Short Paper

Serum protein alterations in goats naturally infected with *Babesia ovis*

Esmaeilnejad, B.\(^1\); Tavassoli, M.\(^{1*}\); Asri-Rezaei, S.\(^2\); Dalir-Naghadeh, B.\(^2\); Mardani, K.\(^3\); Farhaghpajouh, F.\(^4\) and Abtahi, S. M.\(^5\)

\(^1\)Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran; \(^2\)Department of Clinical Sciences, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran; \(^3\)Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran; \(^4\)MSc in Parasitology, Department of Clinical Sciences, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran; \(^5\)Department of Microbiology, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran

\(^*\)Correspondence: M. Tavassoli, Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran. E-mail: m.tavassoli@urmia.ac.ir

(Received 30 Jan 2012; revised version 26 Jan 2013; accepted 23 Feb 2013)

Summary

This study was conducted to determine the electrophoretic pattern of serum protein in goats infected with *Babesia ovis*. Serum total protein was calculated and serum electrophoresis from 15 goats naturally infected with *B. ovis* as well as same number of healthy goats was performed. Microscopic examination of Giemsa-stained peripheral blood smears revealed *B. ovis* infection. The parasitological diagnosis was confirmed using polymerase chain reaction (PCR) assay by using a pair of *B. ovis*-specific primers. Mean values total protein and α and γ globulin fractions in infected goats were significantly higher (P<0.05) than those observed in the healthy group.

Key words: Serum protein, Electrophoresis, *Babesia ovis*, Goats, PCR

Introduction

Serum protein electrophoresis is a valuable tool for evaluating health of body, both in diagnosing and clinical monitoring of several diseases (Abate et al., 2000). Although a specific diagnosis can rarely be made with serum protein electrophoresis, processes of diseases can be recognized by serum protein patterns, and alterations to these patterns are associated with a variety of different conditions and diseases (Lobetti et al., 2000).

Blood serum contains two major proteins including albumin and globulin. Serum protein electrophoresis from healthy goats exhibits four fractions: albumin, α, β and γ fractions, which, in β-globulin was divided to β\(_1\) and β\(_2\) (Alberghina et al., 2010).

Recent studies have focused on serum protein alterations in canine babesiosis (Abate et al., 2000; Camacho et al., 2005); however, there are no data regarding serum protein pattern in goats naturally infected with *B. ovis*. Therefore, this study was conducted to evaluate the specific effects of *Babesia* infection on different serum protein fractions in goats, as well as to assess its application in diagnosis by study of the quantitative alterations in serum proteins associated to the disease.

Materials and Methods

Thirty goats of different local breed (West-Azerbaijan) were studied and classified into two groups. All of the animals were more than 1-year-old (≥1 year). The infected group was comprised of 15 goats (10 female and 5 male) naturally affected by *B. ovis*. As control group, 15 clinically healthy goats (8 female and 7 male) were also sampled from the same farm. Jugular
blood samples were obtained from infected and control goats. Blood serum was then separated by centrifugation at 750 g for 15 min and stored at -20°C until measurements were done. Also, blood samples from ear vein were obtained for the preparation of thin blood smears, stained with Giemsa, for the detection of Babesia piroplasms. PCR was performed not only to detect B. ovis in blood of infected animals but also to rule out the presence of Babesia spp. infection in both healthy and infected animals. DNA was extracted using a DNA purification kit (Fermentas, Germany) according to the manufacturer’s instructions. One pair of primers, P1 (5’-CACAGGGAGGTAGTGA CAAG-3’) and P2 (5’-AAGAATTCACCT ATGACAG-3’), specific for amplification of Babesia species 18S ssu RNA (Shayan et al., 2007), were used in PCR assay as a positive quality control for the Babesia species. Seminested PCR of the PCR products of B. crassa with primer pair of P2 (5’-AAGAATTCACCTATGACAG-3’) and P4 (5’-GTATGGGCCCCTTGCTTAT-3’) and B. motasi with primers P2 (5’-AAGAATTCACCTATGACAG-3’) and P5 (5’-CGCGATTCCGTTATTGGAG-3’) were conducted as well (Shayan et al., 2007). In addition, amplification of B. ovis was performed by species-specific primer pair previously reported and used to amplify a fragment of 549 bp. The sequences of primers were as follows: 

Bbo-F, 5’-TGGGCAGGACCTTGGTTGTTCT-3’
Bbo-R, 5’-CCGCGTAGCGCCGGCTAAATA-3’

PCR was performed in 50 µl total reaction volume containing 5 µl of 10 x PCR buffer, 2 mM MgCl₂, 250 µM of each of the four deoxyribonucleotide triphosphate, 1.25 U Taq DNA polymerase (Fermentas, Germany), 50 pmol of each primer and 50 ng of extracted DNA. For negative control, distilled water was added instead of nucleic acid. PCR reaction was performed in a DNA thermocycler (Model CP2-003; Corbett Research, Australia). Cycling condition was 95°C for 5 min, followed by 45 cycles at 94°C for 45 sec, 63°C for 45 sec and 72°C for 1 min with a final extension step of 72°C for 10 min. Amplified products were electrophoresed on 2% agarose gel and stained with ethidium bromide to visualize the amplified DNA fragments under ultraviolet light. Serum total protein concentrations were determined by Biuret method and spectrophotometer (Perkin-Elmer, Junior model 35). Albumin and globulins were separated by cellulose acetate (Helena, France) electrophoresis in barbital buffer (Helena, France), pH = 8.6 at 180 V, 4 mA, for 15 min using Sebia system (Sebia, France). The separated proteins were stained with Ponceau S (Sigma, Germany), and then destained. After plate drying at 50-60°C, the relative levels of separated proteins were scanned by densitometer at 525 nm. Data was checked graphically (histograms, q-q plots and box plots) for the outliers and normality. No extreme outlier was detected and the assumptions were satisfied. Independent samples t-test was used to compare the differences between groups. The level of significance was set at P<0.05. Statistical analyses were carried out using SPSS (Release 17, SPSS Inc., and Chicago, Illinois). Results are presented as mean±SEM.

**Results**

All of the infected animals were positive by PCR with B. ovis-specific primers (549 bp). On the contrary, there was no amplification of B. ovis DNA in the control animals (Fig. 1).

Serum protein electrophoresis of samples exhibited four fractions: albumin, α, β and γ fractions in goats which, in the samples, α globulin band was divided into α₁ and α₂. Electrophoretic pattern of serum from healthy and infected goats is shown in Fig. 2.

Concentrations (mean±SEM) of serum total protein, albumin and globulins of healthy and affected animals are presented in Table 1.

**Discussion**

Although evaluation of serum proteins and their electrophoretic profiles have been widely used in human medicine since the 1950s, in veterinary medicine the mentioned technique is not used as a common diagnostic method for the evaluation of
dysproteinemias (Attaelmannan and Levinson, 2000). Many researchers stated that fractions display important differences among all domestic animals between healthy and infected animals (Kean and Doxey, 1981). As far as goats are concerned, values of serum protein fractions in healthy animals disagreed with a previous study (Mendes Ahid and Soto-Blanco, 2010).

Earlier studies showed that protein fractions display important differences among all domestic animals between healthy and Babesia-infected animals (Barrera et al., 2010).

In our study, the mean value obtained for serum total protein in the affected animals was significantly higher (P<0.05) than that obtained in the healthy ones. Hyperproteinemia in babesiosis is usually caused by dehydration, resulting from lethargy and anorexia associated with the disease (Divers, 1998). The hydration leads to hemconcentration through reduction in fluid volume and consequent hyperproteinemia (Kaneko et al., 2008).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Control (n=15)</th>
<th>Infected (n=15)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tp†</td>
<td>7.05 ± 0.01</td>
<td>7.50 ± 0.09*</td>
</tr>
<tr>
<td>Alb‡</td>
<td>2.70 ± 0.06</td>
<td>2.22 ± 0.01**</td>
</tr>
<tr>
<td>α1</td>
<td>0.85 ± 0.02</td>
<td>1.31 ± 0.07**</td>
</tr>
<tr>
<td>α2</td>
<td>1.00 ± 0.03</td>
<td>1.04 ± 0.02NS</td>
</tr>
<tr>
<td>β</td>
<td>0.58 ± 0.02</td>
<td>0.63 ± 0.01NS</td>
</tr>
<tr>
<td>γ</td>
<td>1.90 ± 0.03</td>
<td>2.20 ± 0.04**</td>
</tr>
</tbody>
</table>

Asterisks indicate the presence of the significance between the two groups: * P<0.01 and ** P<0.05. NS: Non-statistically significant. Tp†: Total protein, and Alb‡: Albumin.

The mean concentration of albumin in healthy animals was significantly higher (P<0.05) than that obtained in diseased animals. The hypoalbuminemia observed in goats in this study is in agreement with the findings of Apaydin and Dede (2010) and Esmaeilnejad et al. (2012) in ovine babesiosis. The most likely explanation for this finding would be hepatopathy that may develop during the disease (Colville, 2002), to the symptomatic anorexia state (Kaneko et al., 2008) and urinary loss of albumin associated with renal failure (Camacho et al., 2010).
The proteins located in α₂-globulin band are significantly increased (P<0.05) in diseased animals compared with the healthy ones. These results are in accordance with the findings of Camacho et al. (2005). The most likely reason for this elevation is the release of acute phase reactants, such as α₁-antitrypsin, α₁-acid glycoprotein, α₂-macroglobulin and haptoglobin in response to inflammation process (Barrera et al., 2010).

When the result of β-globulin sub-fraction in goats with babesiosis was compared with those obtained in the control group, no significant difference was observed (Table 1). An increase in its concentration related to acute hepatic damage has been described as a consequence of the increase in transferrin concentration (Kaneko et al., 2008). This protein also contributes to the β-globulin decrease if the hepatic disease is chronic (Barrera et al., 2010). Increase in the plasminogen concentration, which is included in the β-globulin fraction, due to intra-vascular coagulation may be explained by elevation of β-globulin concentration (Kaneko et al., 2008). However, further studies are needed to precisely assess the acute phase response in caprine babesiosis. Finally, concentration of β-globulin fraction may be related to the albumin fraction in cases of extra-vascular liquid exudation (Barrera et al., 2010). This fact, namely hypoalbuminemia and lower β-globulin was observed in present study. The immunity mechanisms in babesiosis are mainly of humoral nature (Rahbari et al., 2008), although the protozoa can activate a cellular-type immune response (Tizard, 1996). In accordance with the findings of other studies (Camacho et al., 2005), our results indicated that the mean value obtained for the γ-globulin fraction in infected goats was significantly higher (P<0.05) than the one obtained in healthy goats. This increase, observed in the serum γ-globulins concentration is related to the humoral immunity activation by parasitisation of the animals studied (Barrera et al., 2010).

The present study revealed that the increase of total protein, associated with the increase of α and β globulin fractions, is a common finding in serum electrophoresis of goats suffering from babesiosis, which can be useful for diagnosis and prognosis of caprine babesiosis as a supplementary analysis in combination with clinical, parasitological and molecular findings of this disease.

Acknowledgement

The positive control for B. ovis was kindly provided by Prof. Rahbari (Faculty of Veterinary Medicine, University of Tehran, Iran).

References


