Molecular characterization of *Babesia gibsoni* present in dogs in Sri Lanka

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**Highlights**

- Sequences of 18s rRNA gene of *B. gibsoni* in Sri Lanka were highly similar to Wayanad isolate 8 from India.
- ITS1 genes were highly similar to those of *B. gibsoni* from India.
- *B. gibsoni* in Sri Lanka is genetically similar to a strain present in South India.
Molecular characterization of Babesia gibsoni present in dogs in Sri Lanka

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Abstract: Certain Babesia species that were known as a single species are now re-classified into subspecies or different species. To identify any strain variation in B. gibsoni species which infect dogs in Sri Lanka, sequences of the three genes; 18S rRNA, internal transcribed spacer 1 (ITS1), and B. gibsoni thrombospondin related adhesive protein (BgTRAP) were analyzed in dogs with babesiosis from three geographical locations. Analysis of the sequences of the 18S rRNA gene confirmed that the samples contained B. gibsoni Asian genotype. Analysis of the BgTRAP gene revealed that the B. gibsoni present in Sri Lanka is genetically different from the species present in East Asian countries.

Keywords: Babesia gibsoni; 18S rRNA; ITS1; BgTRAP; variant, Sri Lanka.

INTRODUCTION

Canine babesiosis caused by the intra-erythrocytic apicomplexan parasite is a life-threatening disease (Wozniak et al., 1997). Two morphologically distinct forms named large and small Babesia are causing these infections in dogs (Kjemtrup and Conrad, 2006). The larger form with pear-shaped trophozoites belongs to three sub-species: Babesia canis (B. canis), Babesia rossi (B. rossi), and Babesia vogeli (B. vogeli) (Irwin, 2009). The smaller form which appears as an oval signet ring body in the erythrocytic stage, may represent one of the three different species namely Babesia gibsoni (B. gibsoni), Babesia conradae (B. conradae) or Babesia vulpes (B. vulpes) (syn Babesia microti like/Theliera annae) (Irwin, 2009; Baneth et al., 2019) and of those species, B. gibsoni is highly prevalent in Asian countries (Irwin, 2009). Canine Babesiosis was reported in Sri Lanka as early as 1953 (Seneviratna, 1953; Seneviratna and Jayawickrama 1961; Seneviratna, 1965) and several recent studies have confirmed the high prevalence of the disease in the country (Weerathunga et al., 2019; Jayathilake et al., 2020; Neelawala et al., 2021). As the severity of the clinical signs caused by B. gibsoni shows significant variations, the possibility of the presence of different strains or sub-species of the organism has become a concern, and sequencing of various genes to identify any genetic differences has been attempted (Boström et al., 2008; Mandal et al., 2014; Terao et al., 2015; Singh et al., 2016).

Sequencing of 18S rRNA is widely used to differentiate the genotypes or subspecies of Babesia and the three distinct species of small babesia were identified based on the characterization of this gene (Kjemtrup and Conrad, 2000; Mandal et al., 2014). In addition, sub-species of Babesia are reported to contain dissimilarities in the Internal Transcriber 1 (ITS1) region as well (Baneth et al., 2004). Sequencing of the BgTRAP gene of B. gibsoni species from India and Bangladesh has shown that B. gibsoni species present in these two countries are genetically distinct from those present in East Asian countries (Terao et al., 2015; Singh et al., 2016). The small Babesia species affecting dogs are invariably called B. gibsoni and only two studies conducted recently have attempted to confirm the organism affecting dogs in Sri Lanka as B. gibsoni by molecular methods (Jayathilake et al., 2020; Ranatunga et al., 2020). In this study, we attempted to characterize B. gibsoni which infect dogs in Sri Lanka by analyzing partial sequences of the 18S rRNA, ITS1, and BgTRAP genes.

MATERIALS AND METHODS

Genomic DNA was extracted from blood samples of ten dogs who were confirmed to be infected with small Babesia species by blood smear examination. The dogs were from three different provinces in Sri Lanka namely Central (n = 6), Western (n = 2), and Sabaragamuwa (n = 2) and presented to Veterinary Teaching Hospital, Peradeniya with mild (n = 2), moderate (n = 4) or severe clinical signs (n = 4) of babesiosis in 2017. Three different genes namely 18S rRNA, ITS1, and BgTRAP were amplified using the primers, and the PCR conditions given in Table 1.

The amplicons were separated by electrophoresis on 2.0% agarose gel, stained with Diamond nucleotide dye (Promega, USA) and visualized under a gel imaging system (Geneflash, India).

The PCR products of all three genes (18S rRNA, ITS1 and BgTRAP) were sequenced using forward and or reverse primers at the sequencing facility of the Department of Molecular Biology and Biotechnology, Faculty of Science, University of Peradeniya. The quality of the sequences was analyzed by visualizing the chromatogram on MEGAX. Sequences were BLAST...
searched at BLASTn at NCBI GenBank. Sequences were analyzed using MEGAX software. Reference sequences for each gene were downloaded from the NCBI database. Sequences were aligned by MUSCLE, best-fitted models were identified (Hasegawa–Kishono–Yano model with invariant sites -HKY+I for distance calculation) and Maximum likelihood trees with bootstrap values were generated by the MEGAX.

RESULTS

All three genes were successfully amplified and the PCR amplicons of 619 bp (18s rRNA), 254 bp (ITS1), and 855 bp (BgTRAP) were detected in gel electrophoresis (Figure 1). However, three PCR amplicons of BgTRAP contained non-specific amplification and hence were not sequenced.

Sequence similarity search showed that all 18S rRNA genes of the *B. gisoni* of the present study were highly similar to a *B. gibsoni* Wayanad isolate 8 (Accession MN134517) with 99.6% identity.

ITS1 genes of the *B. gibsoni* strains of this study were highly similar to a *B. gibsoni* strain from India (Accession KF815078) with 98.0% identity. Gene sequences of the ITS-1 region of *Babesia* species were aligned and the Maximum Likelihood tree was constructed using *Plasmodium falciparum* as an out-group. As shown in Figure 2, *B. gibsoni* isolated from Sri Lanka (GenBank accession: MW517166-MW517675) formed a clade with two Indian strains. However, the bootstrap value of the clade (49%) was not supportive to confirm any genetic difference between the two groups.

| Gene       | Primer Sequences and PCR conditions                                                                 | Size  | Reference          |
|------------|------------------------------------------------------------------------------------------------------|-------|--------------------|
| 18srRNA    | Ba103FCCAAATCTGACACAGGGAGGTAGTGAC Ba721RCCCCAGAACCCAAAGACTTTGATTTCTCTCAAG                             | 619 bp| Inokuma et al., 2004 |
| ITS1       | BgITS1F-ACATTGAAACTTGTCGAGCTGCG BgITS1R-AGATCCCGCACCCAGCCA                                       | 254 bp| Terao et al., 2015  |
| BgTRAP     | (F - 5’ - A C C C A G C G A A T A C A T G C A C C A C A C A ) (5’-AGCCCTGCAAAACCGCAAAGTA TG-3’)       | 855 bp| Kjemtrup and Conrad, 2000 |

Figure 1: (a) Agarose gel electrophores of PCR amplicons of 18S rRNA gene (b) ITS1 gene (c) BgTRAP gene of *B. gibsoni*. The first lane contains the 100 bp molecular weight marker and the last two lanes of each gel contain positive and negative controls.
Figure 2: The Maximum Likelihood (ML) tree of ITS1 region of Babesia gibsoni. (Babesia gibsoni from Sri Lanka are in red).

Figure 3: The Maximum Likelihood (ML) tree of the BgTRAP gene of Babesia gibsoni. (Green: East Asia, Blue: India, Purple: Bangladesh, Red: Sri Lanka).
The Maximum Likelihood tree based on the 855 bp region of the BgTRAP gene is presented in Figure 3. As shown in the figure, *B. gibsoni* strains from East Asia, including Taiwan, Malaysia, Japan, and Korea formed a different clade with 100% bootstrap support. All *B. gibsoni* strains from India (KT, KU, and KX isolates), Bangladesh (LC010132 and LC010124), and Sri Lanka (GenBank accession: MW551795-MW551799) clustered on a separate clade. Further, the Sri Lankan strains clustered with a *B. gibsoni* strain from Trivandrum, India.

**DISCUSSION**

The present study reports the genetic characterization of the 18S rRNA gene, ITS1 region, and BgTRAP gene of *B. gibsoni* from dogs in Sri Lanka. Molecular analysis of *B. gibsoni* strains present in several Asian countries including India, Bangladesh, Japan, Korea, Taiwan, and Malaysia has been reported previously (Inokuma et al., 2004; Miyama et al., 2005; Terao et al., 2015; Singh et al., 2016). Homology of the sequences and phylogenetic clustering of the 18S rRNA and ITS1 sequences confirmed that the small *Babesia* species present in Sri Lanka is *B. gibsoni* Asian genotype-2. However, both 18S rRNA and ITS regions of *B. gibsoni* strains from different Asian countries did not show much genetic diversity and appeared to be highly conserved among small *Babesia* species. Bostrom et al. (2008) and Mandal et al. (2014) have made similar observations and our results re-confirmed their findings. Analysis of the 18S rRNA sequences was useful in differentiating *B. gibsoni* from *B. vulpes*, another small *Babesia* species affecting dogs. We only sequenced 619 bp fragment of the 18S rRNA gene and a previous study has shown that the sequencing of 1655 bp fragment of this gene was helpful in differentiating *B. gibsoni* from *B. conradae* (Mandal et al., 2014). Liu et al. (2016) have analyzed 54 sequences of ITS1 of *B. gibsoni* from different geographical regions in Japan. Authors have also reported that those isolates were found interspersed with isolates from Australia, India, Taiwan, and the USA.

The TRAP gene has been used to identify the genetic diversity of the *Babesia* and the regions between TSR and the CTD have shown a variation (Terao et al., 2015). The construction of a phylogenetic tree using the sequences of the BgTRAP gene revealed that the *B. gibsoni* species present in the Indian subcontinent is genetically different from the strains present in East Asian countries. Terao et al. (2015) analyzed the BgTRAP gene sequences of the *B. gibsoni* from Bangladesh and reported that the Bangladesh strains are genetically different from the strains present in East Asian countries. In our phylogenetic analysis also, the Bangladesh strains clustered separately with 88% bootstrap support but that cluster contained a *B. gibsoni* strain from India (KT750255). It is important to note that all five *B. gibsoni* isolates from Sri Lanka were on different genetic clades together with a strain from Trivandrum, India. The number of gene sequences of the BgTRAP gene available in the Genbank is still limited and these gene sequences representing different geographical regions will help to understand the true phylogenetic relationship of the organism in different regions of the world. It warrants further studies to understand whether these genetic differences have caused any difference in the antigenicity and the pathogenicity of the organism.

**CONCLUSION**

*B. gibsoni* present in Sri Lanka is genetically different from the species present in East Asian countries and closely related to strain present in South India.

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**DECLARATION OF CONFLICT OF INTEREST**

Authors have no conflict of interest to declare.

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