Original Article

Molecular Identification and Genotyping of Babesia canis in Dogs from Meshkin Shahr County, Northwestern Iran

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Abstract

Background: Canine babesiosis is one of the mainly worldwide-distributed tick-borne haemoprotozoan parasitic diseases in dogs.

Methods: A total of 43 blood samples were randomly collected from naturally infected dogs in seven villages from different geographical areas of Meshkin Shahr, Ardabil Province, Iran. The presence of Babesia species detected with standard methods including parasitological and gene sequencing techniques targeting the 18S rRNA gene.

Results: Our results revealed that four dogs 9.3% (4/43) including one female and three male dogs were infected with Babesia. All four Babesia-infected dogs were confirmed B. canis by the molecular-based method. Sequence alignments comparison of the B. canis genotypes A and B, it was revealed that all B. canis isolates belonged to genotype B.

Conclusion: This study provides essential data for subsequently define the critical importance of the molecular studies in management and prevention of the canine babesiosis in Iran.

Keywords: Babesia canis; Babesiosis; Dogs; Genotyping; RNA, ribosomal, 18S; Iran

Introduction

Canine babesiosis is a tick-borne parasitic disease with worldwide importance and caused by intra-erythrocytic Babesia species. The identification of each Babesia species routinely is based on the host specificity and the morphological characteristics of piroplasmids (1). The differences in geographical distribution, vector specificity, antigenic properties, genetic characteristics and severity of the clinical manifestations sub divided the former species into the three subspecies, namely B. canis canis (3–5μm) is transmitted by Dermacentor reticulatus in Europe, B. canis vogeli transmitted by Rhipicephalus sanguineus sensu lato in tropical and subtropical regions, and B. canis rossi transmitted by Haemaphysalis leachi in South Africa (1, 2). Babesia gibsoni (1.5–2.5μm) is present in Asia, North America, Africa, Australia and Europe (3–6). The geographical distributions of both species of D. marginatus and D. reticulatus in Europe range from Portugal to Ukraine (continue to the east of Kazakhstan), Turkey and probably to the northern parts of Iran (7-10). The first report of Dermacentor ticks in Iran was documented in 1971 by Mazlum (11). This study performed among the 30 provinces and the results defined that, Dermacentor ticks were found only in six provinces (Semnan, Khorasan, Kurdistan, Ardabil, East Azerbaijan, and Zanjan) with the highest rate of distribution in Ardabil in which ticks was found to be restricted to four species; D. niveus, D. margi-
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...study provides essential and valuable data to insight into the prevalence and distribution of canine babesiosis in Iran. Thereby, regarding to raise of knowledge on this parasite, the detection and characterization of the Babesia species and subspecies from canine babesiosis in Meshkin shahr has a great importance through application of PCR and sequencing of 18S rRNA gene sequences.

Materials and Methods

Study area, blood and spleen samples

From July 2017 to February 2018, a total of 43 blood samples were randomly collected from shepherd dogs (Canis familiaris) (32 males and 11 females, 9 months to 7 years old) in Meshkin Shahr, Ardabil Province, Northwest of Iran. Blood samples were collected into 0.001M EDTA-containing tubes, and transported in ice-boxes to the laboratory of protozoology, faculty of medicine, Iran University of medical sciences. Blood samples aliquoted, smears were prepared from EDTA-sampled, blood air-dried, and stained with Giemsa. Genomic DNA was extracted from each blood samples using a DNA extraction kit (Qiagen DNA Blood Mini-Kit, Germany). All samples were identified and followed the detection process using PCR.

Molecular analysis and characterization of the isolated Babesia species

DNA was extracted from whole blood samples using the DNA extraction kit from blood (Qiagen, Hilden, Germany) through following manufacturer instructions as previously described (22, 31). To detect Babesia species, the gene fragment (~550bp) from 18S rRNA was amplified and sequenced using the primers BAB GF2 (5'-GYYTTGTAATGGAAATGA TG-3') and BAB GR2 (5’- CCAAGAC TTGTTCTC-3'). All stages were performed using the previously described PCR protocol (23). Generally, reactions were performed in a total of 25μl, including 2.5μl of 10X PCR buffer, 2.0μl of dNTP (2.5mM each), 1.25U of Taq...
DNA polymerase (SinaColon Co. Iran) 1.0μl of template DNA, 1.0μl of each primer (10pmol), and 16.25μl of double distilled water (SinaColon Co. Iran). The PCR reaction was 95 °C (3min), [95 °C (30s), 55 °C (30s), 72 °C (90s)]× 35 cycles, 72 °C (5min). In the second round of PCR 418bp of DNA fragments were generated using another pair of primers, PIRO-nest F (5′-GGATAACCGTGST AATTSTAGGGC-3′) and PIRO-nest R (5′-GTGTGTACAAAGGG CAGGGACG-3′) (4). The amplified PCR products were maintained at -20 °C until analyzed. The products were run on electrophoresis in a 1.5% agarose gel containing 0.2μg of safe stain/ml in Trisacetate-EDTA buffer at 120V for 30 min and consequently transilluminated under UV light.

Ethical approve
This study was approved by admission with the ethics procedures and guidelines of the respective national the animal ethics use committees of research issued by the council of the Iran University of Medical Sciences (IR. IUMS.REC. 27899.).

Sequences analysis
Sequences subjected to online BLAST algorithm and were compared with previously registered sequences in the GenBank database. To confirm the classification of the parasite, large fragments of the 18S rRNA gene were amplified from each sample that was positive for Babesia. The18S rRNA genes sequences were analyzed by standard technique using a sequencer and BioEdit software (Perkin-Elmer, USA) (32). Analysis of DNA sequences and phylogenetic relationships for B. canis isolates and the group of isolates from dogs were aligned using Clustal W software (33). A phylogenetic tree was created using alignments performed with neighbor joining (NJ) phylogenetic tree using Kimura-2-Parameter algorithm with bootstrap as the tree construction method (34). Furthermore, phylogenetic analysis of gene sequences were performed with maximum likelihood method with MEGA 7.0 software. The representative sequence was annotated in the GenBank database with accession number MN173220, MN173221, MN173222 and MN173223 (Table 1). To assess B. canis genotypes (4, 35), the obtained sequences were compared with the members from genotype A (AY703072) and genotype B (AY649326).

Results
In the direct microscopic diagnostic investigation of blood smear and molecular study of blood samples revealed that four dogs 9.3% (4/43) including one female and three male dogs were infected with B. canis (Fig 1). In the clinical examinations, all four dogs had major symptoms of babesiosis and most of the infected dogs had fever and splenomegaly. In addition, blood parameters including hemoglobin concentration, hematocrit, RBC count, and direct bilirubin had increased (Table 1). Out of the total samples subjected to PCR, four dogs was Babesia-positive including one female and three males. DNA was purified from all blood samples of the collected dogs and used as the PCR template, which a 550bp band was observed in the analysis. The results of sequence analysis were the same as with the other previously annotated sequences. The nucleotide sequences from canine samples were identical to each other and had shown a 99.6–100% identity with B. canis derived from dogs in GenBank reference sequences originated from different countries such as Turkey (KY247106 and KF499115), China (MK256974), Slovakia (DQ869307), Estonia (KT008057), Romania (HQ662634), and Croatia (AY072926). The comparison of B. canis nucleotide sequences obtained in this study with genotypes A and B revealed that all our isolates were classified as genotype B and the main difference was observed in positions 490 and 491. The difference of the two genotypes in the row of adenine and guanine nucleotides are in genotype B as AG and GA in genotype A (Fig. 2). The results of phylogenetic analysis revealed that the 18S
rRNA gene sequences obtained in this study matched with *B. canis* and alignments showed that all *B. canis* isolates belonged in the category of genotype B (Fig. 3). In present study, the common ancestor of genotype A and B was obtained with confidence level 99%. Genetic confidence intervals can help to better understand genealogical relationships to DNA matches.

![Fig. 1. Direct microscopic detection of *Babesia canis* in the blood of naturally infected dogs. Field-Giemsa stained thin smears showing various forms of *B. canis* in erythrocytes. A: Closed angle pyriform bodies of *B. canis* and B: Wide angles *B. canis* near the margin of the infected RBCs](image1)

![Fig. 2. Multiple sequence alignment of the partial 18S rRNA gene and the sequences of genotype A and B. In this position nucleotide changes can be seen](image2)
Fig. 3. Neighbor-joining analysis of canine *Babesia* sequences obtained from samples submitted. A 550bp fragment of the 18S rRNA was aligned with representative sequences derived from GenBank. Bootstrap values (1000 replications) are shown in the phylogenetic tree. Comparison of the *B. canis* sequences obtained in this study with genotypes A and B. Samples sequenced in the present study are marked with red cycle (MN173220- MN173223). The tree was inferred using the neighbor joining method of MEGA7, bootstrap values are shown at each branch point.
Table 1. Principle information on the animals sampled and the *Babesia* species isolated

<table>
<thead>
<tr>
<th>Breed</th>
<th>Samples</th>
<th>Pathogen</th>
<th>Clinical symptoms</th>
<th>Accession number (s)</th>
<th>Blood analysis*</th>
<th>Diagnostic investigation</th>
<th>Location and Coordinates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mongrel</td>
<td>Mesh 1</td>
<td>Female</td>
<td><em>B. canis</em></td>
<td>MN173220</td>
<td>PCR: positive</td>
<td>Blood smear: positive</td>
<td>Ag bolagh 38°20′57″N 47°39′57″E</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Fever, splenomegaly</td>
<td></td>
<td>Blood smear: positive</td>
<td>Tissue: positive</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mesh 2</td>
<td>Male</td>
<td><em>B. canis</em></td>
<td>MN173221</td>
<td>PCR: positive</td>
<td>Blood smear: positive</td>
<td>Parikhan 38°24′51″N 47°38′38″E</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Fever, vomiting, lethargy</td>
<td>RBC: 4.8</td>
<td>HGB: 90</td>
<td>Direct Bilirubin: 1.01</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mesh 3</td>
<td>Male</td>
<td><em>B. canis</em></td>
<td>MN173222</td>
<td>PCR: positive</td>
<td>Blood smear: Not tested</td>
<td>Qurt tappeh 38°25′43″N 47°37′29″E</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Fever, icter, splenomegaly</td>
<td>RBC: 4.3</td>
<td>HGB: 91</td>
<td>Direct Bilirubin: 1.15</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mesh 4</td>
<td>Male</td>
<td><em>B. canis</em></td>
<td>MN173223</td>
<td>PCR: positive</td>
<td>Blood smear: positive</td>
<td>Qara darvish 38°56′43″N 47°28′48″E</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Cough, splenomegaly</td>
<td></td>
<td>Blood smear: positive</td>
<td>Tissue: positive</td>
<td></td>
</tr>
</tbody>
</table>

*Normal ranges: Red blood cell (RBC) count, 4.6–10×10^9/L; Hemoglobin concentration (HGB), 93–153g/L; Haematocrit (HCT), 28–49%; Direct bilirubin, 0.15±0.01*
Discussion

In this study due to the most availability of 18S rDNA sequences from *B. canis* in the GenBank, the 18S rDNA was used to search for the intraspecific variability and the most available abundant *B. canis* sequence. Out of the 43 samples subjected to PCR, 9.3% (4/43) were found to be positive for *Babesia* infection. This is the first study of a molecular detection and identification of *B. canis* infection in dogs from Iran and our results revealed that *B. canis* was prevalent in Meshkin Shahr, Iran. On the basis of 18S rRNA gene sequence analysis, genetic heterogeneity of *B. canis* has been reported in Poland, Croatia, Estonia, Lithuania, Hungary and China (4, 22, 35). Two genotypes of *B. canis*, includes A and B, have been documented so far, and have shown to have variable virulences (4, 36). The results provided principle information toward a better understanding of the epidemiology of canine babesiosis in Iran and prepared the situation for implementation of an effective control planning on babesiosis. A variable interspecies pathogenicity of the *B. canis* genotypes stated by previous studies (1, 4, 25, 28). The clinical manifestations of *B. canis* infection are mild to acute, and the severity of disease has a significant relationship with the species of *Babesia* causing infection (4). There are few reports and studies on *Babesia* spp. in Iran, while a widespread distribution of the parasite vector and suitable weather condition were observed in some areas of Iran (18, 37). Therefore, there is the probability of canine babesiosis and establishment of an infection chain in some geographic areas of Iran. Niak et al. (1973) studied the blood parasites of 155 dogs and one fox (*Vulpes vulpes*) in the north of Iran, *B. canis* was just found in one splenectomized dog and *B. gibsoni* was found from fox (21). Jalali et al. (2013) applied a PCR method in the study and documented that the prevalence of canine babesiosis was 0.36% (20). In another study, Akhhtardanesh et al. (2016) detected 60 tick-infested anemic dogs, among which three dogs (5%) were positive through using a genus-specific PCR and all infected with *B. gibsoni*. None of the collected ticks was positive at the *Babesia* specific PCR (18). In the collected blood samples of dogs from seven regions of Shiraz in south of Iran, only one positive sample was infected with *B. canis* (19). The results provided useful data on the distribution of *B. canis* genotypes in dogs from Iran, and showed the necessity to use a molecular-based analysis for an accurate diagnosis of canine babesiosis. The PCR-based analysis demonstrated that the molecular techniques can a highly sensitive easy to use and cost-effective tools for the simultaneous detection and differentiation of *B. canis* genotypes. However, since a limited number of target gene sequences are currently available for molecular detection of this parasite, any consideration on the population genetics of *Babesia* in the study areas would be highly scrupulously (38). Genetic intraspecific variability is a vital mechanism for piroplasm parasite survival in hosts (39). It is proven that *B. canis* transmitted by *D. reticulatus*, and the distribution area of the parasite is directly related to the presence of this tick species. Although *B. canis* has been observed in dogs in Iran (19-21, 37), But so far we have no reports of *D. reticulatus* ticks in Iran. These results demonstrate that probably *B. canis* and *D. reticulatus* have infested a dog’s population, at least in the northern part of Iran. *Dermaentor reticulatus*, not occurring in the Mediterranean climatic zone, is a tick of some cool regions generally in wooded areas. This ticks has a wide spread geographical overlap with *D. marginatus*. Preferred habitats are forests and swamps zones where it can survive for long periods (8). The main clinic pathological sings in *Babesia* infections were a moderate to acute disease haemoglobinuria and a mild to very severe normochromic normocytic haemolytic anaemia but, the symptoms of the disease are classified based on clinical sings and severity of the infection (40).
In the present study, the main clinical signs in Babesia infected dogs were fever, splenomegaly, vomiting, cough. Haemoglobinuria and haemolytic anemia was not seen, which may be due to host immune system status, age and stages of infection. Based on clinical signs and mortality rates, genotype B is more virulent than genotype A (4). Considering that, all of the positive cases of Babesiosis in this study were of genotype B and all of them had typical clinical symptoms of the disease, the results of this study are consistent with those of other studies (4, 36, 40).

The babesiosis infection is detected with molecular and serological methods in domestic dogs and other wild canine in the world. The basic method of diagnosis is the observing intracellular parasite, however, this method has limitations such as false positive, co infections and non-identification of the species (41). Serological analysis is a very useful diagnostic method, but has some limitations such as cross-reactivity between different Babesia species and it cannot differentiate between acute infection and prior exposure with the parasites (40, 41). The molecular-based techniques enable differentiation of morphologically indistinguishable Babesia species and the most reliable techniques for Babesial DNA detection in blood and tissue (36, 39, 42). Ardabil Province and especially Meshkin Shahr have cold and mountainous climate with forest and swamp conditions. The presence probability of this tick, because of the proof of B. canis not far-fetched. It has proven that global warming and climate change will lead to a further spread of the vectors and transmitted pathogens (42). Indeed, the climate change is a global challenge, which may explain not only the increase of density and scattering of tick vectors, but also the pattern distribution their hosts, changes in periods of activity, and variations in geographical distribution (42). The studies suggest a possible role of Dermacentor spp. as vectors of tick-borne pathogens that affect human and animal health (12, 19). Fast diagnostic technique is necessary for the accurate determination of Babesia in canine that could be carried and possibly transmitted by Dermacentor or other related spp. More studies are needed to increase the knowledge in the epizootiology, ecology and epidemiology of canine babesiosis in Ardabil area. Epidemiological studies are necessary to provide important data for the development of new vaccines and effective therapies against canine babesiosis (43). Through a novel diagnostic strategy, our study could characterize B. canis infection in dogs in Meshkin Shahr, Iran. Due to the increasing numbers of piroplasm species, infected dogs may state a drastic health position threat to dog’s population and prevalence of animal infectious disease in Iran.

Conclusion

Our study identified the presence of B. canis in dogs in Meshkin Shahr, Iran, but further studies are needed on the prevalence of Babesia spp. in large sample dog populations from extended areas in Iran to understand better about the epidemiology of canine babesiosis and to promote an effective control program to determine the tick species diversity in dogs in different areas of Iran. The finding of this study provides essential data for subsequently define the critical importance of the molecular studies in management and prevention of the canine babesiosis in Iran.

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