

Complexity of the major surface protease (msp) gene organization in *Leishmania (Viannia) braziliensis*: evolutionary and functional implications

K. VICTOIR¹, J. AREVALO², S. DE DONCKER¹, D. C. BARKER³, T. LAURENT¹, E. GODFROID⁴, A. BOLLEN⁴, D. LE RAY¹ and J. C. DUJARDIN^{1*}

¹Laboratory of Molecular Parasitology, Instituut voor Tropische Geneeskunde 'Prins Leopold', 155 Nationalestraat, B-2000 Antwerpen, Belgium

²Departamento de Bioquímica, Biología Molecular y Farmacología, Facultad de Ciencias y Filosofía and Instituto de Medicina Tropical "Alexander von Humboldt", Universidad Peruana Cayetano Heredia, A.P. 5045, Lima 100, Peru

³Cambridge University, Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK

⁴Applied Genetics, IBMM, Université Libre de Bruxelles, Gosselies, Belgium

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SUMMARY

The major surface protease (msp or *gp63*) of *Leishmania* plays a major role in the host–parasite interaction. We analysed here the structure of the msp gene locus in *Leishmania (Viannia) braziliensis* and compared it to results obtained in other species. Physical mapping of cosmid contigs revealed a minimum of 37 genes per haploid genome and at least 8 different msp gene families. Within the same organism, these genes showed a nucleotide sequence varying in certain stretches from 3 to 34%, and a mosaic structure. From an evolutionary point of view, major differences were observed between subgenera *Viannia* and *Leishmania*, both in terms of msp gene number and sequence. Within subgenus *Viannia*, phenetic analysis revealed three clusters in which sequence variants of *L. (Viannia) braziliensis* and *L. (Viannia) guyanensis* were interspersed. Functional implications of our results were explored from predicted *L. (Viannia) braziliensis* protein sequences: regions encoding the msp catalytic site showed a conserved sequence, while regions encoding surface domains possibly involved in the host–parasite interaction (macrophage adhesion sites and immunodominant B-cell and T-cell epitopes) were variable. We speculate that this would be an adaptive strategy of the parasite.

Key words: *gp63*, leishmanolysin, *Leishmania (Viannia) braziliensis*, genome organization, telomere, cosmid, epitopes.

INTRODUCTION

Leishmania are parasitic protozoa responsible for a wide spectrum of clinical forms ranging from self-healing cutaneous lesions to disfiguring mucosal metastasis and life-threatening visceral infection. The parasites are transmitted to their mammalian hosts under a promastigote flagellar form, by the bite of an infected sand fly vector. By receptor-mediated events they will infect the host's macrophages and change into a non-motile amastigote form, which will replicate in the acidic phagolysosomal vacuoles. The ability of a parasite to evade the complement system, attach to the macrophages, invade and finally survive in them likely involves a series of factors. The major surface protease (msp) of *Leishmania*, is thought to be one of them (for a recent review, see Yao, Donelson & Wilson, 2003) and homologous genes have also been described in other digenetic *Trypanosomatidae* such

as *Trypanosoma brucei* (El-Sayed & Donelson, 1997) and *Trypanosoma cruzi* (Grandgenet *et al.* 2000). Noteworthy is that homologues were also reported in monogenetic parasites as *Crithidia fasciculata*, suggesting a primary role of the glycoprotein for the parasite survival in the insect gut (Etges, 1992; Inverso *et al.* 1993). However, this role was not supported in digenetic parasites, at least in *L. (Leishmania) major* (Joshi *et al.* 2002).

The genes encoding msp are arranged in multi-copy tandem arrays in all *Leishmania* species studied so far (Medina-Acosta, Beverley & Russell, 1993; Steinkraus *et al.* 1993; Voth *et al.* 1998). Earlier studies showed that species of subgenus *Viannia* generally have more msp genes than species of subgenus *Leishmania* (Medina-Acosta *et al.* 1993; Steinkraus *et al.* 1993; Victoir *et al.* 1998; Voth *et al.* 1998). In organisms like *Trypanosomatids* which essentially regulate their gene expression at post-transcription level (i.e. not at initiation, Stiles *et al.* 1999), gene repetition is an essential feature to generate a high number of transcripts for proteins needed in large amount. It might also allow the parasite to generate sequence diversity (isogenes) within a same gene array (Victoir & Dujardin, 2002).

* Corresponding author: Laboratory of Molecular Parasitology, Instituut voor Tropische Geneeskunde 'Prins Leopold', 155 Nationalestraat, B-2000 Antwerpen, Belgium. Tel: +32 3 2476358. Fax: +32 3 2476359. E-mail: jcdujard@itg.be

Accordingly, species of subgenus *Viannia* should have a potential for a higher number of different msp isogenes than subgenus *Leishmania*. This hypothesis was supported by data from *L. (Viannia) guyanensis* (Steinkraus *et al.* 1993).

In the present work, we further explored this hypothesis in *L. (Viannia) braziliensis*. Indeed, this is the most pathogenic species of subgenus *Viannia* and previous studies suggested that this species might harbour the highest number of msp genes (Victoir *et al.* 1998). We performed a fine mapping of the msp gene locus of that species and sequenced most of the genes encountered. Results were placed in an evolutionary context by comparing them with all msp sequences described so far, and potential functional consequences of the described polymorphism were studied. Particular attention was paid to major functional domains, such as interaction motifs, B and T-cell epitopes.

MATERIALS AND METHODS

Analysis of the cosmid library

Genomic cosmid clones containing msp genes were isolated from an *L. (Viannia) braziliensis* library (MHOM/BR/75/M2903, cloned in pWE15, gift from Professor D. C. Barker, University of Cambridge, UK) by (i) hybridization with a *L. (Viannia) braziliensis* msp probe (pLb134Sp, Dujardin *et al.* 1993) and (ii) their differential restriction pattern. Isolated clones were purified at least twice, and their genomic stability was checked over time by several complete digestions. In addition, to minimize the possibility that a cosmid clone would contain artefactual re-arrangements, we only considered those in which msp-hybridizing restriction fragments co-migrated with an msp-hybridizing restriction fragment from total genomic DNA of *L. (Viannia) braziliensis*. The fine mapping of 7 selected clones (G3411, C4121, C1211, C711, D9311, A811 and B9211) was done by the T3/T7 method. In brief, inserts were taken out of the cloning site by a complete *Not* I digestion. Then, incomplete digestions were performed with *Bgl*I, *Eco*RI and *Sal*I (serial dilutions of restriction enzyme starting from 1.5 u concentration) and stopped with 0.5 M EDTA after incubation for 15 min. In order to have an optimal resolution in different size ranges, the different restriction fragments were resolved electrophoretically on a 0.5% agarose gel DNA (conventional electrophoresis) or 1% agarose in a field inversion gel electrophoresis configuration (60 V, 2.1 sec forward-0.7 sec backward). DNA was transferred after depurination and denaturation to a Nylon membrane (Hybond-N) according to the manufacturer's instructions (Amersham). Blots were hybridized at 42 °C with T3 and T7 oligonucleotides end-labelled by a kinase reaction

(Sambrook, Fritsch & Maniatis, 1989). Post-hybridization washings were performed in 6 × SSC, 0.1% SDS, the first 2 × 5 min at room temperature followed by 1 min at 42 °C. The msp genes were localized by (i) complete digestion of the cosmid clones and hybridization with an msp probe, and (ii) comparison of restriction patterns of msp genes PCR-amplified from the corresponding cosmid clones (see below).

L. (Viannia) braziliensis sequence analysis

Fragments (1.3 kb) resulting from an amplification of the central portion of the msp genes from different cosmid clones (A 8.1.1., C 7.1.1 and C 4.1.2.1.) were generated by 2 specific msp primers respectively situated at positions 410–422 and 1721–1741 in the lg63c1 cDNA msp sequence of *L. (Viannia) guyanensis* according to Steinkraus *et al.* 1993. Amplicons were cloned in the PCRTM 2.1 vector using the TA-cloning kit from Invitrogen. Clones were selected according to their restriction pattern with *Eco*RI, *Sal*I and *Bgl*I (also used for cosmid clone mapping) and sequenced by PCR using the 'ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit' from Perkin Elmer. The automatic sequencer used was the model 373 of PE Applied Biosystems using the Sanger enzymatic method. Eleven different sequences were obtained (AJ851007–17). The sequence of a cDNA fragment isolated from an msp-specific *L. (Viannia) braziliensis* library (Victoir, 2001) was also included (AJ863117). Sequence treatment was done with Seaview (Galtier, Gouy & Gautier, 1996), alignment was done by ClustalW (Thompson, Higgins & Gibson, 1994) and phenetic analysis done by using DAMBE 4.0.26 (<http://web.hku.hk/~xxia/software/software.htm>). The tree-building method used was the neighbor-joining method (Saitou & Nei, 1987). The genetic distance used for nucleotide sequence analysis is the Poisson correction or the Kimura 80. The following sequences were retrieved from Gene Bank and used for phenetical analysis: *L. guyanensis* c1,7–10 (M85203, L16776, L16777, L16778, L16779), *L. panamensis* c1, g2, g3 (AF038028, AF037166, AF037167), *L. amazonensis* (L46798), *L. mexicana* c1 (X64394), *L. donovani* S2, S4, PAA (L19563, L19562, M60048), *L. major* C (AF039721), *L. major* (Y00647), *L. chagasi* stat., C, log. (M80669, M80671, M80672), *L. infantum* Gen (Z83677), *Crithidia fasciculata* (M94364), *T. brucei* (U86345) and *T. cruzi* g1–4 (AF267161, AF267162, AF267163, AF267505).

Analysis of the protein structure

The crystallographic coordinates of *L. (Leishmania) major* msp (Schlagenhauf, Etges & Metcalf, 1998; id. Code: 1lml) were retrieved from the Protein Data

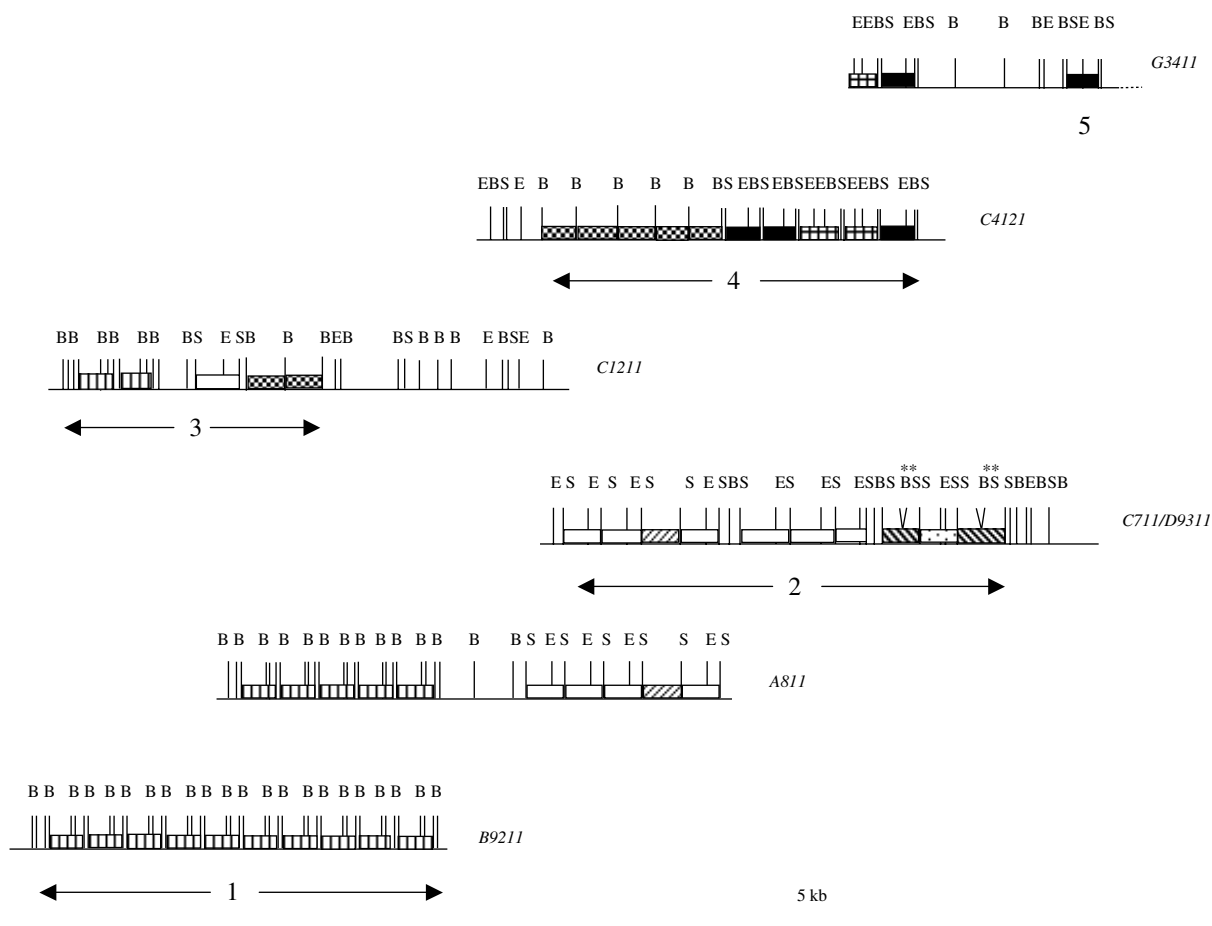


Fig. 1. Physical map of 6 cosmid clones of *Leishmania (Viannia) braziliensis*, containing tandemly repeated msp genes; 8 different msp isogenes were identified, based on the presence and order of restriction sites (B, *Bgl*I; S, *Sal*I and E, *Eco*RI): SEBS, BB, SEEBS, BBBB, SES, SS, SBSS and SESS, (represented by different shading patterns). The 2 copies of the *L. (Viannia) braziliensis*-specific msp isogene (Victoir *et al.* 1998) are marked with a star. Numbers under the maps correspond to the arrays mentioned in the text.

Bank. Specific residues or regions of the gene were localized on the 3-dimensional structure of the protein using the computer program Cn3D 3.0, a 3-D viewer for NCBI Databases, Version 3.0.

RESULTS

Structure of the msp gene locus in L. (Viannia) braziliensis

Seven cosmid clones containing msp genes were mapped and 2 were found to be identical (C711 and D9311); overlapping clones were identified by their restriction pattern (Fig. 1). This allowed identification of 2 different contigs, containing a total of 4 msp tandem arrays (numbered 1 to 4) and 1 single gene (number 5). Arrays were separated by regions in which no msp gene could be detected and of variable length: 7.5 kb (arrays 1 and 2), 18 kb (arrays 3 and 4) and 12.5 kb (array 4 and gene 5). The two contigs would contain 21 and 16 genes respectively. A minimum of 8 different msp isogenes were identified based on the presence and order of restriction sites

(Fig. 1). Previous analysis of natural populations of *Viannia* parasites evidenced a *L. (Viannia) braziliensis*-specific msp isogene, characterized by an internal *Sal*I site (Victoir *et al.* 1998). This isogene was localized (star, Fig. 1) and was found to be surrounded by highly heterogeneous msp repeat units. The nature and distribution of isogenes was totally different between the 2 contigs, so that it seems unlikely that the 2 contigs constitute different alleles of the same locus. Consequently, this strain of *L. (Viannia) braziliensis* would contain a minimum of 37 genes per haploid genome.

Nucleotidic sequence of the L. (Viannia) braziliensis msp genes

Msp genes from cosmid clones C 7.1.1, C 4.1.2.1 and A 8.1.1 (containing the most representative and divergent msp isogenes) were sequenced. The obtained sequence lengths varied between 1325 bp and 1334 bp, with differences ranging from 5 to 21% over the whole sequence and to 34% over some stretches. A closer look at the 11 aligned *L. (Viannia)*

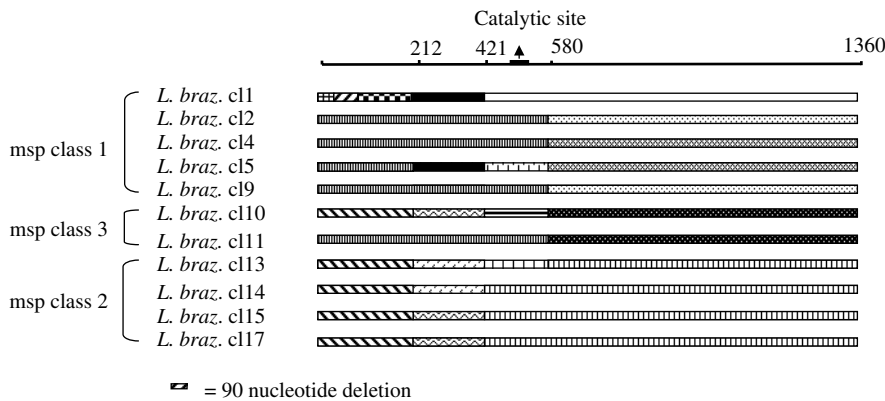


Fig. 2. Representation of the mosaic structure of the different msp genes in a *Leishmania (Viannia) braziliensis* strain (M2903); msp classes 1–3 refer to the 3 major clusters individualized in Fig. 3. Sequence stretches which share a homology between different clones, equal or higher than 95% are represented by the same shading pattern (unrelated to Fig. 1). The corresponding nucleotide positions are given in bp for the different *L. (Viannia) braziliensis* sequences.

braziliensis sequences (named *L. braz.* cl1, 2, 4, 5, 9–11, 13–15, 17) revealed a mosaic structure as well at the level of short stretches (8–15 bp, not shown) as well as longer ones (100 to 500 bp) (Fig. 2). From one variant to the other, sequence stretches were represented in different shading if their nucleotide sequence difference was greater than 5%. A clear example of such a structure is shown in *L. (Viannia) braziliensis* sequences *L. braz.* cl9, *L. braz.* cl10 and *L. braz.* cl11. Indeed, from nucleotide 1 to 580, *L. braz.* cl9 is identical to *L. braz.* cl11 and both clones differ by 122 nucleotides (21%) from *L. braz.* cl10. For the last 780 nucleotides, however, *L. braz.* cl11 differs only by 2 nucleotides from *L. braz.* cl10 and both clones differ from *L. braz.* cl9 by 165 (21.2%) and 163 (20.9%) nucleotides, respectively. Another peculiar mosaic structure was observed in a cDNA msp sequence (Victoir, 2001) here included: this 1.3 kb fragment consisted in a 310-bp msp stretch at its 5' terminal end (corresponding to position 1–310 in genomic sequence of *L. (Viannia) braziliensis* cl2), followed by a sequence presenting 95% identity with a subtelomeric *L. (Viannia) braziliensis* sequence (telo10, Fu & Barker, 1998). This sequence was not a reverse transcription artefact because PCR of genomic DNA with primers targeting each of the two segments generated a fragment of the expected size.

Evolution of msp genes

In order to situate the msp gene polymorphism of *L. (Viannia) braziliensis* in a broader evolutionary context, we performed a phenetic analysis of all known msp sequences of *Leishmania* and outgroups (*C. fasciculata*, *T. cruzi* and *T. brucei*) over a length corresponding to positions 412–1743 of the *L. (Viannia) guyanensis* c1 sequence. *Leishmania* and *C. fasciculata* clustered together, separately from *Trypanosoma* species. *Leishmania* appeared to be monophyletic, and sequences from subgenera

Leishmania and *Viannia* clustered separately (Fig. 3). Within subgenus *Viannia*, 3 clusters were observed in which *L. (Viannia) braziliensis* and *L. (Viannia) guyanensis* sequences were interspersed (here called classes 1 to 3 respectively). The first cluster, containing *L. (Viannia) braziliensis* sequences of class 1 was the most divergent (32%) from sequences of subgenus *Leishmania*. Interestingly, all these *L. (V.) braziliensis* sequences originated from the same region of the msp gene locus, present in clone C.7.1.1.

Structural characteristics: the predicted proteins

Our genomic sequences allowed the prediction of *L. (Viannia) braziliensis* proteins from amino acid 15 to 556 of the *L. (L.) major* msp-6 gene (AF039721). By comparison with the latter species, our predicted *L. (Viannia) braziliensis* sequences presented differences in identity ranging from 6 to 34% (*L. (Viannia) braziliensis* class 1). The heterogeneity between the predicted proteins increased towards the C-terminal end (not shown), and was essentially localized at the exterior part of the molecule, as inferred from the crystal structure of *L. (Leishmania) major* (Schlagenhauf *et al.* 1998). We searched potential implications of this polymorphism at the level of major functional domains of the protein: catalytic site, attachment motifs and reported epitopes.

Analysing the positions of the 16 essential Cys residues assessed the general conformation of the protein. Positions were conserved in all predicted *L. (Viannia) braziliensis* proteins, except in *L. braz.* cl1, which showed a sequence truncated from amino acids 7 to 36 (including one of the Cys residues), which might lead to a difference in conformation. The predicted HexxH motif of the catalytic/zinc-binding site was conserved in all sequences, as well as the 62 aa downstream histidine residue, which is important for the formation of the metalloprotease active groove. Potential N-glycosylation

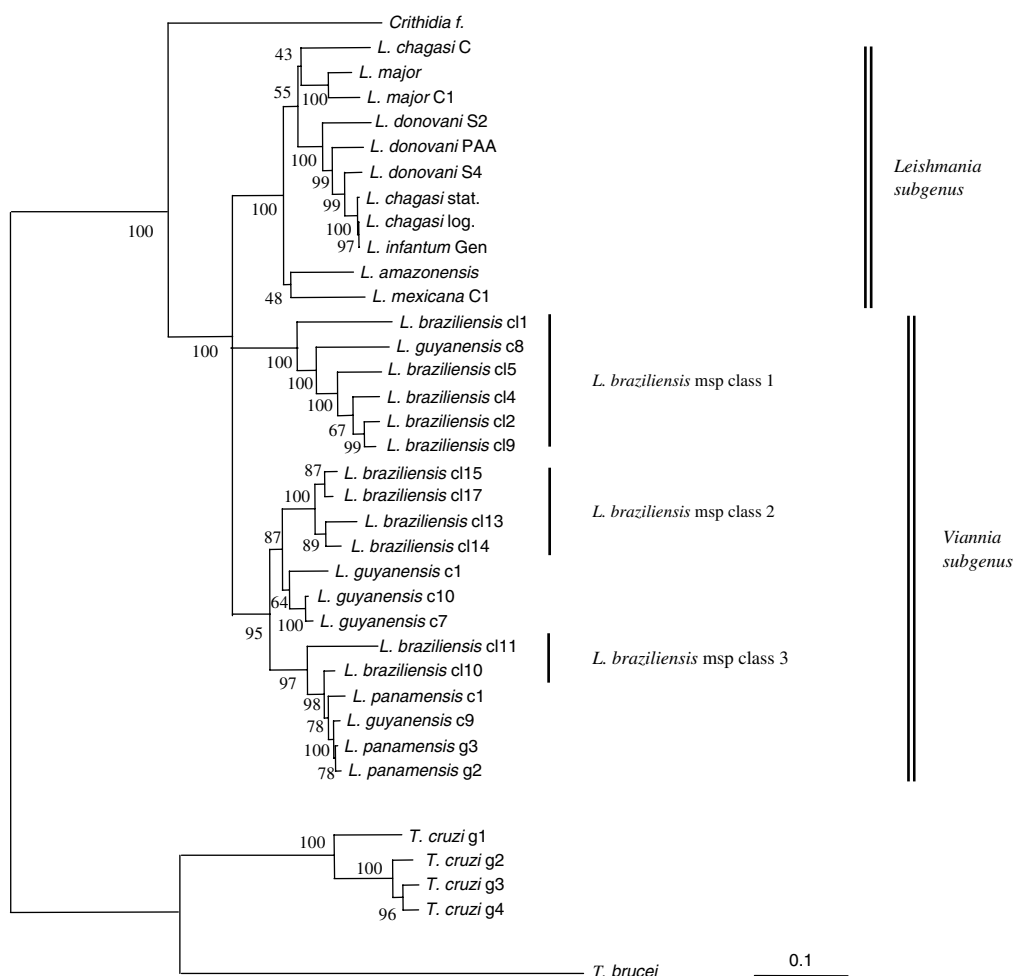


Fig. 3. Phenetical analysis of msp gene heterogeneity: sequences of *Leishmania (Viannia) braziliensis* and other species (accessible in GenBank). Numbers near nodes are bootstrap values (1000 pseudo-replicates). Corresponding GenBank locus names of the sequences are listed in the Materials and Methods section. C (upper case), constitutively expressed, S or stat. (expressed in the promastigote stationary phase), log. (expressed in the promastigote logarithmic phase).

sites, important for the protein structure were conserved in all of the *L. (Viannia) braziliensis* sequences except those of class 1.

Regions reported to play a role in the internalization of the parasites into the macrophages (aa 215–264 and 290–339 of *L. (Viannia) guyanensis* L16779 sequence, Puentes *et al.* 1999) showed heterogeneity among the *L. (Viannia) braziliensis* sequences: from 3 to 19 aa (6 to 38%) in the first region and from 2 to 18 aa (4 to 36%) in the second one. Again, sequences from class 1 were divergent. Within these regions, there are 2 important adhesion motifs (SRYD and EYLEV, Brittingham *et al.* 1999). With respect to SRYD, all sequences of class 1 and *L. braz. cl10* (class 3) showed a 240-Arg/Ala transition (relative amino acid position in *L. (Viannia) guyanensis* msp sequence, L16779), i.e. from a large and basic amino acid to a small and hydrophobic one. Also in the EYLEV motif, sequences of class 1 were distinct from all other *L. (Viannia) braziliensis* sequences, as they showed a T/SFLEL motif. Glu and Tyr, the two first amino

acids of the EYLEV motif, are prone to interact and especially a change from Glu to Thr or Ser would have considerable consequences because Thr and Ser are much smaller than Glu and lack its negative charge.

A last point concerned heterogeneity in major reported epitopes. With respect to potential T-cell epitopes determined in former studies by Russo *et al.* (1993), we found in our *L. (Viannia) braziliensis* sequences a polymorphism ranging from 1/16 (6%) amino acids (peptide 10 in position 116–130 from the *L. (Leishmania) major* protein) up to 13/16 (81%) (peptide 11 in position 171–187 from the *L. (Leishmania) major* protein). This result seems especially noteworthy since this last peptide is especially divergent at the beginning and ending positions of the peptide, which are especially important for T-cell recognition (Janeway & Travers, 1996). With respect to B epitopes, immunodominant determinants of *L. (Leishmania) infantum* msp were shown to be localized in the C-terminal region (Morales *et al.* 1997). *L. (Viannia) braziliensis* msp

showed a heterogeneity for these peptides ranging from 4/20 (25%) to 10/20 a.a. (50%). Also within the same organism, considerable heterogeneity (50% (11/20)) could be observed between sequences from two different *L. (Viannia) braziliensis* phenetic msp classes for an identified immunodominant peptide (position 453 to 475, for the predicted msp amino acid sequence of *L. (Leishmania) infantum*).

DISCUSSION

In this study, we analysed the genomic organization of msp genes of *L. (Viannia) braziliensis*, and distinguished a minimum of 37 genes by haploid genome, distributed in 8 isogenes. This might represent a portion only of the msp gene locus, when considering the gene copy number (70) estimated by densitometry in that species (Victoir *et al.* 1998). In *L. (Viannia) guyanensis*, another species of subgenus *Viannia*, 50 genes constituted by 8 isogenes were reported (Steinkraus *et al.* 1993). The msp gene organization of *Viannia* species thus contrasts with that reported in subgenus *Leishmania* and more particularly in *L. (Leishmania) major* (7 genes, 2 isogenes; Voth *et al.* 1998), the species chosen for the *Leishmania* genome project. Gene amplification, a common phenomenon in *Leishmania* (Iovannisci & Beverley, 1989; Inga *et al.* 1998; Kebede *et al.* 1999) is likely responsible for the difference in the structure of the msp gene locus between the two subgenera. We here demonstrate that it is accompanied by an increase in sequence diversity among genes of the same organism.

The msp gene polymorphism here reported might be generated by synonymous and non-synonymous substitutions (Alvarez-Valin, Tort & Bernardi, 2000). However, another contributing mechanism appeared to be intra-genic recombination as suggested by the mosaic structure observed among *L. (Viannia) braziliensis* msp genes. This phenomenon is generally due to reciprocal crossing over and segmental gene conversion, as reported in *Trypanosoma brucei* (Pays & Nolan, 1998). Loci more prone to this type of recombination are generally localized in the subtelomeres, regions known to be especially 'turbulent' by comparison with the generally stable central core of the chromosomes (Inga *et al.* 1998; Wickstead, Ersfeld & Gull, 2003). This might also be the case in msp genes of *L. (Viannia) braziliensis*, as suggested by the presence of a DNA fragment combining an msp stretch with a subtelomeric sequence. Mosaic patterns have been reported for surface antigens of *Theileria annulata* (major merozoite piroplasm surface antigen, Gubbels *et al.* 2000) and *Plasmodium falciparum* (merozoite surface protein 1, Conway *et al.* 1999). Altogether, the msp gene polymorphism here reported might constitute an adaptive strategy of the parasite (Guerbouj *et al.* 2001). Analysing

functionally important domains in our predicted proteins allowed exploration of this hypothesis.

The conservation of catalytic regions in all *L. (Viannia) braziliensis* predicted msp and also among other species, contrasted with the polymorphism in regions involved in the host-parasite interaction. First, structurally important changes were noted in major macrophage adhesion motifs of a series of *L. (Viannia) braziliensis* isogenes. How this might effectively affect the binding capacities of that species cannot be determined from our data. However, it has been reported elsewhere that inhibition of the internalization of *L. (Viannia) braziliensis* parasites was only partial when blocking well-defined amino acid stretches based on a *L. (Viannia) guyanensis* msp sequence (Puentes *et al.* 1999). Secondly, considerable polymorphism was observed for major epitopes, concerning the primary sequence of T epitopes as well as structural features of B-epitopes. Further work is necessary to understand the functional consequences of the diversity here reported. One should address the hypothesis that this diversity is positively selected because it allows evasion of the host immune response, like in other pathogens: African trypanosomes (VSG, Pays & Nolan, 1998), HIV (gp120, Lewis *et al.* 1998) or *Plasmodium* (pfempI, Conway *et al.* 1999). In addition, reminding that leishmaniasis is an immunopathology, the link between polymorphism of msp (or other immunogens) and clinical pleomorphism should be further explored.

Finally, our results also gave an insight on the evolution of msp genes within the genus *Leishmania*. In terms of genomic structure of the msp gene locus (and particularly the gene copy number) and considering *Crithidia fasciculata* (7 msp genes, Inverso *et al.* 1993) as an outgroup, our results indicate that the *Leishmania* subgenus shows an ancestral character and that the *Viannia* subgenus diverged dramatically. This was not supported by phylogenies based on msp amino terminal sequences (our study and Medina-Acosta *et al.* 1993), but was well supported by those based on msp carboxy terminal sequences (Medina-Acosta *et al.* 1993). Interestingly, phylogenies based on the sequence of another surface membrane glycoprotein, gp46/M-2, also indicated an ancestral character of *Leishmania* subgenus (Kerr *et al.* 2000). Within the *Viannia* subgenus, msp sequences of *L. (Viannia) braziliensis* and *L. (Viannia) guyanensis* were interspersed and clustered in 3 major groups. This could be explained by 2 mechanisms. First, diversification of the corresponding 3 major msp gene classes could have preceded speciation. Secondly, horizontal transfer could have occurred. Indeed, sexual recombination between *L. (Viannia) braziliensis* and *L. (Viannia) guyanensis* has been observed in natural conditions, albeit rarely (Bañuls *et al.* 1997). However, in such a case, the 2 studied strains would be the descendants of a hybridization

event, which was not supported for the *L. (Viannia) braziliensis* strain here studied, by the analysis of other genetic markers.

In conclusion, *L. (Viannia) braziliensis* and *L. (Viannia) guyanensis* show the most complex organization of msp genes in the whole genus *Leishmania*. Why such a structure was selected during evolution and what is the function of the 3 msp classes remain unanswered. We showed that polymorphism in the predicted protein might have fundamental implications for host–parasite interactions. However, this should be further explored, on the one hand by following the expression of the different genes along the parasite life-cycle, and on the other hand, by focusing on the interaction of the most polymorphic domains with the host immune system or with the insect vector.

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