

Molecular detection of *Dirofilaria immitis*, *Hepatozoon canis*, *Babesia* spp., *Anaplasma platys*, and *Ehrlichia canis* in dogs on Costa Rica

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Abstract

Although vector-borne diseases are important causes of morbidity and mortality in dogs in tropical areas, there is little information on these conditions in Costa Rica. In PCRs of blood from dogs in Costa Rica, we did not detect DNAs of *Rickettsia* (*R*.) *felis* and *Coxiella* (*C*.) *burnetii* but we did find evidence of infection with *Dirofilaria* (*D*.) *immitis* (9/40, 22.5%), *Hepatozoon* (*H*.) *canis* (15/40, 37.5%), *Babesia* spp. (10/40, 25%; 2 with *B. gibsoni* and 8 with *B. vogeli*), *Anaplasma* (*A.*) *platys* (3/40, 7.5%) and *Ehrlichia* (*E.*) *canis* (20/40, 50%). Nine dogs (22.5%) were free of any vector-borne pathogens while 14 (35%) were infected with a single pathogen, 11 (27.5%) with two, 4 (10%) with three, 1 (2.5%) with four, and 1 (2.5%) with five pathogens. Dogs in Costa Rica are commonly infected with vector-borne agents.

Keywords

Costa Rica, Dirofilaria immitis, Babesia gibsoni/vogeli, Anaplasma platys, Ehrlichia canis, Hepatozoon canis

Introduction

Canine vector-borne diseases are an important cause of morbidity and mortality in dogs worldwide and many are zoonoses. There is very limited data on vector-borne diseases in dogs from the seven Central American states with reports from only four countries, namely Costa Rica (Romero *et al.* 2011; Scorza *et al.* 2011; Rojas *et al.* 2014), Panama (Bermúdez *et al.* 2011; Pineda *et al.* 2011; Herrer and Christensen 1976) and Guatemala (Ryan *et al.* 2003) and Nicaragua (Wei *et al.* 2014). To provide further information we used PCR to investigate the prevalence of seven vectorborne agents in dogs from Costa Rica.

Materials and Methods

A convenience sample of whole bloods was collected in EDTA from 40 dogs which were neutered in a Volunteers for Intercultural and Definitive Adventure (VIDA) Clinic in the village of Nueva Esperanaza outside Bagaces in Northwestern Costa Rica in 2012. The dogs were 6 months to 3 years of age (average 9 months) and belonged to local people from underprivileged areas (Table 1). The study was approved by the Institutional Animal Care and Use Committee of the Yangzhou University College of Veterinary Medicine of China.

The whole blood samples were stored and transported to the laboratory at 4°C where aliquots (200 µL) were frozen at -80°C until DNA was extracted using the High-Pure PCR Template Preparation Kit (Roche Molecular Biochemicals, Indianapolis, IN, USA) as described before (Zhang *et al.* 2013). The extracted DNA was eluted in 200 µl 1× $T_{10}E_{0.1}$ elution buffer and used in eight qPCRs, seven for vectorborne pathogens and one for the canine HMBS gene as an endogenous internal control. The qPCRs were performed in a 20 µl reaction system of a Roche LightCycler 480-II PCR as described previously: *Anaplasma* spp. 16S rRNA (Kelly *et al.* 2013), *Babesia* spp. 18S rRNA (Wang *et al.* 2010), *C. burnetii IS-1111* (Berri *et al.* 2009), *Dirofiliria immitis* (Wei *et al.* 2014), *E. canis* 16S rRNA (Kelly *et al.* 2013), *Hepatazoon* spp. 18S rRNA (Li *et al.* 2008), *R. felis gltA*

Gender	Age (years)	Weight (lbs)	Tick-borne pathogens*				
			Hepatazoon	Anaplasma	Babesia	Ehrlichia	Dirofilaria
М	0.5	5	_	_	B. gibsoni	E. canis	_
F	1.0	10	_	_	_	E. canis	_
F	0.5	12	_	_	_	_	_
F	0.5	7	_	A. platys	_	E. canis	_
М	6.0	7	_	_	B. gibsoni	_	_
F	0.75	4	_	_	_	E. canis	_
М	1	7	_	_	_	E. canis	_
М	2.5	22	_	_	_	E. canis	_
F	3.0	7	_	_	_	E. canis	D. immitis
М	6	7	_	_	_	E. canis	D. immitis
F	0.5	7	_	_	_	_	—
F	0.5	12	_	_	_	_	_
F	0.75	10	_	_	_	_	_
М	1.0	25	_	_	_	_	_
F	0.83	5	H. canis	A. platys	_	_	—
F	2.0	10	H. canis	_	B. vogeli	_	_
F	4.0	12	H. canis	_	B. vogeli	_	_
F	1.0	14	H. canis	_	B. vogeli	E. canis	D. immitis
F	4.0	12	_	_	_	E. canis	_
М	2.0	18	H. canis	_	_	_	D. immitis
F	2.0	5	H. canis	_	_	E. canis	D. immitis
F	1.0	12	_	_	_	_	_
М	1.5	16	_	_	_	_	D. immitis
F	0.83	6	_	_	_	E. canis	_
F	1.0	11	_	_	_	E. canis	_
F	0.5	5	H. canis	_	_	_	_
F	0.5	18	H. canis	_	_	_	_
М	2.0	8	H. canis	A. platys	B. vogeli	E. canis	D. immitis
F	0.58	13	H. canis	_	B. vogeli	_	_
F	2.0	3	H. canis	_	B. vogeli	_	_
М	5.0	9	H. canis	_	B. vogeli	E. canis	_
F	2.0	16	H. canis	_	_	E. canis	D. immitis
F	0.75	15	H. canis	_	B. vogeli	E. canis	—
М	3.0	11	H. canis	_	_	E. canis	—
М	1.0	10	_	_	_	E. canis	_
F	0.75	10	_	_	_	_	_
F	1.0	6	_	_	_	E. canis	_
F	1.0	14	_	_	_	_	_
F	2.0	6	_	_	_	_	_
F	0.5	9	_	_	_	_	D. immitis

Table I. Prevalence of tick-borne agents in dogs determined by quantitative PCRs

**R. felis* and *C. burnetii* were not detected in the whole blood samples of any those dogs. "-" denotes the absence of bacterial DNA in the whole blood of the designated dog

(Hii *et al.* 2013) and the canine HMBS gene (Wang *et al.* 2012). The melting curve analysis for probes annealing to the PCR products was determined by monitoring the fluo-

rescence from 45°C to 80°C following the completion of PCRs, and the first derivatives of F4/F1 were evaluated to determine the probe melting temperature (T_m) . The PCR

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products were verified by gel electrophoresis and nucleotide sequencing using forward and antisense primers (GenScript, Nanjing, China) was used to confirm the identity of the organism detected.

Results and Discussion

The PCR for the HMBS gene was positive on all samples indicating successful extraction of amplifiable DNA. Our PCRs for pathogens were positive for 5 of the 7 organisms tested, namely *E. canis* (20/40, 50%), *H. canis* (15/40, 37.5%), *Babesia* spp. (10/40, 25%; including 2 dogs with *B. gibsoni* and 8 with *B. vogeli*), *D. immitis* (9/40, 22.5%) and *A. platys* (3/40, 7.5%). *R. felis* and *C. burnetii* were not detected. Altogether, 77.5% (31/40) of the dogs were positive with 35% having evidence of infection with a single agent, 27.5% with two, 10% with three, 2.5% with four, and 2.5% with five agents (Table I).

In a recent PCR study of dogs from the central, northwestern and eastern areas of Costa Rica, a high percentage of dogs (47%; 69/146) was also found positive for vector-borne agents, mainly E. canis (34%), A. platys (10%), B. vogeli (8%) and *H. canis* (8%). Infections with *E. canis* have further been shown to be very prevalent in another study in Costa Rica (47%; 148/310; Romero et al. 2011). The vector of E. canis is Rhipicephalus (R.) sanguineus which occurs worldwide (Dantas-Torres, 2008) and it is likely, then, that infections with E. canis are widespread in Central America. Veterinarians in the region should have a high index of suspicion of infections in their patients (Kelly et al. 2013; Shaw et al. 2001) and, as human cases of infection with E. canis are known (Perez et al. 2006), human health workers should be alerted to the possibility of infections in patients with contact with dogs and their ticks.

R. sanguineus is also the vector of *B. vogeli* (Solano-Gallego and Baneth 2011), H. canis (Baneth et al. 2007) and A. platys (Alleman et al. 2008) and, in the only other report on these organisms in Central America, they were found to be prevalent in Costa Rica with 8%, 7.5% and 10% of dogs positive, respectively (Rojas et al. 2014). As with E. canis the widespread distribution of their vector makes it likely that infections with these organisms are also common in dogs throughout Central America. Although these organisms generally cause few clinical signs (Alleman et al. 2008; Baneth 2011; Solano-Gallego and Baneth 2011) and do not appear to be a major threat to the health of dogs in the region, it should be noted that we and Rojas et al. (2014) both found mixed infections were common and it is possible the effects of one agent may exacerbate (Brown et al. 2006; Kelly et al. 2013; Rojas et al. 2014) or ameliorate (Matthewman et al. 1993) the effects of another. The organisms also appear not to be important zoonotic agents with no reports of B. vogeli or H. canis infections in people (Esch and Petersen 2013) and only one report of A. platys in a person (Maggi et al. 2013).

The PCR we designed for D. immitis was found to be reliable, consistently giving positive results for the positive control, and also sensitive, detecting down to one copy of the standard in a PCR reaction. When used in the study the PCR showed nine dogs (9/40, 22.5%) had evidence of DNA of D. immitis, the agent of mosquito transmitted canine heartworm disease which is an important disease of dogs worldwide (McCall et al. 2008; Cuervo et al. 2013). In the only other report on D. immitis in Central America, 2% of dogs studied in the center of the western region of Costa Rica were seropositive (Scorza et al. 2011). The far higher prevalence in our PCR study might be because our dogs were from underprivileged areas where heartworm preventatives are unaffordable. The current data indicates dogs in Costa Rica, and likely the region, are at risk of infection with D. immitis and animal health workers should be recommending the use of heartworm preventatives where possible. Human health workers should also be aware that D. immitis can infect people (Simon et al. 2005).

Melting point analysis of our Babesia positive PCR reactions and genomic sequencing of the PCR products showed that two of the dogs had DNA of *B. gibsoni* ($T_m \sim 67 \text{ °C}$) and 8 dogs had *B. vogeli* ($T_m \sim 60 \degree$ C) (Wang *et al.* 2010). This organism is found in northern Africa, southern Asia, Australia, Europe, the USA and the Caribbean (Kelly et al. 2013). Babesia gibsoni is thought to be transmitted by dogs fighting or by ticks, in particular R. sanguineus (Taboada and Lobetti 2006). There are no reported human infections (Esch and Petersen 2013) but in dogs infections usually result in acute signs including fever, pallor, splenomegaly and anorexia (Ayoob et al. 2010). Dogs that recover generally become chronic subclinical carriers with significantly reduced platelet counts (Matsuu et al. 2004). Unfortunately diagnosis is not easy, generally requiring serology and PCR (Ayoob et al. 2010), and treatment of B. gibsoni sometimes fails (Iguchi et al. 2013).

Of the agents that were not detected in our study, *C. burnetii* is the agent of Q fever in people which occurs worldwide, apart from New Zealand (Cutler *et al.* 2007). Our negative findings for *C. burnetii* are consistent with there being no reports of *C. burnetii* in people or animals in Central America. We would note, however, that only few seropositive dogs are also PCR positive (1:25) and dogs have only been implicated in one outbreak of Q fever (Buhariwalla *et al.* 1996). Determining the true importance of *C. burnetii* in Central America requires studies of people and livestock which are the major reservoirs and sources of infection.

We also found no evidence of *R. felis*, an emerging pathogen principally associated with cat fleas (*Ctenocephalides* felis) and causing flea-borne spotted fever in people (Abdad *et al.* 2011). It occurs on all continents except Antarctica and recent evidence suggests dogs might be reservoir hosts with only subclinical infections (Hii *et al.* 2011). It is unexpected that we did not find the organism as

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it occurs in cat fleas in Costa Rica (Troyo *et al.* 2012), and also in Guatemala and Panama (Bermudez *et al.* 2011; Hun *et al.* 2011). Further studies are indicated to characterize infections in dogs and their possible role as sentinels of human infections.

In conclusion, our study adds to the scant data on vectorborne diseases of dogs and vector-borne zoonoses in Central America. Further we provide the first evidence of *B. gibsoni* in Central America while confirming the presence of important canine vector-borne pathogens in the region. Finally, many of the pathogens can infect people and health workers need to be aware of the possibility of infections in their patients, particularly those that have contact with dogs and their parasites.

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