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## Molecular detection of *Babesia gibsoni* in stray dogs of Southern Kerala

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### Abstract

A molecular study was conducted to know the prevalence of *Babesia gibsoni* in stray dogs from Southern zone of Kerala. A total of (n=50) blood samples and smears were collected from Animal Birth Control Centers (ABCs) from Southern Zone of Kerala. Peripheral blood smears revealed *B. gibsoni* piroplasms in 20 per cent (10/50) of the samples. Primary PCR targeting 18S rRNA gene showed amplification at ~1665 bp in 42 per cent (21/50) of samples whereas by nested PCR using a set of internal primers which targets primary PCR product showed amplification at ~308 bp fragment in 56 per cent (28/50) of samples. This study showed a higher prevalence of *B. gibsoni* in stray dogs compared to previous studies on the prevalence of *B. gibsoni* in pet dogs. The nested PCR targeting 18S rRNA was more sensitive in detecting *B. gibsoni* compared to primary PCR.

**Keywords:** *Babesia gibsoni*, stray dogs, PCR, 18S rRNA

### Introduction

India's diverse climatic zones, make it ideal for a wide range of vectors and pathogens, whose transmission and geographical distribution are closely linked to regional temperature, humidity and rainfall (Patz *et al.*, 2005) [17]. Babesiosis, hepatozoonosis, trypanosomosis, ehrlichiosis and anaplasmosis are the major vector borne parasitic diseases prevalent in dogs in India. Co-infections of *Babesia* with *Ehrlichia*, *Hepatozoon*, *Bartonella*, *Anaplasma* and *Leishmania* have been reported in dogs (O'Dwyer *et al.*, 2001) [16]. Babesiosis is one of the widespread haemoprotozoan diseases in dogs world-wide (Homer *et al.* 2000) [6]. Taxonomically *Babesia* is under the phylum Apicomplexa, class Aconoidasida, order Piroplasmida and family Babesidae (Taylor *et al.*, 2016) [28]. The babesiosis causing organisms are classified based on the morphology of piroplasm within red blood cell as large (4-5 µm) (Eg: *B. canis*) or small (1-2.5 µm) forms (Eg: *B. gibsoni*) (Gallego *et al.*, 2016) [25]. The *B. gibsoni* was reported first in India by Patton in 1910 (Patton, 1910). *Babesia gibsoni* is the most pathogenic species and is transmitted mainly by ticks (Jefferies *et al.* 2007; Schnittger *et al.* 2012) [9, 21]. There are different modes of transmission for canine babesiosis which include tick bite, blood transfusion, direct contact between dogs through wounds (fighting dogs), saliva or blood ingestion and transplacental transmission (Stegeman *et al.*, 2003; Birkenheuer *et al.*, 2005; Jefferies *et al.*, 2007; Yeagley *et al.*, 2009; Fukumoto *et al.*, 2005, Adaszek *et al.*, 2016) [26, 10, 9, 5, 31]. Canine babesiosis can range from chronic or sub-clinical to per acute and fatal infection (Schoeman 2009) [22]. The clinical signs include fever, anaemia, icterus, thrombocytopenia and splenomegaly. The microscopic examination of peripheral blood smears does not allow for reliable identification of the parasites in sub-clinical and asymptomatic carriers (Rani *et al.*, 2011) [18]. Parasite morphology being a poor guide to speciation, polymerase chain reaction (PCR) differentiates piroplasm species with higher specificity and sensitivity. Highly conserved 18S rRNA is used to differentiate genotype or sub-species of canine *Babesia* (Kjemtrup *et al.*, 2000) [10].

### Materials and Methods

A total of (n=50) peripheral blood smears and whole blood samples from saphenous vein of stray dogs in EDTA (ethylene diamine tetra acetic acid) vials were collected from apparently healthy animals brought to the Animal Birth Control centers and stored at -20°C until further processing. Peripheral blood smears were stained with Giemsa stain for 45 min. Genomic DNA was isolated from the blood samples using DNeasy blood and tissue kit (Qiagen,

Germany) according to the manufacture's protocol. The isolated DNA was stored at -20 °C. All the PCR reactions were conducted in an automated thermal cycler with heated lid (M/s. Eppendorf, Hamburg, Germany). The PCR reaction was set up in a total volume of 25 µL reaction mixture as follows 12.5 µL of Master-mix, 1 µL of forward and reverse primer, 1.5 µL of template DNA and 9 µL of Nucleus free water. The primers targeting 18S rRNA gene were showed in (Table 1).

Primary PCR was performed based on the protocol described by Jefferies *et al.* (2007) [9] for the amplification of ~1665 bp fragment of 18S ribosomal RNA gene. The cycling conditions are as follows: initial denaturation at 94 °C for 5 min followed by 35 cycles, consisting of a denaturation step of 1 min at 92°C, an annealing temperature of 45sec at 52 °C and an extension step of 2 min at 72 °C. The final extension was performed at 72 °C for 10 min.

The primary PCR products were used as a template for nested PCR. *B. gibsoni* species specific PCR based on the protocol described by Jefferies *et al.* (2007) [9] for the amplification of ~330 bp fragment of 18S ribosomal RNA gene. The cycling conditions are as follows: initial denaturation at 92 °C for 2 min followed by 35 cycles, each consisting of denaturation at 92 °C for 45sec, annealing temperature of 45 sec at 52 °C and an extension step of 5 min at 72 °C. the final extension was performed at 72 °C for 5 min.

## Results

The Peripheral blood smears (n=50) were examined under 100X objective of a compound microscope (Leica, Germany) of which (10/50) samples (20 per cent) were positive for *B. gibsoni* organisms (Fig. 1). The genus specific primers targeting 18S rRNA gene of *Babesia* spp. amplified at ~1665 bp fragment during primary PCR in 21/50 (42 per cent) samples (Fig. 2). The nested PCR using a set of internal primers amplified at ~308 bp fragment of 18S rRNA gene when the product of the primary PCR ~1665 bp was used as the template (Fig. 3). A total of 28/50 (56 per cent) samples

were positive for *B. gibsoni* by nested PCR.

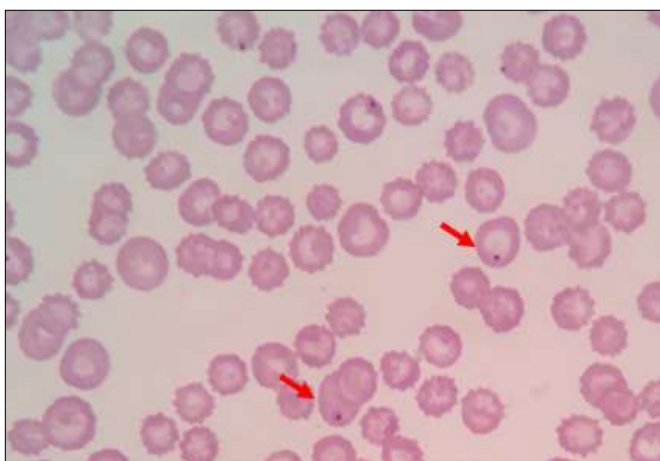
## Discussion

Ticks and tick-borne diseases (TTBDs) cause severe impediments to human and animal health. The blood sucking habits of ticks complement the transmission of various pathogens like bacteria, virus, rickettsia and haemoprotozoans. Among the haemoparasitic infections in mammals, babesiosis caused by the organisms of the genus *Babesia*, occupies the second place after trypanosomosis (Schnittger *et al.*, 2012) [21]. Both large and small forms of *Babesia* can cause considerable morbidity and mortality if they are not diagnosed and treated at the appropriate time. *Babesia vogeli* and *B. gibsoni* are the commonly distributed canine *Babesia* in the tropical and subtropical areas of the world. *Babesia gibsoni* is widely distributed in the Indian subcontinent and east Asian countries (Lee *et al.*, 2010; Mandal *et al.*, 2014; Laha *et al.*, 2014; Terao *et al.*, 2015) [12, 14, 11, 29]. The distribution of these organisms not only depend on the presence of ticks but also can be transmitted by dog bite, transplacental transmission and blood transfusion (Birkenheuer *et al.*, 2005; Fukumoto *et al.*, 2005; Adaszek *et al.*, 2016) [5, 10].

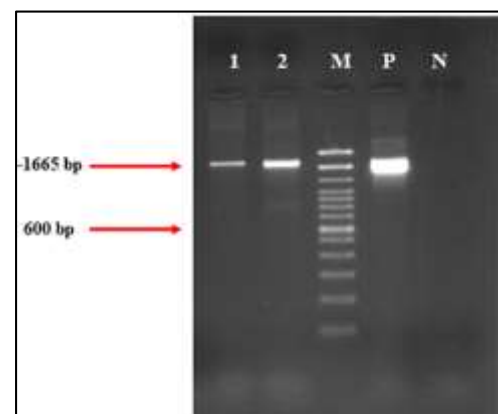
In the present study, the prevalence of *B. gibsoni* in stray dogs was very high compared to that of previous reports from pet dogs of Kerala (Jain *et al.*, 2017, Bora *et al.*, 2021) [8, 3] as well as from other states of India (Rani *et al.*, 2011; Singh *et al.*, 2016; Mahalingaiah *et al.*, 2017; Chandra *et al.*, 2018; Sarma *et al.*, 2019, Manoj *et al.*, 2020, Sindhu *et al.*, 2020) [18, 4, 23, 15]. The reasons could be due to the abundance of tick vectors (Rani *et al.*, 2011, Sahu *et al.*, 2014) [18] and absence of treatment in community owned dogs (Traub *et al.*, 2014; Sudan *et al.*, 2015) [27]. Moreover, there are reports for possible transmission *B. gibsoni* through direct contact through wounds, saliva or blood ingestion (Irizarry-Rovira *et al.*, 2001) [7]. These findings corroborates with the high prevalence of *B. gibsoni* in community owned dogs in the present study.

**Table 1:** Primers used for the detection of *Babesia gibsoni*

Target gene	Primer name	Oligonucleotide sequence (5' 3')	Product size (bp)	Reference
18S rRNA	Bg18S F (Primary)	TGGTTGATCCTGCCAG TA	1665 bp	(Jefferies <i>et al.</i> 2007) [9]
	Bg18S R (Primary)	CTTCTCCTTCCTTTAAGTGA		
	Bg18S F (Nested)	ATAACCGTGCTAATTGTAGG	308 bp	
	Bg18S R (Nested)	TGTTATTTCTTGTCACTACC		

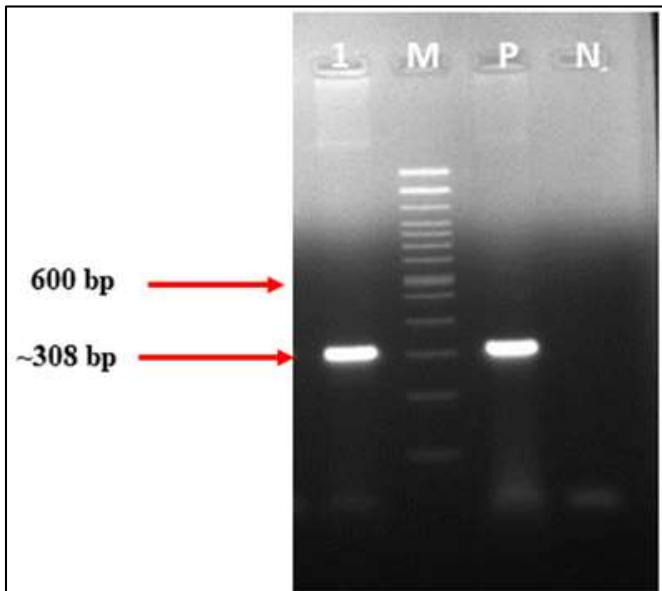


**Fig 1:** Blood smear of a stray dog showing ring shaped piroplasms of *B. gibsoni*



Lane 1,2: Samples, Lane M: 100 bp plus ladder, Lane P: Positive control, Lane N: Negative control

**Fig 2:** PCR amplification of 18S rRNA gene (~1665 bp) of *Babesia* spp.



Lane 1: Sample, Lane M: 100 bp plus ladder, Lane P: Positive control, Lane N: Negative control

**Fig 3:** Nested PCR amplification of 18S rRNA gene (~308 bp) of *Babesia gibsoni*.

### Conclusion

In the present investigation, the prevalence of *B. gibsoni* in stray dogs was very high compared to that of previous reports from pet dogs of Kerala. The nested PCR targeting 18S rRNA was more sensitive in detecting *B. gibsoni* compared to primary PCR.

### Acknowledgements

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