Molecular investigation of tick-borne bacterial microorganisms from *Amblyomma* (Acari: Ixodidae) ticks collected from reptiles in South Africa

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INTRODUCTION

Tick-borne pathogens (TBPs) are responsible for some of the most serious emerging infectious diseases across the world (Parola et al. 2005; Omondi et al. 2017). The wildlife-domestic-human interaction has the potential to accelerate the spread of zoonotic tick-borne pathogens that cause significant diseases, and eventually death (Uilenberg 1995; Omondi et al. 2017). To date, about 61% of human diseases have been documented to have a zoonotic origin, and wildlife is associated with approximately 75% of emerging zoonotic infections globally (Warwick and Corning 2013). An increasing number of studies have implicated reptiles and their associated ticks as potential reservoirs involved in the transmission cycles of TBPs (Peter 2000; Omondi et al. 2017).

JUSTIFICATION AND AIM

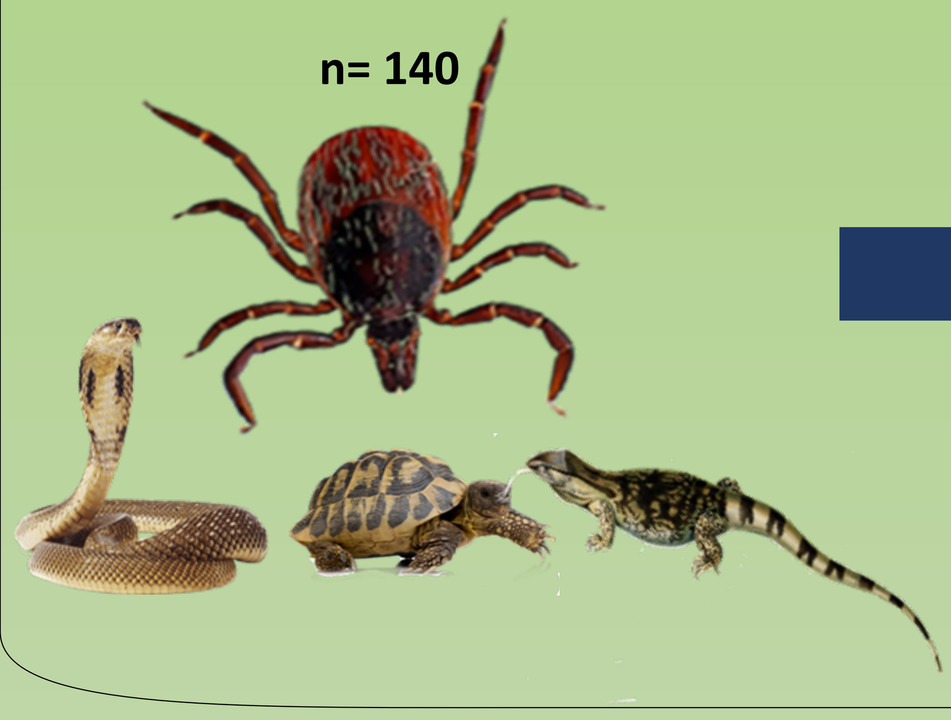
Although diverse tick-borne pathogens are emerging across the world, with documented impact on the health of humans and livestock, studies into their diversity and specific interactions with ticks and their reptilian host species in South Africa are lacking. In particular, the role of these ectotherms in the epidemiology of TBPs remains unknown, despite the fact that exported ticks and reptiles (*Amblyomma marmoreum*, tortoises and lizards) have been implicated with TBPs of livestock (Peter et al. 2000; Omondi et al. 2017).

The aim of this study is to screen for the presence of bacterial microorganisms from reptilian and reptile-associated ticks from South Africa.

MATERIALS AND METHODS

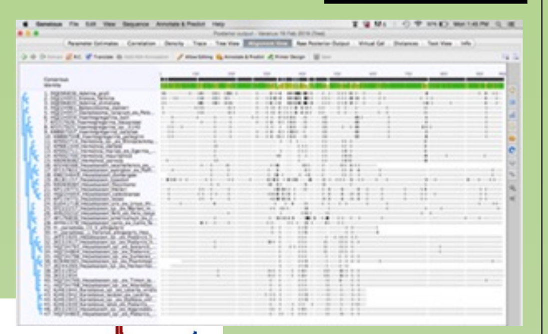
1. Collection of samples

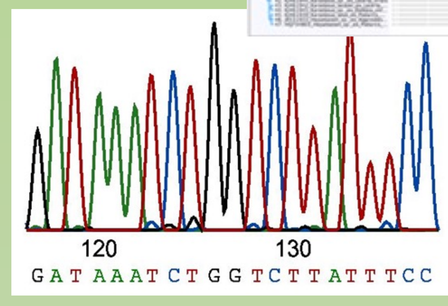
n= 140



2. Identification of ticks

3. Amplification and phylogenetic analysis





RESULTS

Table 1. Prevalence of *Borrelia* and *Rickettsia* species from reptilian *Amblyomma* ticks

Province	Tick species	n	Host	*Rickettsia* spp.	*Borrelia* spp.
KZN	*Amblyomma marmoreum*	4	*Varanus albigularis (1)*	-	-
	Amblyomma marmoreum	13	*Kinixys sp. (1)*	-	46.12%(6/13)
	Amblyomma marmoreum	4	*Kinixys zombensis (1)*	-	25% (1/4)
	Amblyomma marmoreum	4	*Stigmochelys pardalis (1)*	-	-
	Amblyomma latum	2	*Naja mossambica (1)*	-	-
	Amblyomma exornatum	2	*Varanus albigularis (1)*	-	-
WC	*Amblyomma marmoreum*	21	*Kinixys zombesis (3)*	-	4.76% (1/21)
	Amblyomma marmoreum	37	*Stigmochelys pardalis (2)*	-	-
	Amblyomma marmoreum	15	*Chersina angulata (9)*	46.67% (7/15)	20% (3 /15)
	Amblyomma sylvaticum	38	*Chersina angulata*	31.58% (12/38)	-
Total		140	20	13.57% (19/140)	7.86% (11/140)

*** *Anaplasma* species and *Coxiella burnetii* were not detected**

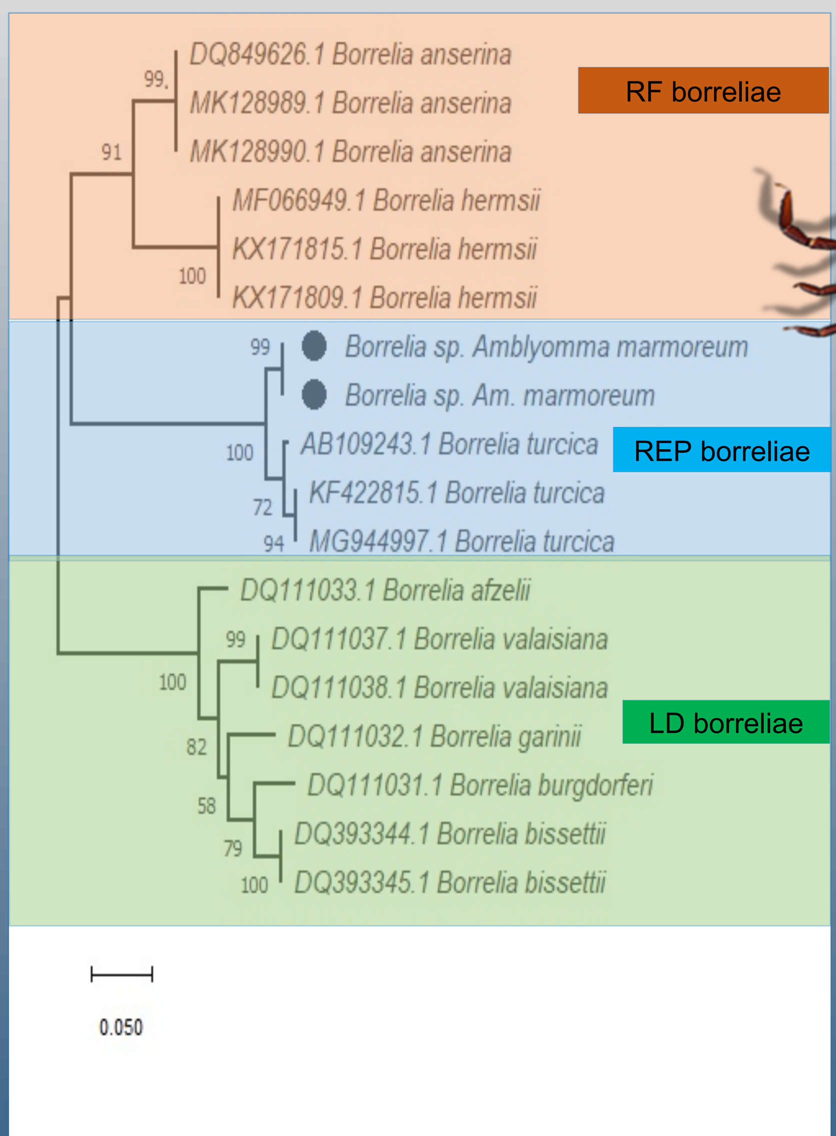


Figure 1. Maximum likelihood analysis of *Borrelia* spp. based on *Fla* gene sequences.

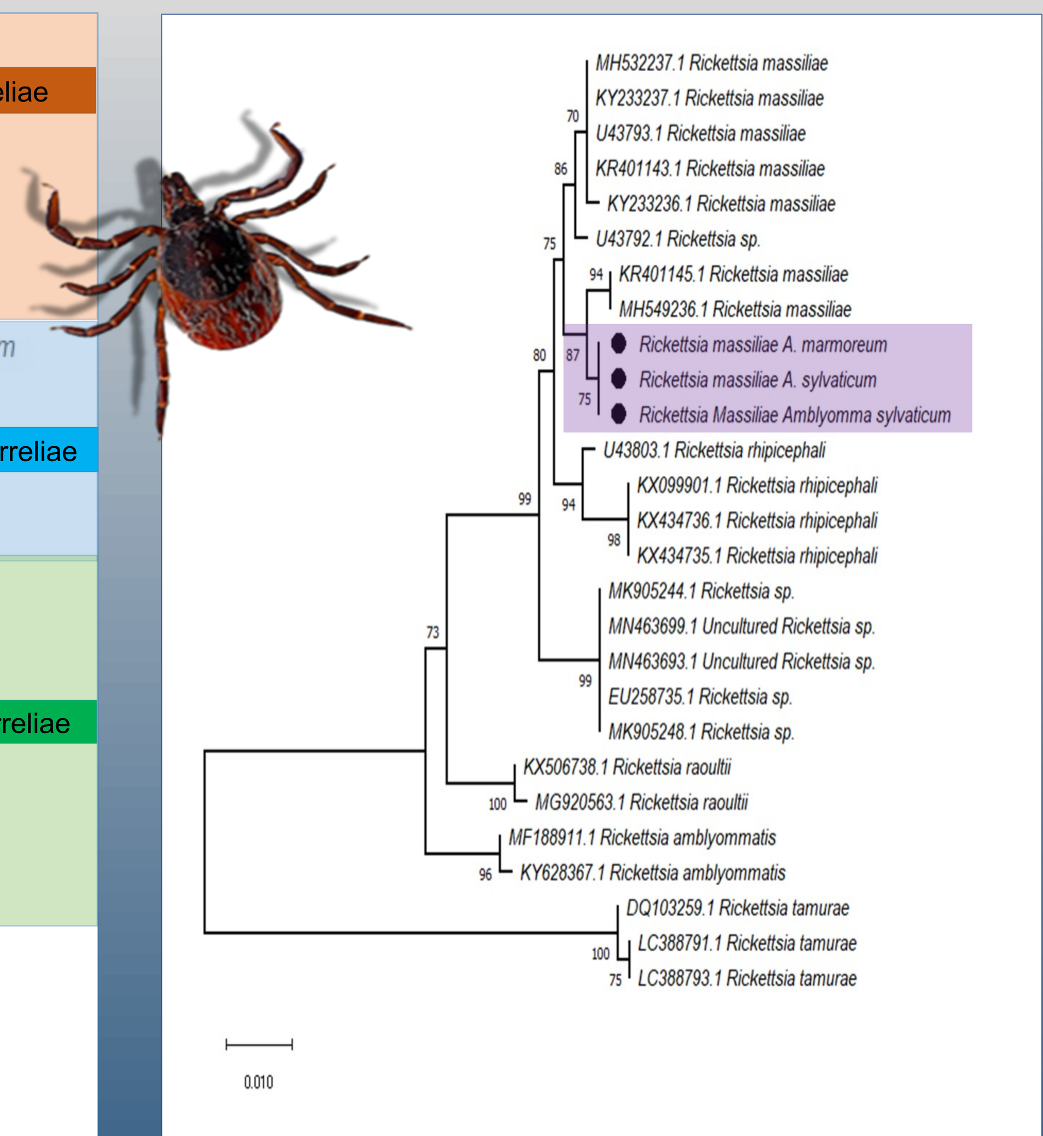


Figure 2. Maximum likelihood analysis of *Rickettsia* spp. based on the *OmpA* gene sequences.

DISCUSSION

Despite the fact that tick-borne bacterial microorganisms represent serious emerging and re-emerging health problems to humans and other vertebrates, the surveillance of these pathogens in wildlife has focused mainly on mammals, birds and their ectoparasites, whereas reptiles and their associated ectoparasites remain unexplored (Sanchez-Montes et al. 2019).

The finding of *R. massiliae* in reptilian ticks from South Africa suggests that human cases of this pathogen can occur. Therefore, ticks associated with reptiles should be considered in the epidemiology of *R. massiliae*, although more studies investigating the potential role of these ticks as vectors and reservoirs of this pathogen are needed.

This study observed for the first time the presence of REP *Borrelia* in *A. marmoreum* in South Africa. The latter tick species has been reported feeding on mammals and exported reptiles (Horak et al. 2006), which causes a serious concern on the distribution of pathogens by these *Amblyomma* ticks. Thus far, the impact of REP borreliae in humans and animals in South Africa is unknown.

Although *Anaplasma* spp. and *Coxiella burnetii* were not detected, they cannot be completely neglected and their absence could be attributed to the limited number of hosts and ticks analysed in the current study to date.

CONCLUSION

The present study demonstrates the presence of REP *Borrelia* in *A. marmoreum* infesting tortoises, and corroborates the existence of *R. massilae* in South Africa. These results should increase the awareness on the emergence of these pathogens in the country, and additional studies should elucidate the role of these ectotherms in the transmission of different tick-borne bacterial microorganisms to domestic animals and humans.

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