

A new *Leishmania*-specific hypothetical protein and its non-described specific B cell conformational epitope applied in the serodiagnosis of canine visceral leishmaniasis

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Abstract The serodiagnosis of canine visceral leishmaniasis (CVL) presents problems related to its sensitivity and/or specificity. In the present study, a new *Leishmania*-specific hypothetical protein, LiHyD, was produced as a recombinant protein (rLiHyD) and evaluated in ELISA experiments for the CVL serodiagnosis. LiHyD was characterized as antigenic in a recent immunoproteomic search performed with *Leishmania infantum* proteins and the sera of dogs developing visceral leishmaniasis (VL). Aiming to compare the efficacy between whole proteins and synthetic peptides, two linear and one conformational B cell epitopes of LiHyD were synthesized

and also evaluated as diagnostic markers. The four antigens were recognized by the sera of dogs suffering VL. On the contrary, low reactivity was observed when they were assayed with sera from non-infected healthy dogs living in endemic or non-endemic areas of leishmaniasis. In addition, no reactivity was found against them using sera from dogs experimentally infected by *Trypanosoma cruzi*, *Babesia canis*, or *Ehrlichia canis*, or sera from animals vaccinated with the Leish-Tec[®] vaccine, a prophylactic preparation commercially available for CVL prevention in Brazil. As comparative diagnostic tools, a recombinant version of the amastigote-specific A2 protein and a soluble crude *Leishmania* extract were studied. Both antigens presented lower sensitivity and/or specificity values than the LiHyD-based products. The rLiHyD presented better results for the CVL serodiagnosis than its linear epitopes, although the peptide recreating the conformational epitope resulted also appropriate as a diagnostic marker of CVL. To the best of our knowledge, this is the first study showing the use of a conformational epitope derived from a *Leishmania* protein for serodiagnosis of CVL.

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Introduction

Leishmaniasis is a disease complex that presents a high morbidity and mortality in the world, where about 380 million people are at risk in 98 countries, with approximately 1.5 to 2.0 million new cases being registered annually (Alvar et al.

2012). Zoonotic visceral leishmaniasis (VL) is a disease caused by *Leishmania infantum* in the Mediterranean area, Middle East, Africa, Asian countries, and Latin America (WHO 2010), and dogs are considered important domestic reservoirs of parasites (Petersen 2009). The disease is also emerging in the USA, Canada, Northern Italy, and Germany and in the Americas, with about 95 % of the cases registered in Brazil (Ready 2010; Alvar et al. 2012).

Upon infection, dogs can develop asymptomatic or symptomatic forms of disease (Solano-Gallego et al. 2011). In symptomatic canine VL (CVL), cutaneous and organic alterations are observed correlating with the presence of high parasite burdens, and the disease usually results in the death of the infected animals (Ciaramella et al. 1997). For diagnosis, parasitological methods based on direct demonstration of amastigote forms by direct staining or amplification of the parasite DNA by the polymerase chain reaction (PCR) in collected samples from infected organs or tissues can be employed. PCR-based tests applied for *Leishmania* detection are more reliable than direct observation of parasites (Antinori et al. 2007). However, these methods require invasive procedures for sample collection and false negative results can be obtained when diagnosing individuals with low parasite burdens, like in asymptomatic patients (Coura-Vital et al. 2011). In addition, for PCR-based diagnosis, a careful standardization of protocols is needed in terms of design of primers and DNA extraction procedures (Alvar et al. 2004; Baneth & Aroch 2008; Deborggraeve et al. 2008; Maia & Campino 2008).

Serological tests have been recommended for the CVL diagnosis due to the fact that they use less invasive methods of sample collection. Infected dogs can present a moderate to strong humoral response, which generally accompanies the development of disease (Porrozzi et al. 2007; Maia & Campino 2008). However, antigens used present cross-reactivity with antibodies generated against proteins of other pathogens, leading to the occurrence of false positive results (Coura-Vital et al. 2011; Almeida-Leal et al. 2014). Moreover, in areas in which CVL is endemic, non-infected animals can also develop an antileishmanial serology, and they can be confused with infected dogs (Courtenay et al. 2002; Moshfe et al. 2009).

The Brazilian Ministry of Health has recommended that, for a CVL serological diagnosis, the “Dual Path Platform” (DPP®; Bio-Manguinhos, Fiocruz, Rio de Janeiro, Brazil) combined with the “Canine Leishmaniasis ELISA Kit” (EIE-LVC kit; BioManguinhos, Fiocruz, Rio de Janeiro, Brazil) should be employed (Coura-Vital et al. 2014; Laurenti et al. 2014). However, their efficacy has been hampered by factors affecting their sensitivity and/or specificity, mainly related to the antigens employed. Thus, it is necessary to find new antigenic proteins that serve to design serodiagnostic systems with higher degree of sensitivity and

specificity than current kits. Different recombinant proteins have been evaluated as diagnostic markers of disease (Soto et al. 1998; Candido et al. 2008; Martins et al. 2013), although a precise antigen does not exist. In parallel to the use of recombinant proteins, synthetic peptides could be also considered, since these antigens are simpler, stable, and cheaper to produce (Noya et al. 2003; Chávez-Fumagalli et al. 2013).

In a recent immunoproteomic search performed with *L. infantum* proteins, a *Leishmania*-specific hypothetical protein was recognized by CVL sera (Coelho et al. 2012). This protein, namely, LiHyD (LinJ.33.3150), was obtained as a recombinant molecule in the present study (rLiHyD). It was chosen because it is only present in the *Leishmania* genus, it is highly conserved among *Leishmania* species, and it is predicted to have B cell epitopes. Aiming to evaluate new candidates for the CVL serodiagnosis, this study employed the rLiHyD protein and three of its specific B cell epitopes (two linear and one conformational) contained in three different synthetic peptides. Also, to the best of our knowledge, this study evaluates for the first time the diagnostic properties of a conformational epitope derived from a *Leishmania* hypothetical protein.

Materials and methods

Ethics statement

This study was approved by Committee on the Ethical Handling of Research Animals from Federal University of Minas Gerais (UFMG), Belo Horizonte, Brazil, under the protocol number 043/2011.

Canine sera

The sample size used was composed of 177 domestic animals (*Canis familiaris*) and consisted of males ($n=100$) and females ($n=77$), of different breeds and ages. CVL-positive animals presented positive parasitological results for *L. infantum* DNA assayed by a PCR technique (Reis et al. 2013). All of them presented positive serological results in two commercial tests (IFAT-LVC Bio-Manguinhos kit and EIE-LVC Bio-Manguinhos kit). Symptomatic VL dogs (CVLS, $n=44$) were those with positive parasitological and serological results, as well as showing three or more clinical signals and/or symptoms. Asymptomatic VL dogs (CVLA, $n=9$) were those presenting positive parasitological and serological results, but without any clinical signals of leishmaniasis. Non-infected dogs were selected from endemic (HEA, $n=44$; Belo Horizonte, Minas Gerais, Brazil) or non-endemic (HNEA, $n=20$; Poços de Caldas, Minas Gerais, Brazil) areas of leishmaniasis. All of them presented negative serological results, as well as were free of any signal of

disease. In this study were also included sera samples of healthy animals vaccinated with Leish-Tec[®] (HV, $n=30$), and sera from dogs infected with *Ehrlichia canis* (EC, $n=10$), *Babesia canis* (BC, $n=10$), or *Trypanosoma cruzi* (TC, $n=10$). These last animals were maintained in kennels to prevent their contact with transmitting vectors of leishmaniasis.

Parasite

The *L. infantum* (MHOM/BR/1970/BH46) strain was used. Parasites were grown at 24 °C in Schneider's medium (Sigma, St. Louis, MO, USA) supplemented with 10 % inactivated fetal bovine serum (FBS, Sigma), 20 mM L-glutamine, 200 U/mL penicillin, and 100 µg/mL streptomycin, at pH 7.4. The soluble *Leishmania* antigenic extract (SLA) was prepared from 1×10^9 stationary-phase promastigote cultures (5–7 days old), as described (Coelho et al. 2003).

Sequence analysis of the LiHyD protein

The process of in silico analysis of the *L. infantum* LiHyD sequence consisted of (i) the search for similarity among sequences deposited in non-redundant protein databases, (ii) comparison with the databases of other trypanosomatids whose genomes have been sequenced completely or are in the phase of annotation, i.e., *Leishmaniamajor*, *Leishmania mexicana*, *Leishmania braziliensis*, *T. cruzi*, *Trypanosoma brucei*, and *Trypanosoma congolenses* (all available at www.genedb.org), and (iii) evaluation of the sequence for analysis of its physicochemical properties using the ProtParam tool in the ExPASy server (Gasteiger et al. 2005). The parameters computed by the program and reported here include the molecular weight, theoretical isoelectric point, amino acid composition, total number of positive and negative residues, extinction coefficient, instability index, aliphatic index, and grand average of hydropathicity (GRAVY).

Cloning, expression, and purification of recombinant LiHyD protein

The cloning, expression, and purification of the LiHyD protein were performed as described by Lage et al. (2015). The *L. donovani* A2 recombinant protein used as an antigen control was produced as described by Zhang et al. (1996). After purification, the recombinant proteins were passed through a polymyxin-agarose column (Sigma), in order to remove residual endotoxin content (<10 ng of LPS per 1 mg of recombinant protein, measured by the Quantitative Chromogenic Limulus Amebocyte Assay QCL-1000, BioWhittaker, MD, USA).

Mapping of specific B cell epitopes of the LiHyD protein

Two linear and one conformational B cell epitope of LiHyD were synthesized. Two peptides containing the linear sequences (Peptide-1, PQQGYQPPPPMEHALP, 262–277 positions; and Peptide-2, SSLRRQNSMRRNE, 296–307 positions) were predicted using the ABCpred Prediction Server software (www.imtech.res.in/raghava/abcpred/), as described by Saha and Raghava (2006). The second epitope was also predicted using the Emini Surface Accessibility Scale algorithm, based on the program IEDB (Immune Epitope DataBase and Analysis Resource; available at www.iedb.org), as described by Emini et al. (1985). The conformational epitope (Peptide-3) was predicted using a combination of three algorithms, ABCpred Prediction Server, Bepipred Linear Epitope Prediction (www.tools.immuneepitope.org/bcell), and Kolaskar and Tongaonkar antigenicity scale (www.tools.immuneepitope.org/bcell/), following technical protocols described by Kolaskar and Tongaonkar (1990), Larsen et al. (2006), and Saha and Raghava (2006). This epitope contains a combination of amino acids from two different protein regions of LiHyD: LYHPAPSSL (221–229 positions) and PQQGYQPP (262–269 positions). All peptides were synthesized by the F-moc technique of Merrifield (1963), with modifications following Machado-de-Ávila et al. (2011). Briefly, peptides were released from the amine resin by trifluoroacetic acid treatment in the presence of the appropriate scavengers. Then, they were diluted in Milli-Q water and purified by high-performance liquid chromatography (HPLC) on a C18 reverse phase column (flow rate 1.0 mL/min; Vydac). Finally, they were submitted to a MALDI-TOF-TOF analysis.

ELISA for CVL serodiagnosis

Previous titration curves were performed to determine the most appropriate concentration of antigens and sera sample dilutions to be used in the ELISA experiments. Microtiter immunoassay plates (Falcon) were coated with rLiHyD, rA2, Peptide-1, Peptide-2, Peptide-3, or *L. infantum* SLA (1.0, 1.0, 20.0, 20.0, 20.0, and 2.0 µg per well, respectively), dissolved in 100 µL coating buffer (50 mM carbonate buffer, pH 9.6), for 18 h at 4 °C. Next, free binding sites were blocked using 200 µL of PBS-T (phosphate-buffered saline plus Tween 20 0.05 %), containing 5 % albumin, for 1 h at 37 °C. After washing the plates three times with PBS-T, they were incubated with 100 µL of canine sera (1:100, diluted in PBS-T), for 1 h at 37 °C. Plates were subsequently washed four times in PBS-T and incubated with anti-dog IgG horseradish-peroxidase-conjugated antibody (1:5000, diluted in PBS-T; catalog A6792, Sigma Aldrich, USA), for 1 h at 37 °C. After washing the plates five times with PBS-T, the reactions were developed by incubation with 100 µL per well of a solution consisting of 2 µL H₂O₂, 2 mg orto-

phenylenediamine, and 10 mL citrate-phosphate buffer at pH 5.0, for 30 min and in the dark. Reaction was stopped by adding 25 μ L 2 N H₂SO₄. The optical density was read in an ELISA microplate spectrophotometer (Molecular Devices, Spectra Max Plus, Canada) at 492 nm.

Statistical analysis

The results were entered into Microsoft Excel (version 10.0) spreadsheets and analyzed using GraphPad Prism™ (version 6.0 for Windows). The mean optical density (OD) value was calculated by subtracting the mean blank OD from the mean OD for each individual sample. The lower limits of positivity (cutoff) for the diagnostic antigens were established for optimal sensitivity and specificity using the receiver operating characteristic (ROC) analysis. The curves were plotted with the values from symptomatic and asymptomatic CVL groups versus the control groups, following a sick/non-sick rating method. The result of the division between the mean OD obtained for the sample and its respective cutoff was called “optical density index” (ODI). The D’Agostino & Pearson normality test was used to determine whether a variable was normally distributed. An unpaired Students *t* test was also used, and significant differences were considered with $P < 0.05$. The diagnostic capacity of each antigen was measured by assessing its sensitivity (95 % confidence interval, CI 95%), specificity (CI 95%), area under the curve (AUC), and accuracy (AC). The degree of agreement between the assays was determined by kappa (κ) index (with CI 95%) and classified according to the Fleiss scale: 0.00–0.20 (poor), 0.21–0.40 (fair), 0.41–0.60 (moderate), 0.61–0.80 (good), 0.81–0.99 (very good), and 1.00 (perfect).

Results

Sequence database and physicochemical evaluation of LiHyD protein

In the present study, the hypothetical LiHyD protein was defined as a *Leishmania* spp. specific protein, and its identity degree found was 60, 79, and 80 % for the *L. braziliensis*, *L. major*, and *L. mexicana* species, respectively. No orthologue sequence was found in the *T. cruzi*, *T. brucei*, *Trypanosoma vivax*, and *T. congolenses* species. Based on the fact that LiHyD is a hypothetical protein, a physicochemical evaluation was in silico performed (Table 1). The results showed that it presents 327 amino acids in its primary sequence, having a molecular weight of 36 kDa, and an isoelectric point of 9.49.

Table 1 Physicochemical evaluation of the LiHyD protein

Parameters	Results
Number of amino acids	327
Estimated molecular weight (kDa)	36.0
Theoretical isoelectric point	9.49
Total number of negatively charged residues	20
Total number of positively charged residue	28
Ext. coefficient (M ⁻¹ cm ⁻¹)	33810
Instability index (classification)	56.4
Aliphatic index	56.15
Grand average of hydrophobicity (GRAVY)	-0.806

Evaluation of the rLiHyD protein for CVL serodiagnosis

The rLiHyD protein was evaluated for CVL serodiagnosis (Fig. 1). For comparison, a recombinant version of the A2 protein and the *L. infantum* SLA were also employed in the ELISA assays. The results showed that 100 % of the CVL sera presented OD values over the cutoff, when rLiHyD was employed as an antigenic source (Fig. 1a). The ODI value of reactivity of rLiHyD was calculated and is also shown (Fig. 1b). The cutoff values for accessing the sensitivity and specificity of antigens were determined using receiver operating characteristic (ROC) analysis, and the area under the curve (AUC) was calculated to assess the accuracy of the tests (Fig. 1c). When the rA2 protein was used as a comparative diagnostic marker, its sensitivity and specificity values were 100 and 72.6 %, respectively (Fig. 2). The *L. infantum* SLA was not able to identify the asymptomatic animals. In addition, a poor specificity was observed, since it was recognized by 30 % of the sera from *T. cruzi*-infected dogs (Fig. 2a). The ODI values (Fig. 2b) and the result of the ROC analysis for rA2 and SLA (Fig. 2c) are also shown. The individual evaluation of each antigen for the CVL serodiagnosis was performed (Table 2). The AUC was used to compare the efficacy between the different evaluated diagnostic antigens. The rLiHyD protein presented the highest AUC value (1.000), followed by rA2 (0.992) and *L. infantum* SLA (0.964). The maximum sensitivity and specificity values (100.0 % in both cases), the maximum accuracy value (100.0%), and a total agreement were obtained using the rLiHyD protein. On the other hand, when the rA2 and *L. infantum* SLA were used, they presented sensitivity values of 98.1 and 83.0 %, respectively, and accuracy values of 96.0 and 93.0 %, respectively.

Comparative efficacy between the rLiHyD protein and its linear and conformational B cell epitopes for CVL serodiagnosis

Next, the antigenicity of the linear and conformational epitopes was investigated by an ELISA assay. Results are shown

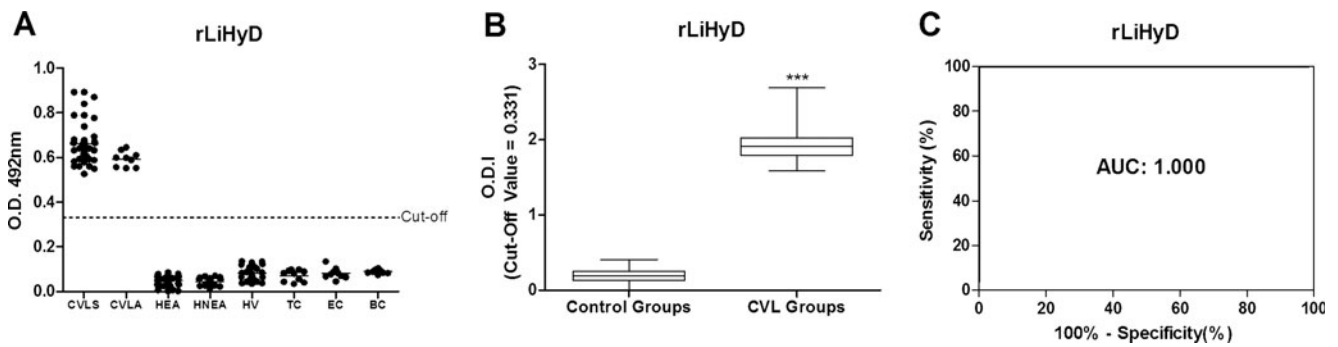


Fig. 1 Evaluation of ELISA reactivity with the rLiHyD protein using a canine serological panel. The recombinant LiHyD protein was employed as an antigen for ELISA assays performed with canine sera samples obtained by the next animal groups: symptomatic (CVLS, $n=44$) or asymptomatic (CVLA, $n=9$) visceral leishmaniasis (VL) dogs, healthy dogs living in endemic (HEA, $n=44$) or non-endemic (HNEA, $n=20$) areas of leishmaniasis, dogs immunized with Leish-Tec[®] vaccine (HV, $n=30$), and animals infected with *Trypanosoma cruzi* (TC, $n=10$),

Ehrlichia canis (EC, $n=10$), or *Babesia canis* (BC, $n=10$). The individual OD values are shown (a). The dotted line represents the cutoff value calculated by a ROC analysis. The box and whisker plots of the ODI values from sera grouped in non-infected (control) or CVL (*Leishmania*-infected) groups are also shown (b), as well as the ROC curves obtained for LiHyD protein (c). Statistically significant differences ($***P<0.001$) were observed between the CVL group and the control groups

in Fig. 3. The three peptides were recognized by CVL sera. However, an unexpected reactivity against Peptide-1 and Peptide-2 was observed when sera from non-infected dogs living in endemic area of leishmaniasis were employed. Of note, Peptide-3 was able to react specifically with CVL samples, irrespective of the presence of clinical signs (Fig. 3a). In

fact, this antigen presented the best results to distinguish the CVL sera from the other samples, since all sera reactivities were higher than the cutoff value calculated by ROC analysis. The ODI values from *L. infantum*-infected dogs and those from non-infected animals were also determined (Fig. 3b). The AUC was used to compare the efficacy between the

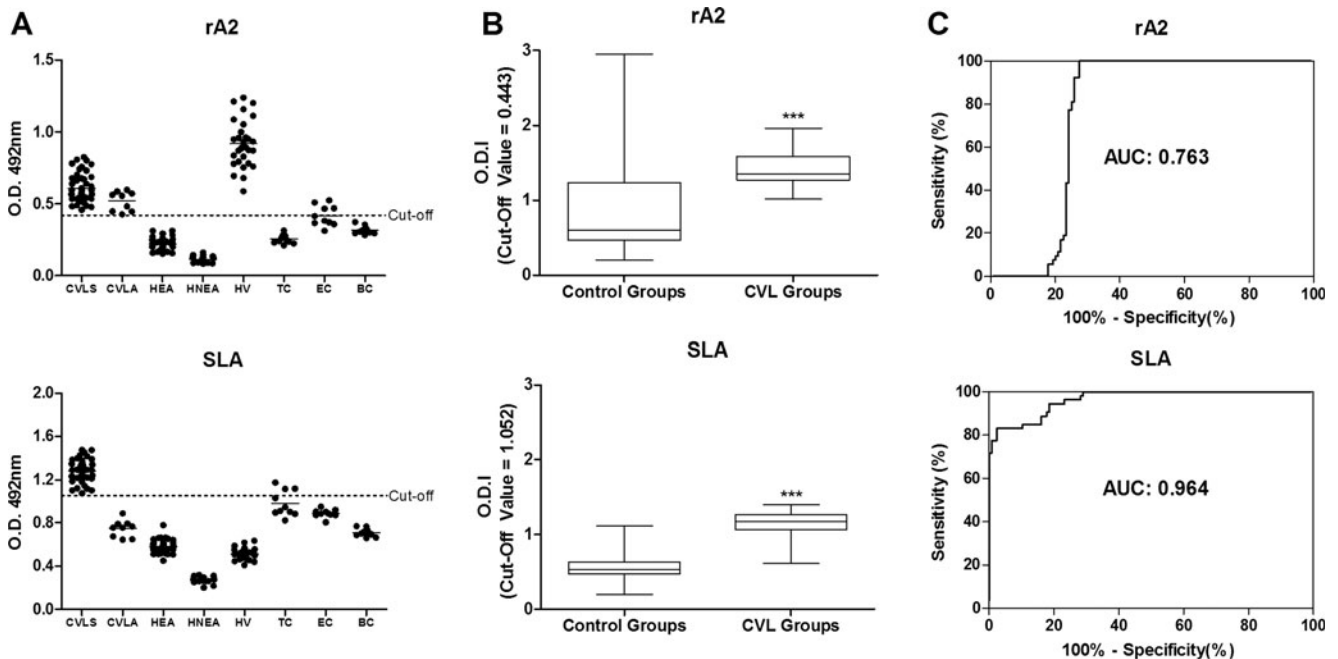


Fig. 2 Evaluation of ELISA reactivity using the rA2 and *L. infantum* SLA against a canine serological panel. Two antigenic preparations were studied: the recombinant A2 protein (upper panels) and a soluble *L. infantum* antigenic (SLA) preparation (bottom panels). ELISA assays were performed using sera samples obtained by the next animal groups: symptomatic (CVLS, $n=44$) or asymptomatic (CVLA, $n=9$) visceral leishmaniasis (VL) dogs, healthy dogs living in endemic (HEA, $n=44$) or non-endemic (HNEA, $n=20$) areas of leishmaniasis, dogs immunized with Leish-Tec[®] vaccine (HV, $n=30$), and animals infected with

Trypanosoma cruzi (TC, $n=10$), *Ehrlichia canis* (EC, $n=10$), or *Babesia canis* (BC, $n=10$). The individual OD values are shown (a). The dotted line represents the cutoff value calculated by a ROC analysis. The box and whisker plots of the ODI values from sera grouped in non-infected (control) or CVL (*Leishmania*-infected) groups are also shown (b), as well as the ROC curves obtained for LiHyD protein (c). Statistically significant differences ($***P<0.001$) were observed between the CVL group and the control groups

Table 2 Diagnostic efficacy of rLiHyD protein for CVL serodiagnosis

Antigen	Parameters ^a					
	Se (%) (CI 95%)	Sp (%) (CI 95%)	AUC (CI 95%)	κ (CI 95%)	Agreement ^b	AC (%)
rLiHyD	100.0 (93.3-100.0)	100.0 (97.1-100.0)	1.000 (1.000-1.000)	1.0 (1.0-1.0)	Perfect	100.0
rA2	100.0 (93.3-100.0)	72.6 (63.9-80.2)	0.760 (0.690-0.840)	0.6 (0.5-0.7)	Good	80.9
SLA	83.0 (70.0-91.9)	97.6 (93.1-99.5)	0.960 (0.940-0.990)	0.9 (0.8-1.0)	Very Good	93.2

ROC curves were used to determine ELISA sensitivity (Se), specificity (Sp), confidence interval (CI 95%), and area under curve (AUC) of each diagnostic antigen

^a Parameters were calculated using all 177 samples presented in this study

^b Agreement was calculated using parasitological assay (PCR technique) as a gold standard

Se, sensitivity, Sp specificity, CI confidence interval, AUC area under curve, κ kappa index, AC accuracy

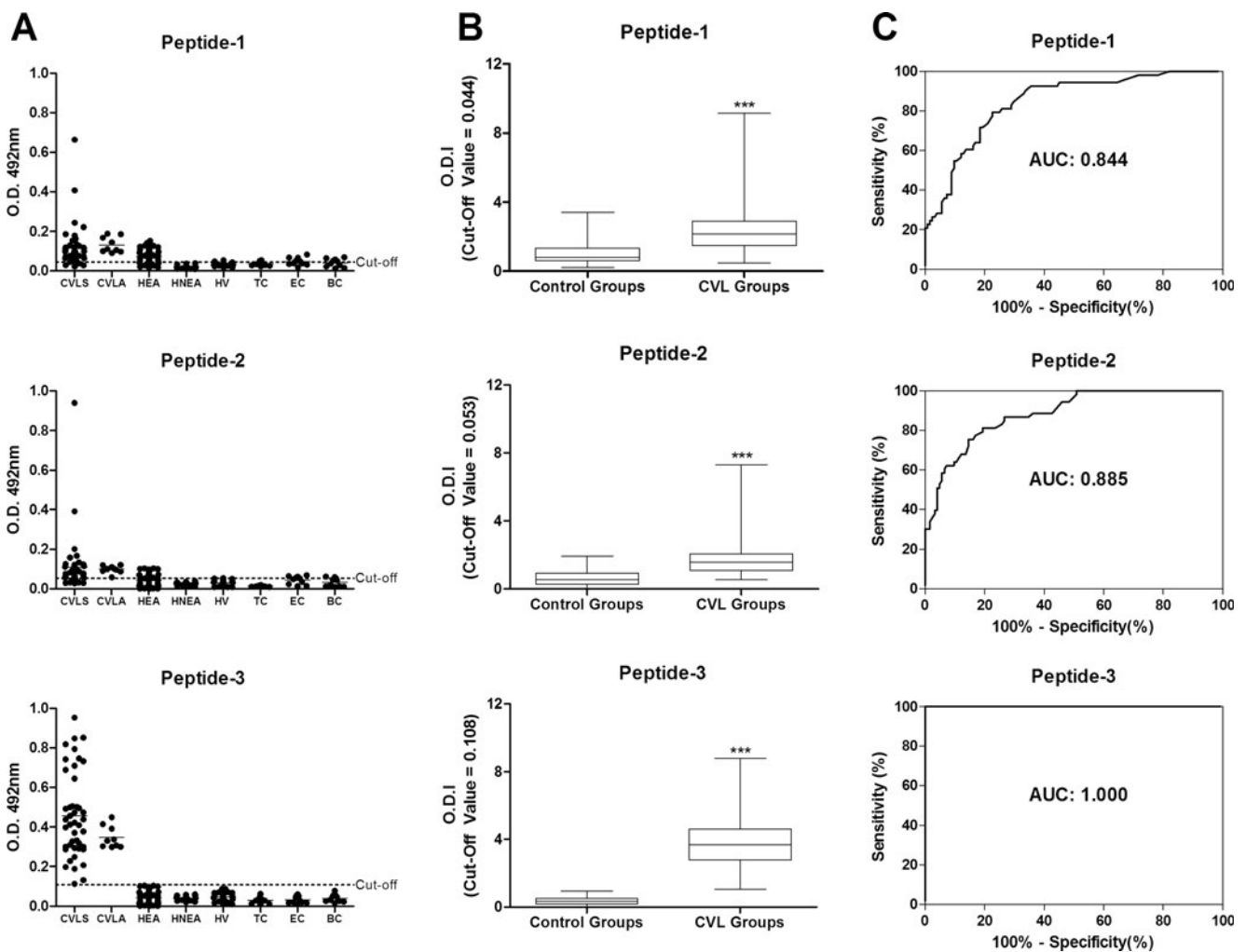


Fig. 3 Analysis of the specific B cell epitopes derived from LiHyD protein for CVL serodiagnosis. ELISA assays were performed using three synthetic epitopes designed on the basis of a computation analysis looking for linear (Peptide-1 [upper panels] and Peptide-2 [middle panels]) and the conformational epitopes (Peptide-3). Sera samples were obtained from symptomatic (CVLS; $n=44$) or asymptomatic (CVLA; $n=9$) visceral leishmaniasis (VL) dogs, from healthy dogs living in endemic (HEA; $n=44$) or non-endemic (HNEA; $n=20$) areas of leishmaniasis, and from dogs immunized with Leish-Tec[®] vaccine

(HV; $n=30$) or from animals infected with *Trypanosoma cruzi* (TC; $n=10$), *Ehrlichia canis* (EC; $n=10$), or *Babesia canis* (BC; $n=10$). The individual OD values are shown (a). The dotted line represents the cut-off value calculated by a ROC analysis. The box and whisker plots of the ODI values from sera grouped in non-infected (control) or CVL (*Leishmania*-infected) groups are also shown (b), as well as the ROC curves obtained from the same groups (c). Statistically significant differences (***) were observed between the CVL group and the control groups

different peptides (Fig. 3c). Peptide-3 presented the highest AUC value (1.000), followed by Peptide-2 (0.885) and Peptide-1 (0.844). Parameters related to the sensitivity and specificity of these antigens applied in the CVL serodiagnosis were determined and are also shown (Table 3). Peptide-3 presented the maximum sensitivity and accuracy values (100.0 % in both cases), similar to the values obtained using the rLiHyD protein. Peptide-1 and Peptide-2 showed sensitivity values of 92.5 and 81.1 %, respectively, and an accuracy of 72.8 and 80.8 %, respectively (Table 3). Evaluating the specificity of the synthetic epitopes, Peptide-3 showed the highest value (100.0 %), followed by Peptide-2 (80.7 %) and Peptide-1 (64.5 %).

Discussion

The development of a cost-effective and affordable diagnostic tool for CVL is still needed. It will allow the establishment of field assays within the national control strategic programs of the endemic countries for detecting canine infections (Desjeux 2004). Similarly, some problems have been reported for an accurate CVL serodiagnosis. The first one is the variable sensitivity of the tests, especially in determining asymptomatic but infected animals that can present low titers of antileishmanial antibodies. An additional difficulty is the low specificity of the tests when they are employed in areas endemic for other pathogens related or not to *Leishmania spp.* This lack of specificity usually produces false positive results (Coelho et al. 2009; Laurenti et al. 2014; Wolf et al. 2014; Peixoto et al. 2015).

In recent years, studies have been developed aiming to improve the quality of the CVL serodiagnosis. Some of these were directed to produce and characterize recombinant versions of parasite individual antigens to be employed for CVL diagnosis (Celeste et al. 2004; Fonseca et al. 2014; Menezes-Souza et al. 2015). Derived from this line of investigation, detection of the major antigenic determinants within these

proteins and construction of synthetic peptides able to diagnose the disease are also the focus of current research (Costa et al. 2011; Martins et al. 2015). It should be noted that peptides are usually more stable, easier to produce, and cheaper than recombinant proteins (Chávez-Fumagalli et al. 2013). In this light, the present study evaluated the antigenic properties of a *Leishmania* hypothetical protein that was recently identified by an immunoproteomic study performed with *L. infantum* total extracts (Coelho et al. 2012). Aiming to compare the efficacy between different antigenic compositions based on the same protein, studies were completed using three putative B cell epitopes derived from LiHyD, two being linear and the other a conformational epitope.

SLA-based ELISA has been evaluated in the CVL serodiagnosis (Coelho et al. 2009; Chávez-Fumagalli et al. 2013). The main inconvenience is that total *Leishmania* preparations share common epitopes with other microbial antigens, resulting in the cross-reaction with serum samples from dogs infected with related diseases (De Arruda et al. 2013; Kubar & Fragaki 2005). Another limitation has been related to the standardization of the production of these extracts, affecting the reproducibility of the tests. In fact, the commercial EIE-LVC® kit can present false positive results. Marcondes et al. (2011) reported a high degree of cross-reactivity between *Leishmania spp.* and *T. cruzi* (57%) species, as well as between *Leishmania spp.* and *E. canis* (57%) species. Zanette et al. (2014), using three serological methods for the CVL serodiagnosis, showed cross-reactivity among the sera from dogs infected with *E. canis*, *B. canis*, *Toxoplasma gondii*, *Neospora caninum*, and *T. cruzi*.

In the present study, it was observed that all CVL sera recognized the rLiHyD protein. In addition, a null cross-reactivity was observed when sera of *T. cruzi*-, *B. canis*-, or *E. canis*-infected dogs were evaluated. When the putative B cell epitopes were studied, different results were obtained. Although the three peptides were clearly antigenic, only Peptide-3, designed to contain a conformational epitope, presented the same sensitivity and specificity values as the

Table 3 Diagnostic evaluation of specific linear and conformational B cell epitopes for CVL serodiagnosis

Antigen	Parameters ^a					
	Se (CI 95%)	Sp (CI 95%)	AUC (CI 95%)	κ (CI 95%)	Agreement ^b	AC (%)
Peptide-1	92.5 (81.8–97.9)	64.5 (55.4–72.9)	0.844 (0.783–0.905)	0.5 (0.4–0.6)	Moderate	72.8
Peptide-2	81.1 (68.0–90.6)	80.7 (72.6–87.2)	0.885 (0.834–0.925)	0.6 (0.5–0.7)	Moderate	80.8
Peptide-3	100.0 (93.3–100.0)	100.0 (97.1–100.0)	1.000 (1.000–1.000)	1.0 (1.0–1.0)	Perfect	100.0

ROC curves were used to determine ELISA sensitivity (Se), specificity (Sp), confidence interval (CI 95%), and are under curve (AUC) of each diagnostic peptide

^a Parameters were calculated using all 177 samples presented in this study

^b Agreement was calculated using parasitological assay (PCR technique) as a gold standard

Se sensitivity, Sp specificity, CI confidence interval, AUC area under curve, κ kappa index, AC accuracy

recombinant protein. The development and use of a new generation of biotechnological products has been based on identification of linear or conformational epitopes. Peptides recognized by the antibodies present in sera of patients developing different diseases can be employed for their diagnosis (Chávez-Fumagalli et al. 2013; Menezes-Souza et al. 2014). Also, peptides have emerged as vaccine candidates against rotavirus infection (Jafarpour et al. 2015) or dengue (Amatur-Rasool et al. 2015). However, to the best of our knowledge, the present study is the first to employ a peptide containing a conformational *Leishmania* epitope for CVL serodiagnosis. The better results observed for the conformational peptide relative to the linear ones offers an alternative approach to find new antigenic molecules that can be easily constructed and reproduced for diagnostic purposes.

Aiming to compare the diagnostic efficacy of the rLiHyD with other known diagnostic antigenic markers, the rA2 protein (Porrozzini et al. 2007; Akhoundi et al. 2013) was included in the analysis. This antigen is expressed in the amastigote stage of some *Leishmania* species and belongs to a protein family that displays a variable number of repeated sequences of 10 amino acid residues (Zhang et al. 1996). In 2007, the Brazilian Ministry of Agriculture licensed the use of Leish-Tec[®] vaccine (based the recombinant A2 protein) to prevent CVL. One problem associated with this vaccination is that about 30.9 % of the vaccinated dogs tested seropositive when an SLA-based ELISA is employed (Fernandes et al. 2014). Data obtained here showed that the rA2-based ELISA failed not only to distinguish between *Leishmania*-infected dogs from those vaccinated with Leish-Tec[®] but also between *Leishmania* and *E. canis*-infected dogs. The possibility to distinguish Leish-Tec[®] vaccinated dogs from the *Leishmania*-infected ones is another advantage of using the rLiHyD protein or Peptide-3. Both molecules have improved the diagnostic values found with other antigens, such as other recombinant single proteins (Fonseca et al. 2014; Rodríguez-Cortés et al. 2013) or chimeric proteins (Boarino et al. 2005; Faria et al. 2015), synthetic linear peptides (Chávez-Fumagalli et al. 2013), and phage-derived mimotopes (Costa et al. 2013).

One drawback of this work is that we have not demonstrated the presence of the LiHyD protein in *Leishmania*. However, the presence of antibodies recognizing this protein in the sera of infected dogs may be taken as an indication that it is expressed by the parasites during the active disease. Database searches performed in this study demonstrated the presence of LiHyD encoding genes in different *Leishmania* species. The protein is highly conserved in *Leishmania* spp. and no orthologue form was found in other Trypanosomatidae. This specificity together with its high antigenicity allows its use as a diagnostic tool for VL. However, further studies should be performed to understand its expression pattern, as well as the biological function that the protein plays in the parasite.

Although nearly 200 serum samples had been used in the present work, other studies are also necessary to evaluate a larger canine serological panel, in order to further corroborate the efficacy of these diagnostic markers for the CVL serodiagnosis. For instance, our panel did not contain samples from *L. braziliensis*-infected dogs, although in Brazil there are endemic areas for both tegumentary and visceral leishmaniasis (Courtenay et al. 2002; Coura-Vital et al. 2011). In this context, the present study should be taken as a proof-of-concept of the capacity of the proposed antigens for the CVL serodiagnosis and may well serve as a reference for further assays. However, due to scarcity of antigens to diagnose this important neglected disease, this study irradiates new possibilities to use both the rLiHyD protein and its conformational epitope as possible diagnostic markers for CVL.

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Compliance with ethical standards

Conflict of interest The authors confirm that they have no conflicts of interest in relation to this work.

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