their feces, milk, and most crucially, placental tissues and birth fluids (Maurin et al. 1999; Bouvery et al. 2003). As an emerging zoonosis, sheep and goats are linked to several human Q fever outbreaks (Van den Brom et al. 2015). The detection of *C. burnetii* DNA in ticks collected from sheep and goats in this study is in consonance with the results of previous research in Ghana (Johnson et al. 2019; Folitse et al. 2020; Paintsil et al. 2022). An increase in trade and sales of livestock across Ghana will likely increase the risk of *C. burnetii* transmission to naive animals and humans.

The use of insect repellents and protective garments have been found to lower the likelihood of tick bites and, as a result, the transmission of pathogens (Rahlenbeck et al. 2016). Education, the intake of only pasteurized milk and milk products, and the wearing of protective clothes, particularly when working with animals, are other ways to prevent infections (Honarmand 2012).

Conclusion

This study reports the prevalence of ixodid ticks infesting livestock in the Kassena-Nankana Districts of Ghana and the presence of the DNA of *R. africae*, *R. aeschlimannii* and *C. burnetii*. These findings are of veterinary and public health significance considering the involvement of the human population in livestock-related activities. There is an increased risk of ticks and zoonotic tick-borne pathogens being imported into Ghana due to the transboundary movement of herders and their livestock from numerous African countries. Thus, there is a need for further research to update the information on the status of ticks and zoonotic tick-borne pathogens in Ghana for the formulation of effective control measures.

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Author contributions SOA wrote the first draft of the manuscript. SOA, REB, BOAB, KNY, BA and AAN conducted the laboratory analysis. EB performed the data analysis. JAL, PKB, MDW, VA, MS, JCD and SKD supervised the study. SOA, SM, JWD and SKD designed the study. All authors reviewed and approved the final manuscript.

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Data availability All the data supporting this study are included in the article.

Declarations

Competing interests The authors declare no competing interests.

Ethical approval For this study was obtained from the University of Ghana Institutional Animal Care and Use Committee (UG-IACUC; UG-IACUC 001/19–20). The views expressed in this article are those of the authors and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, or the US Government. Opinions, interpretations, conclusions, and recommendations are those of the authors and are not necessarily endorsed by the US Army. Joseph W. Diclaro II, James C. Dunford and Suzanne Mate are military service members or employees of the US Government. This work was prepared as part of their official duties. Title 17 USC § 105 provides that 'Copyright protection under this title is not available for any work of the United States Government'. Title 17 USC § 101 defines US Government work as work prepared by a military service member or employee of the US Government as part of that person's official duties.

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Authors and Affiliations

Seth Offei Addo[1,2] · Ronald Essah Bentil[1] · Bernice Olivia Ama Baako[3] · Kevin Nii Yartey[1] · Eric Behene[1] · Benjamin Asiamah[1] · Abena Akyeamaa Nyarko[1] · Victor Asoala[3] · Mohamed Sallam[4] · Suzanne Mate[5] · James C. Dunford[6,7] · John Asiedu Larbi[2] · Philip Kweku Baidoo[2] · Michael David Wilson[1] · Joseph W. Diclaro II[8] · Samuel K. Dadzie[1]

✉ Seth Offei Addo
sethaddo40@gmail.com

✉ Samuel K. Dadzie
SDadzie@noguchi.ug.edu.gh

[1] Parasitology Department, Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Accra, Ghana

[2] Department of Theoretical and Applied Biology, College of Science, KNUST, Kumasi, Ghana

[3] Navrongo Health Research Centre, Upper East Region, Navrongo, Ghana

[4] Public Health and Biostatistics Department, Uniformed Services University of the Health

Sciences, Bethesda, MD, USA

5 U.S. Army Emerging Infectious Diseases Branch, Walter Reed Army Institute of Research, Silver Spring, MD, USA

6 Navy Entomology Center of Excellence, Jacksonville, FL, USA

7 Uniformed Services University of Health Sciences, Bethesda, MD, USA

8 Navy Entomology Center of Excellence, Center for Disease Control and Prevention Detachment, Atlanta, GA, USA