



First molecular detection of *Borrelia theileri* subclinical infection in a cow from Brazil

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Abstract

Borrelia theileri is a relapsing fever group *Borrelia* that is transmitted to cattle by ticks of the genus *Rhipicephalus*. In this study, we describe the first molecular detection of *B. theileri* subclinical infection in a cow in Brazil. During the examination of stained blood smears of 10 cows from a farm with a recent history of fatal *Trypanosoma vivax* trypanosomiasis, spirochete-like structures were incidentally detected in one of the cows. The animal presented good body score, normal hematocrit and normal-colored ocular mucosa. Temperature, heart rate and respiratory rate were all normal. The animal was infested by ticks, which were morphologically identified as *Rhipicephalus microplus*. The diagnosis was confirmed by testing DNA extracted from a blood sample using a PCR targeting a \approx 650 bp fragment of the flagellin B (*flaB*) gene of *Borrelia* spp. The partial *flaB* sequence obtained showed 99.83% similarity with *B. theileri*. Phylogenetically, the *flaB* partial sequence generated herein clustered with other *B. theileri* sequences, being separated from *B. lonestari*. This is the first molecular detection of *B. theileri* subclinical infection in a cow in Brazil. The possible implications of this finding are discussed.

Keywords Spirochete · Bovine borreliosis · Cerrado · PCR

Borrelia theileri is a relapsing fever group *Borrelia* known to infect cattle, horses, sheep, goats, deer, impala and other wild ruminants (Theiler 1904; Dodd 1906; Neitz 1935; Callow 1967; Aouadi et al. 2017; Morel et al. 2019; Scoles et al. 2021; Abdullah et al. 2021; Qiu et al. 2021). This bacterium has been reported in Africa, Australia, Europe and

South America, where it is transmitted by *Rhipicephalus* ticks of the subgenus *Boophilus*, including *Rhipicephalus microplus* (Theiler 1905, 1909; Brumpt 1919; Callow 1967; Trees 1978; Faccini-Martínez et al. 2022).

Bovine borreliosis caused by *B. theileri* is considered a mild disease associated with fever, lethargy, hemoglobinuria, anorexia and anemia (Theiler 1905; Callow 1967; Trees 1978; Smith et al. 1978; Faccini-Martínez et al. 2022). The disease usually occurs in association with other vector-borne diseases such as babesiosis and anaplasmosis (Theiler 1904; Van Heerden and Reyers 1984; Koch et al. 1990; Sharma et al. 2000; Abanda et al. 2019). The circulation of *B. theileri* may be of concern for products derived from bovine blood, such as live vaccines against anaplasmosis and bovine babesiosis (Martins et al. 1996).

Information regarding bovine borreliosis in Latin America is scant. For instance, the presence of *B. theileri* in a bovine from Argentina was only recently confirmed (Morel et al. 2019). Furthermore, while *B. theileri* has been molecularly detected in ticks (Cordeiro et al. 2018), this bacterium has never been molecularly detected in cattle in Brazil. In this context, the objective of this study is to report the

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microscopic and molecular detection of *B. theileri* in a cow from the Cerrado biome of Brazil.

In April 2020, blood samples were collected by jugular venipuncture in sterile EDTA tubes from 10 cows in a farm in the municipality of Hidrolândia, Goiás State, Brazil. These samples were primarily collected to investigate the presence trypanosomes, due to a recent history of fatal *Trypanosoma vivax* trypanosomiasis in some animals of this farm. Samples were sent to the Laboratory of Parasitic Diseases of the Veterinary and Animal Science School of the Federal University of Goiás. From each sample, stained blood smear slides (Panótico Rápido rapid hematology stain, Laborclin®, Brazil) and Woo's test (hematocrit centrifuge technique) were performed. The hematocrit was determined by the microhematocrit method (reference range: 24–46%) (Radostits et al. 2000).

All animals were negative for trypanosomes, but spirochete-like structures were incidentally found in the blood smear of one cow (Fig. 1). This animal was clinically evaluated by measuring rectal temperature (reference range: 38–39.5 °C) (Robinson 1999; DuPreez 2000), respiratory rate [reference range: 24–36 respiratory movements per minute (mpm)] (Stöber 1993) and heart rate [reference range: 60–80 beats per minute (bpm)] (Detweiler 1996; Naas and Arcaro Júnior 2001). The animal had good body score, normal-colored ocular mucosa, normal hematocrit value (25%), rectal temperature (39.3 °C), heart rate (84 bpm), and respiratory rate (62 mpm). A total of 20 ticks (two males and 18 females) were collected and morphologically (Barros-Battesti et al. 2006) identified as *R. microplus*; the remaining nine animals were not evaluated for tick infestation.

An aliquot (200 µl) of the blood sample taken from the infected cow was subjected to DNA extraction using DNeasy Blood & Tissue Kit (Qiagen, Valencia, California),

following the manufacturer's instructions. The extracted DNA was tested by a conventional PCR targeting a ≈650 bp fragment of the flagellin B (*flaB*) gene from *Borrelia* spp., using primers FlaLL and FlaRL (Stromdahl et al. 2003). PCR products of the expected size were purified with ExoSap (USB, Cleveland, OH, USA) and DNA sequenced in an ABI automated sequencer (Applied Biosystems/Thermo Fisher Scientific, model ABI 3500 Genetic Analyzer, Foster City, California, USA) with the same primers used for PCR. The obtained sequence was submitted to BLAST analyses (www.ncbi.nlm.nih.gov/blast) to infer the closest similarities available in GenBank. An alignment with our sequence and a subset of relapsing fever and Lyme group *Borrelia* spp. was constructed with MAFFT (Kato and Standley 2013), and a phylogeny using the maximum likelihood method implemented in PhyML (Guindon and Gascuel 2003) with the HKY85 substitution model as selected using the Bayesian Information Criterion in MEGA 5 (Tamura et al. 2011).

PCR testing was positive and the *flaB* partial sequence obtained showed 99.83% identity (592/593 bp) to a sequence of *B. theileri* (KF569936) detected in *Rhipicephalus geigy* from Mali (McCoy et al. 2014). These sequences differed by a single nucleotide that corresponds to a silent mutation (i.e., a nucleotide change in the third codon position which does not alter the encoded amino acid). The partial *flaB* sequence of *B. theileri* generated in this study is deposited in GenBank (accession number: ON191583). Phylogenetically, the partial *flaB* sequence generated in this study clustered with other *B. theileri* sequences, being separated (100% bootstrap value support) from *B. lonestari*, its closest congener (Fig. 2).

More than a century ago, Brumpt (1919) reported the presence of *B. theileri*-like spirochetes (referred to as *Spirochaeta theileri*) in cattle and transmission through

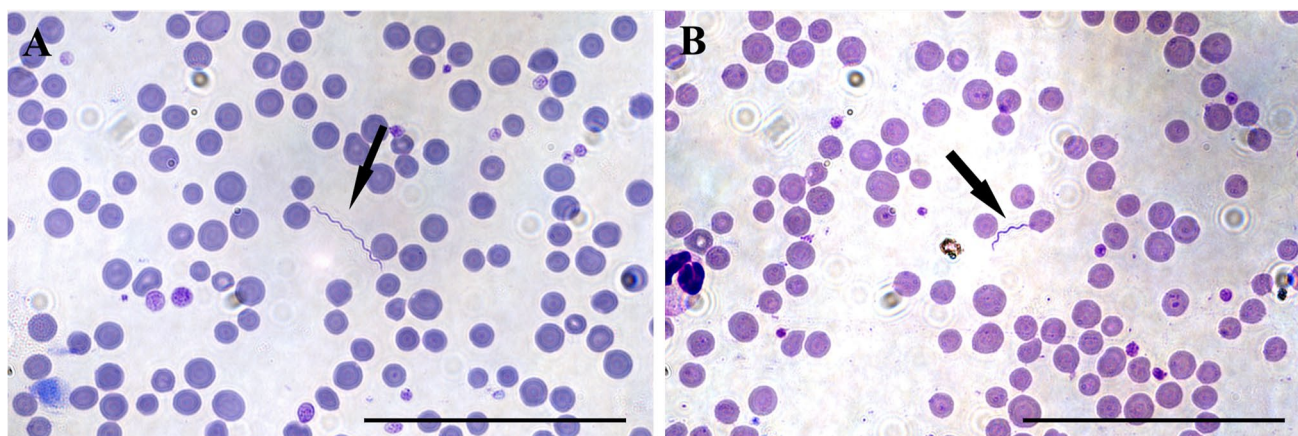


Fig. 1 Stained blood smear of a cow positive to *Borrelia theileri*, presenting typical spirochetes (black arrows in images A and B; 1000 x magnification). Scale bars = 50 µm

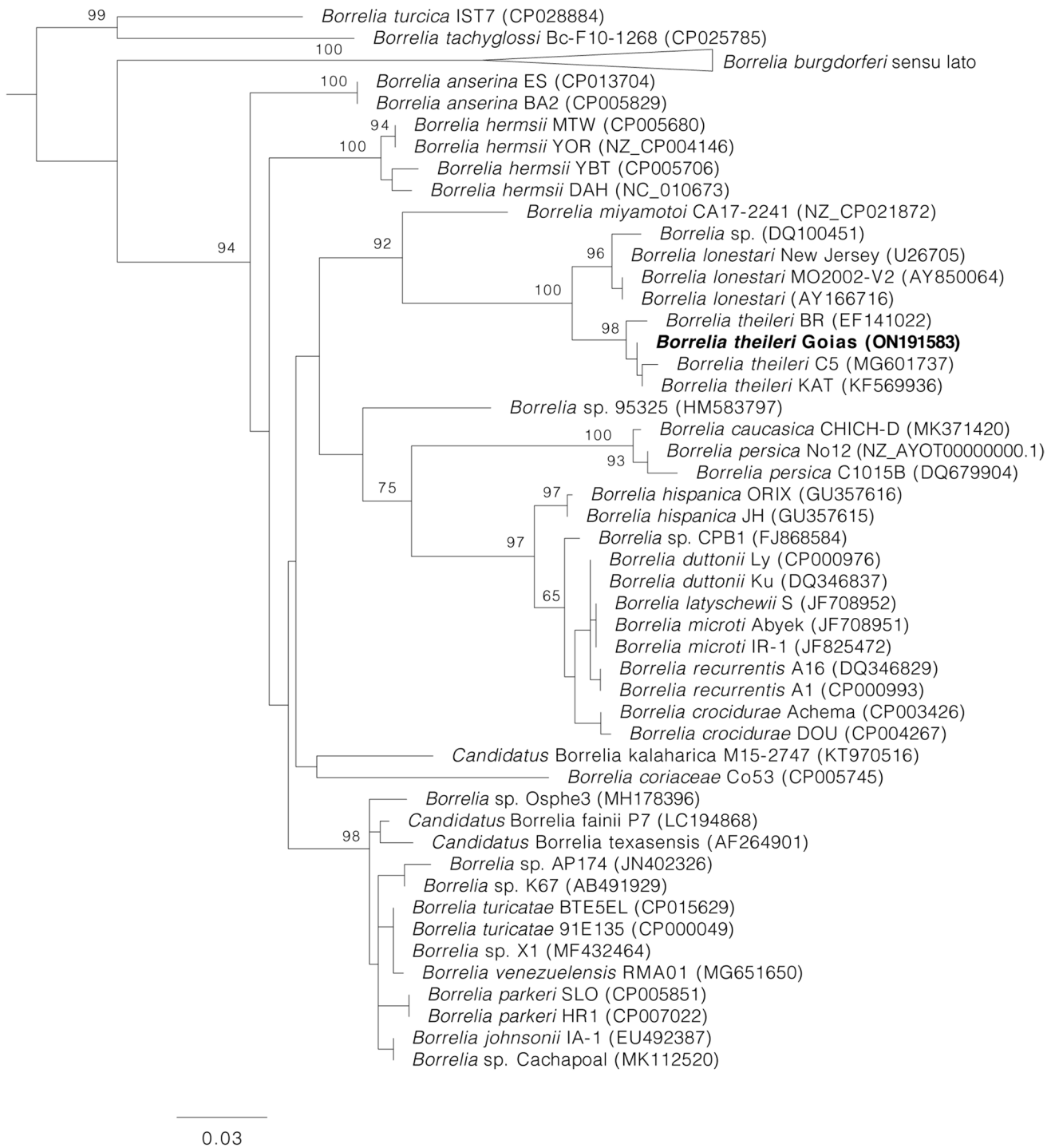


Fig. 2 Maximum likelihood phylogenetic tree of *Borrelia* genus highlighting the position of *Borrelia theileri* detected in this study in bold. *Borrelia turcica* IST7 and *Borrelia tachyglossi* Bc-F10-1268 rooted the tree. Only bootstrap values above 60% are shown

ticks, after these animals were infected by successive generations of *R. microplus* ticks (referred to as *Margaropus australis*) from Brazil. After several decades, *B. theileri* was reported in *R. microplus* ticks from Brazil through incidental findings in hemolymph smears (Martins et al.

1996; Rezende et al. 2008). In addition, Yparraguirre et al. (2007) reported the molecular detection of a *Borrelia* sp. in a *R. microplus* tick in the southeastern Brazil, which was highly correlated with *B. theileri* and *B. lonestari*. More recently, Cordeiro et al. (2018) used morphological,

molecular and phylogenetic data to confirm the presence of *B. theileri* in an engorged *R. microplus* female removed from a bovine in the state of Rio de Janeiro, Brazil.

We detected spirochetes in the stained blood smear from only one out of 10 cows, which could be related to the low parasitemia observed in *B. theileri* infections. According to experimental studies, *B. theileri* becomes detectable in blood smears 2–4 weeks after exposure to infected ticks (Theiler 1905; Callow 1967; Trees 1978; Smith et al. 1978). Occasionally, new peaks of parasitemia may occur, but without signs of illness; the short periods of fever usually coincide with the presence of observable spirochetes on blood smears (Trees 1978; Smith et al. 1978; Van Heerden and Reyers 1984).

During the parasitemia, cattle infected with *B. theileri* may exhibit a mild rise in temperature, fever, anorexia, depression, and anemia (Theiler 1905; Callow 1967), with the presence of hemoglobinuria (Callow 1967). The infected animal in the present study did not present any clinical signs.

Borrelia theileri is transmitted by *Rhipicephalus* ticks belonging to the subgenus *Boophilus* (e.g., *R. annulatus*, *R. microplus*, *R. decoloratus*, and *R. evertsi*) that preferentially parasitize cattle (Theiler 1905, 1909; Brumpt 1919; Callow 1967; Trees 1978). This agrees with our finding of *R. microplus* ticks parasitizing the infected cow. In addition to transmit *B. theileri*, *R. microplus* is reputed to be a vector of *Babesia bigemina*, *Babesia bovis* and *Anaplasma marginale* in some tropical regions (Theiler 1904; Neitz 1956; Callow and Hoyte 1961; Smith et al. 1978; Scoles et al. 2021).

Previous studies reported serologic cross-reactivity of cattle anti-*Borrelia* IgG antibodies to whole-cell antigens of *B. theileri*, *Borrelia burgdorferi* and *Borrelia coriacea* (Ji et al. 1994; Rogers et al. 1999). Thus, caution is needed when using serological tests for diagnosing borreliosis in regions where *B. theileri* co-exists with other tick-borne *Borrelia* species (Rogers et al. 1999).

In a recent study, Scoles et al. (2021) tested cattle blood samples using a PCR assay targeting the flagellin gene and confirmed the presence of *B. theileri* in three (out of 135) stray Mexico origin cattle captured in Texas (Scoles et al. 2021). To our knowledge, our study reports the first molecular detection of *B. theileri* subclinical infection in cattle in Brazil. Further research is needed to assess the prevalence of *B. theileri* and its possible impact on the livestock industry in Brazil.

Author contribution WVFP, MBL and FSK conceived and designed the study, and critically revised the manuscript. WVFP, MBL, FDT, SML and FSK performed the experiment, analyzed the data, and drafted the manuscript. WVFP, LCN, LGFP, MCAS, FPO helped in the implementation and execution of the study. WVFP, MBL, FDT,

SML and FSK performed and interpreted the laboratory analyses. All authors read and approved the final manuscript.

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Data availability The data presented in this study are available within the article.

Declarations

Ethics approval The farm was visited during routine veterinary care of the Veterinary School of the Federal University of Goiás. Animal examination and blood collection were performed under a signed consent of the farmer.

Consent to participate All authors give their consent to participate in this article.

Consent of publication All authors consent to publication of this manuscript.

Competing of interest Authors declare they have no competing interest.

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