

Hepatozoon canis and Babesia vogeli infections of dogs in Tunisia

Ali Bouattour, Ahmed Chabchoub, Iheb Hajjaji, Youmna M'Ghirbi

► To cite this version:

Ali Bouattour, Ahmed Chabchoub, Iheb Hajjaji, Youmna M'Ghirbi. Hepatozoon canis and Babesia vogeli infections of dogs in Tunisia. Veterinary Parasitology: Regional Studies and Reports, 2021, 23, pp.100512. 10.1016/j.vprsr.2020.100512 . hal-03493214

HAL Id: hal-03493214 https://hal.science/hal-03493214

Submitted on 15 Dec 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License

1	Hepatozoon canis and Babesia vogeli infections of dogs in Tunisia
2	
3	Ali Bouattour ^{a*} , Ahmed Chabchoub ^{ab} , Iheb Hajjaji ^b , Youmna M'ghirbi ^a
4	
5	^a Laboratoire de Virus, Vecteurs et Hôtes, Institut Pasteur de Tunis, Université Tunis El
6	Manar, 13, Place Pasteur, 1002, Tunis-Belvédère. Tunisia.
7	^b Ecole Nationale de Médecine Vétérinaire, Sidi Thabet, Université Manouba- Tunisia
8	Ahmed Chabchoub : chabchoubahmed2009@yahoo.fr
9	Iheb Hajjaji : ihebhajjaji@hotmail.fr
10	Youmna M'ghirbi : youmna.mghirbi@pasteur.tn
11	Corresponding author.
12	E-mail: ali.bouattour@pasteur.tn
13	Postal address: Institut Pasteur de Tunis, 13 Place Pasteur, 1002 Tunis
14	Tele: +2016 71893340, Fax: +21671791833
15	
16	Abstract
17	A paucity of studies is available on haemoparasites in dogs in Tunisia. In this study, we
18	used molecular techniques (PCR/sequencing) to detect and characterize haemoprotozoa
19	in sick dogs from Tunisia. A total of 99 dogs displaying such clinical symptoms as
20	fever, anorexia, and depression were presented for treatment to the hospital of the
21	Veterinary School of Sidi Thabet (Tunisia). Among dogs screened by PCR, five (5%)
22	proved to be infected with a hemoprotozoa species.
23	An analysis of all the sequences that were obtained enabled us to identify two species of
24	Protozoa: Babesia vogeli (in three dogs) and Hepatozoon canis (in two other dogs). This
25	is the first time that an infection of dogs by Hepatozoon canis in Tunisia has been

26	reported. Veterinary practitioners should be aware that these two hemoparasites can
27	infect dogs and should include them in any differential diagnosis of clinical illnesses
28	with manifestations compatible with tick-borne diseases.
29	
30	Keywords: Canine Babesiosis, Babesia, Hepatozoon, Dogs, Tunisia, Rhipicephalus
31	sanguineus.
32	
33	1. Introduction
34	
35	Species of Babesia and Hepatozoon infect a wide variety of mammals, including dogs
36	(Smith, 1996; Solano-Gallego and Baneth, 2011). Some of the pathogens transmitted to
37	dogs by ticks, such as hemoprotozoa, cause severe disease and serious illness. Several
38	Babesia species, including B. canis, B. rossi, B. vogeli and B. gibsoni, which are the
39	primary causes of babesiosis, have been reported in dogs (Carret et al., 1999; Irwin,
40	2009; Solano-Gallego et al., 2016; Baneth et al., 2019) and can cause infections whose
41	clinical and pathological signs range from subclinical to severe (fever, haemolytic
42	anemia, splenomegaly, thrombocytopenia) and even death (Solano-Gallego and
43	Baneth, 2011).
44	Small animal practitioners in Tunisia have frequently reported cases of canine
45	babesiosis, which is most commonly caused by Babesia vogeli and transmitted by the
46	dog brown tick Rhipicephalus sanguineus (M'ghirbi and Bouattour, 2008). Considered
47	to be the least pathogenic species (Köster et al., 2015), Babesia vogeli has also been
48	reported in other African countries (Collett, 2000; Oyamada et al., 2005), in southern
49	Europe (Caccio et al., 2002; Solano-Gallego et al., 2016; Solano-Gallego and Baneth,

2011), in North and South America (Birkenheuer et al., 2005; Passos et al., 2005), Asia
(Abd Rani et al., 2011) and in Australia (Jefferies et al., 2003).

Active during the warm season in Tunisia, R. sanguineus heavily infests dogs and can 52 be a vector for several pathogens. In addition to B. vogeli, this tick species was reported 53 to be infected with Anapalsma platys, Rickettsia massiliae Bar 29 and Rickettsia conorii 54 (Bouattour et al., 1999; Sarih et al., 2005; M'ghirbi and Bouattour 2008; Khrouf et al., 55 56 2014). However, haemoparasites of the genera *Hepatozoon* have never been reported in dogs in Tunisia. Canine infections with H. canis have been reported in many parts of 57 Africa (Ibrahim et al., 1989; Oyamada et al., 2005, Medkour et al., 2020), Europe, 58 59 America, Asia, and Australia (Eiras et al., 2007; Li et al., 2008; Abd Rani et al.; 2011; Barker et al., 2012). The cosmopolite brown dog tick R. sanguineus was ascertained to 60 be the primary invertebrate host for this Protozoa (Christophers, 1907). 61

Babesia and *Hepatozoon* are known to occur in endemic areas, which could partially explain the variations in clinical presentation and pathogenicity in infected dogs (Shaw et al., 2001). When examining tick-infested dogs that show clinical signs suggestive of hemoprotozoosis, veterinary practitioners often presume the cause to be babesiosis and omit hepatozoonosis as a possible cause without seeking laboratory confirmation.

67 68

Infection with *Hepatozoon canis* (Family Hepatozoidae) is also part of the differential
diagnosis of hemoprotozoosis affecting dogs as intermediate hosts; the brown dog tick *R. sanguineus* is the definitive host and vector (Baneth et al., 2001). Dogs with canine
hepatozoonosis are often asymptomatic with low levels of parasitaemia whereas dogs
with high levels of parasitaemia can present severe disease and show fever, lethargy,
anaemia, and cachexia (Ivanov and Tsachev, 2008). A diagnosis of *Hepatozoon* cannot

rely only on clinical or biological observations. The detection of other haemoprotozoa 75 such as small Babesia is not obvious even after an examination of blood smears stained 76 with Giemsa. The diagnosis of these parasites is even more problematic in chronic cases 77 of infection because of less virulent species. A blood smear examination by light 78 microscopy remains the easiest, most accessible and least expensive diagnostic test for 79 most veterinarians, but this technique detects less commonly small hemoprotozoa such 80 as B. gibsoni and H. canis. The development of more sensitive molecular tools such as 81 PCR and sequencing has made it possible to identify and differentiate the various 82 species of Babesia (Baneth et al., 2000; Caccio et al., 2002; Inokuma et al., 2004) and 83 84 active Hepatozoon (Oyamada et al., 2005; Medkour et al., 2020) infections in dogs. This study therefore aimed to diagnose the causal agents of infections in dogs presenting 85 suspected haemoparasitosis using PCR and sequencing methodologies. 86

- 87
- 88

2. Materials and methods

89 2.1. Dogs and blood samples

Our study was carried out during the warm season (April-July 2018) during which ticks 90 are active. A total of 99 dogs of various breeds with clinical manifestations compatible 91 with tick-borne diseases including apathy, dehydration, fever, anorexia, weight loss, and 92 pale mucous membranes, were presented to Veterinary School of Sidi Thabet Hospital 93 (Tunisia) for treatment. The dogs underwent clinical examinations and blood samples 94 were collected from the radial vein in 5 mL tubes containing ethylene-95 diaminetetraacetic acid (EDTA)-anticoagulated. Whole blood was collected for DNA 96 extraction and hematological analysis. 97

98 2.2. DNA extraction

We used the QIAmp®DNA Mini kit (Qiagen GmbH, Hilden, Germany) for DNA
extraction as per the manufacturer's instructions, adjusted to 100 μL with the elution
buffer (AE) provided with the kit, and stored at -20°C for further use. To verify
contamination, a control tube (distilled water) for each of the ten samples was included
in the extraction protocol. The DNA yield was determined with a NanoDrop_ND-1000
Spectrophotometer (NanoDrop Technologies, DE, USA).

105

106 2.3. PCR

107PCR was performed using a set of primers that amplified a 460 to 520 bp fragment in108the V4 variable region of the 18S rRNA of *Babesia* and *Theileria* species (Georges et109al., 2001). Sequences of genus-specific primers were used to amplify the V4 region of110the 18S rDNA were RLB-F2 5'-GACACAGGGAGGTAGTGACAAG-3' and RLB-R2111-5'-CTAAGAATTTCACCTCTGACAGT-3'. In our experiments, sequencing showed112that these primers, previously reported as being able to amplify the *Babesia* and113*Theileria* genus, also amplified *Hepatozoon*.

114 The PCR reactions were performed in a final volume of 25 μ L containing 75 ng of 115 genomic DNA, 200 nM of each primer, 1× PCR buffer, 1.5 mM MgCl₂, 200 μ M of 116 each dNTPs and 1 U of Taq Platinum Polymerase (Invitrogen, CA, USA).

117 The reactions were performed on an automated DNA thermal cycler (Perkin-Elmer

118 2720, CA) as follows: starting with 15 min at 95° C and followed by 45 cycles of 94° C

for 35 sec; 51° C for 35 sec and 72° C for 35 sec and a final elongation, 72° C for 10

min. Extraction controls and PCR negative (water) controls were included in each PCR

reaction. Plasmid including the amplicon of the V4 region of the 18S rRNA gene of

122 *Babesia canis* species was used as a positive control.

- 123 The PCR products were separated by electrophoresis using 2% agarose gel containing
 124 ethidium bromide (10 mg/mL) before it was analyzed by sequencing.
- 125
- 126
- 127 2.4. DNA sequencing and data analysis

To confirm the PCR results, positive *BabesialTheileria* amplified DNA (n=5) was analyzed by sequencing. The PCR products were purified using the ExoSAP clean-up procedure (Amersham Biosciences, Germany). All nucleotide sequences were obtained using the Big Dye Terminatorv.3.1 Cycle Sequencing Kit (Applied Biosystems) and the 3130 automated sequencer (Applied Biosystems).

The sequences generated in this study were edited and aligned using BioEdit (Hall, 134 1999) and ClustalW software programs (Thompson et al., 1994). The BLAST program 135 (http://www.ncbi.nlm.nih.gov/BLAST) was used to compare and analyze the data 136 sequences.

137 2.5. Phylogenetic analysis

A phylogenetic tree was inferred using neighbor-joining analysis with MEGA5.2 software with a bootstrap of 1000 replications and evolutionary distances adjusted through Kimura-2 parameter nucleotide substitution (Tamura et al., 2007). The sequence of *Plasmodium falciparum* (M19172.1) was used as distant phylogenetic organisms to root the tree.

143 2.6. Nucleotide sequences data

144 Nucleotide sequences data reported in this paper is available in the GenBankTM, EMBL

and DDBJ databases under the accession numbers MT588813-MT588817.

146 2.7. Hematological analysis

147	White blood cell counts, Hematocrit, Hemoglobin, and platelet counts were performed							
148	by a fully automatic hematology analyzer the BC-2800 Vet (Mindray, China).							
149								
150								
151								
152								
153	3. Results							
154	Of the 99 dogs examined by PCR, five (5%) showed a specific band of 460 bp for							
155	Protozoa. The sequences obtained were analyzed using Bioedit® software and then							
156	compared with the reference sequences in the GenBank							
157	(www.ncbi.nlm.nih.gov/BLAST). This enabled us to identify two species of Protozoa:							
158	Babesia vogeli and Hepatozoon canis. Three sequences (354 sequenced nucleotides)							
159	were found to be 100% identical to the partial sequence of B. vogeli (MK910150)							

nucleotides) were 100% identical to the partial sequence of *H. canis* (MN628318)
isolated in India (Fig. 1).

reported in a dog from Colombia. In addition, two sequences (339 sequenced

163 All positive dogs had a fever (39.4-41.3 °C) and were anorexic (Table1). Of these, only 164 dogs 51 and 93, which were infected by *B. vogeli* and *H. canis* respectively, developed a 165 mild non-regenerative anaemia. The hematocrit showed low values in dogs 32, 93 and 166 51. Dog 51 also presented a leukopenia (WBC = $5.2 \times 10^3/\mu$ L). Dogs 15, 18 and 51 167 suffered from thrombocytopenia (Table1). All dogs had at least two specimens of 168 *Rhipicephalus sanguineus* ticks on their ears.

169

160

170 **4. Discussion**

Infections with *Babesia* or *Hepatozoon* provoked a wide range of clinical manifestations 171 172 in dogs from asymptomatic to severe disease. Acute clinical and hematological signs include fever, lethargy, hemolytic anemia, and thrombocytopenia, (Criado-Fornelio et 173 al., 2007; Irwin, 2009; Solano-Gallego and Baneth, 2011; Baneth et al., 2003, Kamani et 174 al., 2019). However, clinical manifestations caused by haemoprotozoa are not so clearly 175 defined that veterinary practitioners can make a diagnosis and adapt their treatments. 176 Molecular methods must be used to identify the causative species. Several techniques 177 have been described, and conventional PCR used on blood proved more sensitive and 178 specific than classical methods for diagnosing haematozoa (Oyamada et al., 2005; 179 Wahlang et al., 2019). In addition, sequencing facilitated the identification of 180 hemoparasite species (Solano-Gallego and Baneth, 2011). 181

In our study, the DNA of 99 dogs presenting various clinical manifestations to the 182 183 hospital of the Veterinary School of Sidi Thabet (Tunisia) was screened by PCR using a set of a genus-specific primers amplifying Babesia and Theileria species (Georges et al., 184 2001). After sequencing the positive amplicons, we discovered that these same primers 185 can also amplify *Hepatozoon*. Oyamada et al. (2005) have reported similar results using 186 Babesia spp. primers. Sequencing analysis of the positive amplicons that were obtained 187 188 revealed that *Babesia vogeli* was present in three dogs (15, 18 and 51) and *Hepatozoon* canis was present in two dogs (32 and 93). 189

Our results support and confirm the presence of *B. vogeli* in dogs in Tunisia as we have previously reported. However, in the investigated sick dogs, the prevalence of the infection was only 3%, which is lower than that reported in our previous investigation (6.6%) on randomly studied dogs (M'ghirbi and Bouattour, 2008). In fact, infections in dogs with this large *Babesia* have been reported with prevalence range values that vary widely by locality: *B. vogeli* prevalence was 13.2% among 227 dogs screened by PCR

8

in Algeria a neighboring country (Medkour et al., 2020); 2% in 78 randomly chosen 196 dogs from eastern Sudan (Oyamada et al., 2005); 0.6% in dogs with clinical 197 manifestations in Nigeria, (Kamani et al., 2013); in southern France, the prevalence was 198 13.6 % in 140 dogs tested by nested PCR (René-Martellet et al., 2015); in southeastern 199 Rio de Janeiro (Brazil), the prevalence was 15.66 % in 390 dogs tested by qPCR 200 (Paulino et al., 2018). The variation in prevalence might be attributable to several 201 202 factors including the DNA extraction methodology, the primers that were used and the targeted gene, which can have different sensitivities (Valkiunas et al., 2008). In 203 addition, host-related variables such as age or breed and mainly tick infestations should 204 205 also be considered when comparing varying levels of regional prevalence.

In addition to B. vogeli, we detected H. canis in the group of investigated dogs. This 206 study is the first molecular report of *H. canis* in Tunisia. This parasite has been reported 207 208 recently in dogs in Algeria with a prevalence of 41% (Medkour et al., 2020). In addition, this Hepatozoon species was recorded in several countries of Africa: Sudan, 209 210 Nigeria and Zambia with prevalence rates of 42.3%, 41.4%, and 13% respectively 211 (Oyamada et al., 2005; Kamani et al., 2013, 2019; Williams et al., 2014). Studies in several European countries have reported different prevalence rates from low (1% and 212 3% in France and Spain respectively; Criado-Fornelio et al., 2009; Tabar et al., 2009) to 213 high (50.6% in southern Italy; Otranto et al., 2011). The prevalence of H. canis 214 similarly varies by country in America: 53.3% in Brazil (Rubini et al., 2008) to 2.5% in 215 the USA, where *H. canis* occurs together with *H. americanum* (Allen et al., 2008). Dogs 216 in several counties in Asia were also reported to show prevalence: in India where the 217 hemoparasite was identified for the first time, the rate of prevalence was 30% (Abd 218 Rani et al., 2011). 219

Babesia vogeli and Hepatozoon canis are canine hematic Protozoa that are widespread
due to the cosmopolitan nature of their main vector, *Rhipicephalus sanguineus* (Shaw et
al., 2001; M'ghirbi and Bouattour, 2008; Irwin, 2009; Solano-Gallego and Baneth,
2011), the most prevalent tick species infesting dogs worldwide. However, while *Babesia* is transmitted to a dog by the tick's salivary gland during the blood meal
(Solano-Gallego et al., 2016), *H. canis* is transmitted by the ingestion of ticks
containing mature oocysts (Baneth et al., 2001, 2003).

In our study, infections with B. vogeli, considered to be the least virulent Babesia 227 species, caused clinical diseases in three infected dogs that displayed fever, anorexia, 228 dehydration depression, lethargy and weakness. All three dogs also suffered from 229 thrombocytopenia whereas only one dog (number 51) had mild regenerative anaemia 230 since it was infected with B. vogeli (30% hematocrit; 9g/dl hemoglobin). Similar 231 232 clinical signs (fever, anorexia and weakness) were observed in the two dogs infected with H. canis; hematological abnormalities (anemia and low hematocrit) were also 233 noted. Similar clinical and hematological manifestations caused by these two parasites 234 were reported (Sasanelli et al., 2009; Solano-Gallego and Baneth, 2011; Solano-Gallego 235 et al., 2016). H. canis also causes subclinical infections in apparently healthy dogs. 236 237 Indeed, infection with this protozoon can induce severe illness and can be fatal; dogs with high levels of *H. canis* parasitaemia that often approaches 100% of the peripheral 238 blood neutrophils can display lethargy, cachexia and anaemia (Baneth et al., 2003). Two 239 dogs presented to the clinic showed mild disease, which is the most common 240 presentation of infection that is usually associated with low levels of H. canis 241 parasitaemia (1-5% of neutrophils are infected) (Baneth et al., 2003; Ivanov and 242 Tsachev, 2008). 243

244

5. Conclusion

246 In Tunisia, warm weather from March to October prolongs the active season of *Rhipicephalus sanguineus* ticks that heavily infest dogs. This tick is a vector of several 247 pathogens such as species of *Ehrlichia* and *Babesia*, previously reported (Sarih et al., 248 2005; M'ghirbi and Bouattour, 2008), and Hepatozoon canis that is described in this 249 work. It should be noted that co-infections can occur in dogs, which might partially 250 explain the variations in often unspecific clinical presentations (Shaw et al., 2001; 251 Sasanelli et al., 2009; Kamani et al., 2013). It is therefore clinically important that these 252 diseases be diagnosed with a sensitive, specific, simple method and that the veterinary 253 254 practitioner be aware of the existence of these pathogens in Tunisia and select a treatment adequate to each one. 255

256

257 Ethical statement

All dogs were examined and sampled by the veterinary clinicians according to the procedures and the ethics committee of the Veterinary School of Sidi Thabet, and after the consent of the owner. Owners presented their dogs to the Veterinary School Hospital for diagnosis and treatment.

- 262 **Conflict of interest**
- 263 The authors declare that there is no conflict of interest.
- 264 Acknowledgments

We thank Ministry of High Education and Research of Tunisia (Direction Generale de
la Recherche) for financial support. We thank also Dr. Deborah Glassman, Washington
D.C., for English corrections.

268	Authors' contribution: A.B (MDV, PhD) conceived, designed and wrote the
269	manuscript. A. Ch (MDV, Professor) and I. H. (MDV) were the veterinary clinicians
270	who examined the dogs and performed the hematological analysis.

- 271 Y.M (PhD) performed the molecular analysis and contributed to the manuscript.
- All authors read and approved the final manuscript.
- 273 **References**
- Abd Rani, P.A.M., Irwin, P.I., Coleman G.T., Gatne, M., Traub R.J., 2011. A survey of
 canine tick-borne diseases in India. Parasit. Vectors, 4:141-148.
- Allen K.E, Li, Y., Kaltenboeck, B., Johnson, E.M., Reichard, M.V., Panciera, R.J.,
- Little, S.E., 2008. Diversity of *Hepatozoon* species in naturally infected dogs in the
 southern United States. Vet. Parasitol. 154:220–225.
- Baneth, G., Barta, J.R., Shkap, V., Martin, D.S., Macintire, D.K., Vincent-Johnson N.,
- 280 2000. Genetic and antigenic evidence supports the separation of *Hepatozoon canis* and
- 281 *Hepatozoon americanum* at the species level. J. Clin. Microbiol. 38:1298–1301.
- Baneth, G., Cardoso, L., Brilhante-Simoes, P., Schnittger, L., 2019. Establishment of
- 283 *Babesia vulpes* n. sp. (Apicomplexa: Babesiidae), a piroplasmid species pathogenic for
- domestic dogs. Parasite. Vector, 12:129-137.
- Baneth, G., Mathew, J.S., Shkap, V., Macintire, D.K., Barta, J.R., Ewing, S.A., 2003.
- 286 Canine hepatozoonosis: two disease syndromes caused by separate *Hepatozoon* spp.
- **287** Trends. Parasitol. 19:27–31.
- Baneth, G., Samish, M., Alekseev, E., Aroch, I., Shkap, V., 2001.Transmission of
- *Hepatozoon canis* to dogs by naturally-fed or percutaneously injected *Rhipicephalus sanguineus* ticks. J. Parasitol, 87: 606-611.

291	Barker, E.N., Langton D.A., Helps C.R., Brown, G., Malik, R., Shaw, S.E.,
292	Tasker, S., 2012. Haemoparasites of Free-Roaming Dogs Associated With Several
293	Remote Aboriginal Communities in Australia. BMC Vet. Res., 14; 8:55.
294	Birkenheuer, A.J., Correa, M.T., Levy, M.G., Breitschwerdt, E.B., 2005. Geographic
295	distribution of babesiosis among dogs in the United States and association with dog
296	bites: 150 cases (2000–2003). J. Am. Vet. Med. Assoc. 227, 942–947.
297	Bouattour, A., Darghouth, M.A., Daoud, A., 1999. Distribution and ecology of ticks
298	(Acari: Ixodidae) infesting livestock in Tunisia: an overview of eight years of field
299	collection. Parassitologia 41:5–10.
300	Caccio, S.M., Antunovic, B., Moretti, A., Mangili, V., Marinculic, A., Baric, R.R.,
301	Slemenda, S.B., Pieniazek, N.J., 2002. Molecular characterisation of Babesia canis
302	canis and Babesia canis vogeli from naturally infected European dogs. Vet. Parasitol.
303	106, 285–292.
304	Carret, C., Walas, F., Carcy, B., Grande, N., Precigout, E., Moubri, K., Schetters, T.P.,
305	Gorenflot, A., 1999. Babesia canis canis, Babesia canis vogeli, Babesia canis rossi:
306	differentiation of the three subspecies by a restriction fragment length polymorphism
307	analysis on amplified small subunit ribosomal RNA genes. J. Eukaryot. Microbiol. 46,
308	298–303.
309	Christophers, S.R., 1907. The sexual life cycle of Leucocytozoon canis in the tick.
310	Scientific Memoirs by the Officers of the Medical and Sanitary Departments of the
311	Government of India 28: 1–11.
312	Collett, M.G., 2000. Survey of canine babesiosis in South Africa. J. S. Afr. Vet. Assoc.
313	71:180–186.

- Criado-Fornelio, A., Buling, A., Pingret J.L., Etievant, M., Boucraut-Baralon, C.,
 Alongi, A., Agnone, A., Torina, A., 2009. Hemoprotozoa of domestic animals in
 France: prevalence and molecular characterization. Vet Parasitol. 159.1:73-76.
- 317 Criado-Fornelio, A., Rey-Valeiron, C., Buling, A., Barba-Carretro, J.C., Jefferies, R.,
- 318 Irwin, P., 2007. New advances in molecular epizootiology of canine hematic Protozoa
- from Venezuela, Thailand and Spain. Vet. Parasitol. 144, 261–269.
- Eiras, D.F., Basabe, J., Scodellaro, C.F., Banach, D.B., Matos, M.L., Krimer, A., Baneth, G., 2007. First molecular characterization of canine hepatozoonosis in Argentina: evaluation of asymptomatic *Hepatozoon canis* infection in dogs from Buenos Aires. Vet. Parasitol. 149, 275–279.
- 324 Georges, K., Loria, G.R., Riili, S., Greco, A., Caracappa, S., Jongejan, F., Sparagano,
- O., 2001. Detection of haemoparasites in cattle y reverse line blot hybridisation with a
 note on the distribution of ticks in Sicily. Vet. Parasitol. 99, 273-86.
- Hall, T.A. 1999. BioEdit: A user-friendly biological sequence alignment editor and
 analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser., 41:95–98.
- 329 Ibrahim, N.D., Rahamathulla, P.M., Njoku, C.O., 1989. Neutrophilmyeloperoxidase
- deficiency associated with canine hepatozoonosis. Int. J. Parasitol. 19:915–918.
- Inokuma, H., Yoshizaki, Y., Matsumoto, K., Okuda, M., Onishi, T., Nakagome, K.,
- 332 Kosugi, R., Hirakawa, M., 2004. Molecular survey of *Babesia* infection in dogs in
- 333 Okinawa, Japan. Vet. Parasitol. 121:341–346.
- Irwin, P.J., 2009. Canine babesiosis: From molecular taxonomy to control. Parasite.
- 335 Vector. 2 (Suppl. 1): S4.
- Ivanov, A., Tsachev, I., 2008. *Hepatozoon canis* and hepatozoonosis in the dog. TJS. 6.
- 337 2. 27-35

338	Jefferies, R., Ryan, U.M., Muhlnickel, C.J., Irwin, P.J., 2003. Two species of canine
339	Babesia in Australia: detection and characterization by PCR. J. Parasitol. 89, 409–412.
340	Kamani, J., Baneth, G., Mumcuoglu, K.Y., Waziri, N.E., Eyal, O., Guthmann, Y.,
341	Harrus, S., 2013. Molecular detection and characterization of tick-borne pathogens in
342	dogs and ticks from Nigeria. PLoS Negl. Trop. Dis. 7 (3), e2108.
343	Kamani J., Baneth G., Shimon Harrus S., 2019. An Annotated Checklist of Tick-Borne
344	Pathogens of Dogs in Nigeria. Vet Parasitol. Reg. Stud. Reports. 15,100255-1-9.
345	Khrouf, F., M'ghirbi, Y., Znazen, A., Ben Jemaa, M., Hammami, A., Bouattour, A.,
346	2014. Detection of Rickettsia in Rhipicephalus sanguineus ticks and Ctenocephalides
347	felis fleas from southeastern Tunisia by reverse line blot assay. J. Clin. Microbiol. 52(1).
348	268-274.
349	Köster, L., Lobetti, R., Kelly, P., 2015. Canine babesiosis: a perspective on clinical
350	complications, biomarkers, and treatment. Vet. Med.: Res. and Reports. 6. 119-128.
351	Li, Y., Wang, C., Allen, K.E., Little, S.E., Ahluwalia, S.K., Gao, D., Macintire, D.K.,
352	Blagburn, B.L., Kaltenboeck, B., 2008. Diagnosis of canine Hepatozoon spp. infection
353	by quantitative PCR. Vet Parasitol. 157. (1-2), 50-58.
354	M'ghirbi, Y., Bouattour, A., 2008. Detection and molecular characterization of Babesia
355	canis vogeli from naturally infected dogs and Rhipicephalus sanguineus ticks in
356	Tunisia. Vet. Parasitol. 152, 1–7.
357	Medkour, H., Laidoudi, Y., Lafri, I., Davoust, B., Mekroud, A., Bitam, I., Mediannikova,
358	O., 2020. Canine vector-borne Protozoa: Molecular and serological investigation for
359	Leishmania spp., Trypanosoma spp., Babesia spp., and Hepatozoon spp. In dogs from
360	Northern Algeria. Vet Parasitol. Reg. Stud. Reports. 19, 100353,

- Otranto, D., Dantas-Torres, F., Weigl, S., Latrofa, M.S., Stanneck, D., Decaprariis, D.,
 Capelli, G., Baneth, G., 2011. Diagnosis of *Hepatozoon canis* in young dogs by
 cytology and PCR. Parasit. Vectors, 4:55.
- 364 Oyamada, M., Davoust, B., Boni, M., Dereure, J., Bucheton, B., Hammad, A., Itamoto,
- 365 K., Okuda, M., Inokuma, H., 2005. Detection of *Babesia canis rossi*, *B. canis vogeli*,
- and *Hepatozoon canis* in dogs in a village of eastern Sudan by using a screening PCR
- and sequencing methodologies. Clin. Diagn. Lab. Immunol. 12, 11, 1343–1346.
- Passos, L.M., Geiger,S.M, Ribeiro,M.F., Pfister, K., Zahler-Rinder,M., 2005. First
 molecular detection of *Babesia vogeli* in dogs from Brazil. Vet. Parasitol. 127, 81–85.
- 370 Paulino, P.G., Pires, M.S., da Silva, C.B., Peckle, M., da Costa R.L., Vitari, G.L.V., de
- Abreu A.P.M., Massard, C.L., Santos, H.A., 2018. Molecular epidemiology of *Babesia*
- *vogeli* in dogs from the southeastern region of Rio de Janeiro, Brazil. Vet. Parasitol.
 Reg. Stud. Reports, 13,160-165.
- René-Martellet, M., Moro, C.V., Chêne, J., Bourdoiseau, G., Chabanne, L., Mavingui,
- P., 2015. Update on epidemiology of canine babesiosis in Southern France. BMC Vet.
 Res. 11:223-234.
- Rubini, A.S., Paduan, K.S., Lopes, V.V.A., O'Dwyer, L.H., 2008. Molecular and
 parasitological survey of *Hepatozoon canis* (Apicomplexa: Hepatozoidae) in dogs from
 rural area of São Paulo state, Brazil. Parasitol. Res. 102, 895–899.
- Sarih, M., M'ghirbi Y., Bouattour, A., Gern, L., Baranton, G, Postic, D., 2005.
 Detection and identification of *Ehrlichia* spp. in Ticks collected in Tunisia and
 Morocco. J. Clin. Microbiol. 43:1127–1132.
- Sasanelli, M., Paradies, P., Lubas, G., Otranto, D., de Caprariis D., 2009. Atypical
 clinical presentation of coinfection with *Ehrlichia*, *Babesia* and *Hepatozoon* species in a
 dog. Vet. Record. 164, 22-23.

386	Shaw S.E., Day M.J., Birtles R.J. Breitschwerdt, E.B., 2001. Tick-borne infectious
387	diseases of dogs. Trends in Parasitology.17(2).74-80
388	Smith, T.G., 1996. The genus Hepatozoon (Apicomplexa: Adeleina). J. Parasitol. 82,
389	565-585.

- Solano-Gallego, L., Baneth, G., 2011. Babesiosis in dogs and cats-Expanding
 parasitological and clinical spectra. Vet. Parasitol.181. 48–60,
- Solano-Gallego, L., Sainz, A., Roura, X., Estrada-Peña, A., Miró, G., 2016. A review of
 canine babesiosis: the European perspective. Parasit. Vectors. 9: 336.
- Tabar, M.D., Francino, O., Altet, L., Sánchez, A., Ferrer, L., Roura, X., 2009. PCR
 survey of vector borne pathogens in dogs living in and around Barcelona, an area
 endemic for leishmaniasis. Vet. Rec. 24;164 (4):112-116.
- Tamura, K., 2007. Mega4, Molecular Evolutionary Analysis (MEGA) software, version
 4.0. Mol. Biol. Evol., 24, 1, 1596-1599.
- Thompson, J.D., Higgins, D.G., Gibson, T.J., Clustal, W., 1994. improving the
 sensitivity of progressive multiple sequence alignment through sequence weighting,
 position-specific gap penalties and weight matrix choice. Nucleic Acids Res., 22:4673–
 4680.
- Valkiunas, G., Iezhova, T.A., Krizanauskiene, A., Palinauskas, V., Sehgal, R.N.M.
 Bensch, S., 2008. A comparative analysis of microscopy and PCR-based detection
 methods for blood parasites. J. Parasitol. 94: 1395–1401.
- 406 Wahlang, L., Lakshmanan, B., Thomas, N., Bosewell, A., Jain, J.K., Sunanda, C.,
- 407 Aravindakshan, T. V., 2019. Comparative analysis of conventional and real time PCR
 408 for detection of haemoparasites in dogs. IJBT 18.1. 9-15.
- 409 Williams, B.M., Berentsen, A., Shock, B.C., Teixiera, M., Dunbar, M.R., Becker, M.S.,
- 410 Yabsley, M.J., 2014. Prevalence and diversity of *Babesia*, *Hepatozoon*, *Ehrlichia*, and

411	Bartonella in wild and domestic carnivores from Zambia, Africa. Parasitol. Res., 113,
412	911-918.
413	
414	
415	
416	
417	Table 1. Results of sequencing PCR products and hematological values in dogs that
418	showed positive for the first PCR
419	
420	Fig. 1: A phylogenetic tree obtained using a small ribosomal subunit sequence Theileria
421	annulata, 10 Babesia species/isolates and 6 Hepatozoon canis isolates. The Kimura-2
422	method was used to calculate distances, and tree topology was inferred by neighbour
423	joining (MEGA 5.2 software). A total of 354 informative positions were used in the
424	analysis. Numbers at the nodes represent the bootstrap support in 1000 replications.
425	Scale bar indicates an evolutionary distance of 0.02 nucleotides per position in the
426	sequence. New sequences are marked in bold.



0.02

Dog	Age	Babesia	Н.	Accession	Red blood	White	Hematocrit	Hemoglobin	Platelet		Clinical signs
no.	/	vogeli	canis	number	cells	blood cells	(%)	(g/dl)	Count	T °C	
	year				(10 ⁶ /µl)	(10³/µl)			(10³/µl)		
Reference range*			5.50 - 8.50	6.00 -17.0	37.0 - 55.0	12.0 - 18.0	200.0 -	38-39			
									500.0		
15	2	+		MT588815	6.40	11.1	44	13	66	40.3	Anorexia, dehydrated,
4.0				N 4750004 4	7.00	_		45.0	420	44.0	depression
18	1	+		M1588814	7.09	/	54.4	15.8	120	41.3	Anorexia, dehydrated, depression
32	3		+	MT588816	5.11	15.4	28	11.4	569	39.5	Anorexia, lethargy
51	1.5	+		MT588813	5.20	5.2	30	9	140	39.4	Anorexia, lethargy,
											weakness
93	1		+	MT588817	5.54	9.9	25	8.63	292	39.7	Anorexia, Weakness

Table1. Results of sequencing PCR products, clinical signs, and hematological values in dogs revealed positive by the PCR

*From Sasanelli et al. (2009)

+ = sequencing PCR products result