



Leishmania infantum Lipophosphoglycan-Deficient Mutants: A Tool to Study Host Cell-Parasite Interplay

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Lipophosphoglycan (LPG) is the major surface glycoconjugate of metacyclic *Leishmania* promastigotes and is associated with virulence in various species of this parasite. Here, we generated a LPG-deficient mutant of *Leishmania infantum*, the foremost etiologic agent of visceral leishmaniasis in Brazil. The *L. infantum* LPG-deficient mutant ($\Delta lpg1$) was obtained by homologous recombination and complemented via episomal expression of *LPG1* ($\Delta lpg1 + LPG1$). Deletion of *LPG1* had no observable effect on parasite morphology or on the presence of subcellular organelles, such as lipid droplets. While both wild-type and add-back parasites reached late phase in axenic cultures, the growth of $\Delta lpg1$ parasites was delayed. Additionally, the deletion of *LPG1* impaired the outcome of infection in murine bone marrow-derived macrophages. Although no significant differences were observed in parasite load after 4 h of infection, survival of $\Delta lpg1$ parasites was significantly reduced at 72 h post-infection. Interestingly, *L. infantum* LPG-deficient mutants induced a strong NF- κ B-dependent activation of the inducible nitric oxide synthase (iNOS) promoter compared to wild type and $\Delta lpg1 + LPG1$ parasites. In conclusion, the *L. infantum* $\Delta lpg1$ mutant constitutes a powerful tool to investigate the role(s) played by LPG in host cell-parasite interactions.

Keywords: Lipophosphoglycan, *Leishmania infantum*, gene targeting, lipid droplets, macrophage

INTRODUCTION

Lipophosphoglycan (LPG) is one of the most abundant components of *Leishmania* membranes (Turco and Descoteaux, 1992). In the course of parasite interaction with invertebrate hosts, LPG binds to the midgut epithelium of specific species of the sandfly vectors (Sacks et al., 2000), and protects parasites against the digestive enzymes present in the peritrophic matrix following blood feeding (Sacks and Kamhawi, 2001). In vertebrate hosts, LPG contributes to virulence by shielding *Leishmania* against the complement system (Spath et al., 2003) and by inhibiting phagolysosomal

biogenesis (Desjardins and Descoteaux, 1997; Vinet et al., 2009; Moradin and Descoteaux, 2012). Purified LPG has been considered as a pathogen-associated molecular pattern molecule (PAMP) that triggers Toll-like receptors (TLR) and is also known to interfere with pro-inflammatory and signaling pathways in host cells (Descoteaux et al., 1991; Descoteaux and Turco, 1993; Becker et al., 2003; de Veer et al., 2003; Kavooosi et al., 2009; Rojas-Bernabé et al., 2014; Tavares et al., 2014; Lima et al., 2017).

This complex glycolipid is organized in four domains: a conserved 1-O-alkyl-2-lyso-phosphatidyl(myo)inositol membrane anchor, a conserved diphosphoheptasaccharide core structure, a polymer of repeating phosphodisaccharide units (phosphoglycan or PG) carrying species-specific side chains and variable, often mannose-rich cap structures (Turco and Descoteaux, 1992; McConville and Ferguson, 1993). Although the biosynthesis of LPG has attracted considerable interest, to date only few enzymes and transporters involved in this process have been identified either biochemically, genetically, or both (Ryan et al., 1993; Descoteaux et al., 1995, 1998, 2002).

One of the key enzymes in the biosynthesis of LPG is *LPG1*, a putative galactofuranosyl transferase specifically involved in the synthesis of the LPG glycan core (Ryan et al., 1993). Consequently, parasites lacking the *LPG1* gene (Δ lpg1) express a truncated LPG without the PG domain; they nonetheless assemble and secrete other PG-containing molecules (Dermine et al., 2000; Späth et al., 2000). Both *L. major* and *L. donovani* require *LPG1* for the establishment of infection within macrophages, as evidenced by the elimination of *LPG1*-null mutants following phagocytosis; yet, restoration of LPG expression by genetic complementation restored the capacity to replicate within macrophages (Späth et al., 2000; Lodge et al., 2006). Interestingly, phosphoglycan synthesis does not seem to be an absolute requirement for virulence in all *Leishmania* species, since *L. mexicana* phosphoglycan-deficient parasites were found to be similarly virulent to their wild-type (WT) counterparts (Ilg et al., 1999, 2001; Ilg, 2000). This difference in LPG requirement for the establishment of infection within macrophages may be related to the fact that *L. mexicana* resides in large fusogenic communal vacuoles, as opposed to the non-fusogenic, tight individual vacuoles in which *L. major* and *L. donovani* replicate. The role played by *LPG1* in *L. infantum* infectivity in mammals remains to be established.

This report describes the disruption of *LPG1* in *L. infantum*, the main etiological agent of visceral leishmaniasis in Brazil. While deletion of *LPG1* did not alter parasite morphology *in vitro* or the presence of subcellular organelles, e.g., lipid droplets (LD), Δ lpg1 parasites experienced distinct infection outcomes in comparison to WT parasites. Hence, the *L. infantum* *LPG1*-null strain described in the present study constitutes a powerful tool to investigate the role of LPG in host-parasite interactions.

METHODS

Ethics Statement

This study was carried out in accordance with the recommendations of Institutional Review Board for Animal Experimentation (CEUA), Gonçalo Moniz Institute, Fundação

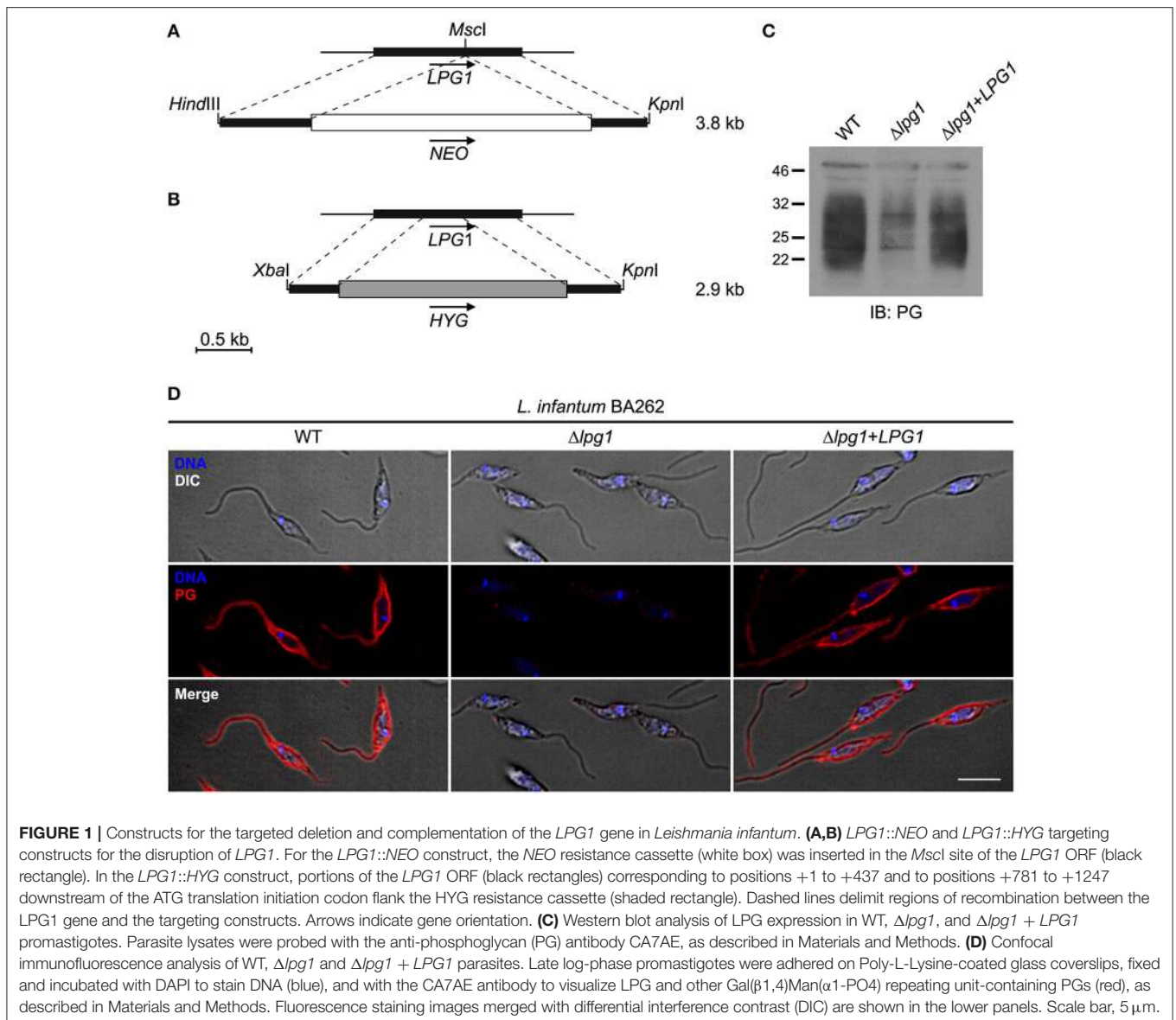
Oswaldo Cruz. The protocol was approved by the Institutional Review Board for Animal Experimentation (CEUA), Gonçalo Moniz Institute, Fundação Oswaldo Cruz (Protocol No. 021/2015).

Animals

Inbred male C57BL/6 mice, aged 6–8 weeks, were obtained from the animal care facility of the Gonçalo Moniz Institute, Fundação Oswaldo Cruz (IGM-FIOCRUZ, Bahia, Brazil).

Targeted Deletion of the *LPG1* Gene and Complementation

The constructs for *LPG1* (beta galactofuranosyl transferase) gene targeting were designed based on the *L. infantum* *LPG1* gene sequence (GenBank accession No. GU233511). Homozygous *LPG1*-null mutants (Δ lpg1) were obtained using two targeting constructs (Figures 1A,B). For the *NEO* targeting construct, the entire *LPG1* gene was amplified by PCR from *L. infantum* BH46 (MCAN/BR/89/BH46) DNA using *Taq* DNA polymerase (New England Biolabs) and oligodeoxynucleotides AD-358 (forward) (5'-gtacaagcttccatATGGCGCCGCTCGCTG-3') and AD-359 (reverse) (5'-gctactcgagTTAGCTGGGGTCAACAG-3'). This fragment was digested with *Hind*III and *Xho*I, and then ligated with the *Hind*III-*Xho*I-digested pBluescript II SK⁻ vector, yielding pBS-*LPG1*. The *NEO* resistance cassette from pLeishNeo (unpublished) was extracted with *Not*I and *Eco*RV, blunted and inserted in the *Msc*I site of pBS-*LPG1*, within the *LPG1* gene, yielding pBS-*LPG1*::*NEO*. For the *HYG* targeting construct, nucleotides 1–437 of the *LPG1* gene were amplified by RT-PCR from *L. infantum* BH46 mRNA using oligodeoxynucleotides AD-53 (forward) (5'-cgggatccatATGGCGCCGCTCGCTG-3') and AD-357 (reverse) (5'-ggaattcTCGGGGTGGTGAATG-3'). This fragment was digested with *Bam*HI and *Eco*RI, and then ligated with the *Bam*HI-*Eco*RI-digested pBluescript II SK⁻ vector. A 467-bp fragment containing nucleotides 781–1,247 of the *LPG1* ORF was amplified by PCR from *L. infantum* BH46 genomic DNA using oligodeoxynucleotides AD-355 (forward) (5'-gcaagcttGGCATCTATTACACAGACCACAAGG-3') and AD-356 (reverse) (5'-caggtcgacTGGCAGCGAATGTTTTACC-3'). This fragment was digested with *Hind*III and *Sal*I, then ligated with the same vector, downstream of the first *LPG1* sequence, at the *Hind*III and *Sal*I restriction sites. The *HYG* resistance cassette from pX63-*HYG* was excised with *Sal*I and *Bam*HI, blunted and inserted between the two *LPG1* sequences, at the *Eco*RV restriction site, yielding pBS-*LPG1*::*HYG*. For genetic complementation of the Δ lpg1 mutant, the entire *LPG1* ORF was amplified by PCR from *L. infantum* BH46 genomic DNA using Native *Pfu* polymerase (Stratagene, La Jolla, CA, USA) and oligodeoxynucleotides AD-358 (forward) (5'-gtacaagcttccatATGGCGCCGCTCGCTG-3') and AD-359 (reverse) (5'-gctactcgagTTAGCTGGGGTCAACAG-3'). This fragment was digested with *Hind*III and *Xho*I, and then ligated with the *Hind*III-*Xho*I-digested pBluescript II SK⁻ vector, yielding pBSII-*LPG1*. The absence of mutations in the amplified *LPG1* ORF was verified by Sanger sequencing (Génome Québec; GenBank accession No. GU233511). The *LPG1* gene was then excised from pBSII-*LPG1* with *Eco*RV and *Xho*I, blunted and



ligated with the *EcoRV*-digested pLeishZeo vector (unpublished), yielding pLeishZeo-*LPG1*.

Transfection and Selection of *L. infantum* Δ *lpg1* Promastigotes

Log-phase WT *L. infantum* BA262 (MCAN/BR/89/BA262) promastigotes were first electroporated with the purified *LPG1*::*HYG* targeting construct (excised as a 2.9-kb *XbaI*-*KpnI* fragment from pBS-*LPG1*::*HYG*) using 0.2 cm electroporation cuvettes, at 0.45 kV and a high capacitance of 500 μ F as previously described (Turco et al., 1994). Following electroporation, promastigotes were incubated for 24 h in drug-free, complete M199 medium and subsequently grown in the presence of 50 μ g/mL Hygromycin B (Roche Diagnostics). To generate *LPG1*-null mutants, log-phase *lpg1*^{+/HYG} heterozygous *L. infantum* BA262 promastigotes were electroporated with

purified *LPG1*::*NEO* targeting construct (excised as a 3.8-kb *HindIII*-*KpnI* fragment from pBS-*LPG1*::*NEO*) and grown after 24 h in the presence of both 50 μ g/mL Hygromycin B and 70 μ g/mL G418 (Life Technologies). Absence of *LPG* in the resulting double drug-resistant Δ *lpg1* promastigotes was verified by Western blot analysis and confocal immunofluorescence. To restore *LPG1* expression, log-phase *L. infantum* BA262 Δ *lpg1* cells were electroporated with pLeishZeo-*LPG1*. Complemented mutants (Δ *lpg1* + *LPG1*) were selected with 80 μ g/mL Zeocin (in addition to G418 and Hygromycin B at concentrations specified above) and verified by Western blotting and confocal immunofluorescence.

Parasite Cultures

L. infantum promastigotes were cultured in HOMEM medium supplemented with 10% inactivated Fetal Bovine Serum (FBS),

100 U/mL penicillin, 100 μ g/mL streptomycin and 2 mM L-glutamine in 25 cm² flasks at 24°C until late log-phase. For *L. infantum* BA262 $\Delta lpg1$, Hygromycin (50 μ g/mL) and G418 (70 μ g/mL) were added to the medium. For *LPG1*-complemented parasites ($\Delta lpg1 + LPG1$), Hygromycin (50 μ g/mL), G418 (70 μ g/mL), and Zeocin (100 μ g/mL) were added to the medium.

Western Blotting

Late log-phase promastigotes were washed with ice-cold PBS containing 1 mM Na₃VO₄, then lysed in 50 mM Tris-HCl pH 8, 150 mM NaCl and 1% Nonidet P-40, containing complete protease inhibitors (Roche Applied Science) and phosphatase inhibitors (1 mM Na₃VO₄, 50 mM NaF, 1.5 mM EGTA and 10 mM Na₄P₂O₇). Samples were sonicated briefly, and insoluble material was removed by centrifugation for 10 min at 4°C. Protein concentrations were determined using the Pierce BCA protein assay kit (Pierce). Proteins were separated by SDS-PAGE and then transferred to Hybond-LFP PVDF membranes (GE Healthcare Life Sciences) using a Trans-Blot SD Semi-Dry Transfer Cell apparatus (BioRad). Membranes were blocked with 5% BSA and incubated with the mouse monoclonal antibody CA7AE (MediMabs). For immunodetection, goat anti-mouse IgM Heavy Chain Secondary antibody conjugated with horseradish peroxidase (HRP), and enhanced chemiluminescence (ECL) detection reagents from GE Healthcare Life Sciences were used.

Confocal Immunofluorescence Microscopy

Late log-phase promastigotes were adhered on Poly-L-Lysine-coated glass coverslips (BD Biosciences, San Jose, CA) by centrifugation, fixed with 4% paraformaldehyde (Canemco and Marivac) for 20 min and simultaneously blocked and permeabilized with a solution of 0.1% Triton X-100, 1% BSA, 6% non-fat dry milk, 20% goat serum and 50% FBS for 20 min. The distribution of LPG and other PGs containing the Gal(β 1,4)Man(α 1-PO₄) repeating unit epitope was visualized using the mouse monoclonal antibody CA7AE (MediMabs, 1:2,000) after 2 h incubation followed by Alexa Fluor 568 goat anti-mouse IgM (Molecular Probes) at 1:500 for 30 min incubation. Parasite nuclei were stained with DAPI (Molecular Probes) at 1:17,000. All steps were performed at room temperature. Coverslips were then mounted in Fluoromount-G (Interscience) and sealed with nail polish. Promastigotes were observed with a Plan APOCHROMAT 63x oil-immersion DIC 1.4 NA objective on a Zeiss LSM780 confocal microscope equipped with a 30 mW 405 nm diode laser, 25 mW 458/488/514 argon multiline laser, 20 mW DPSS 561 nm laser and 5 mW HeNe 633 nm laser, coupled to a Zeiss Axio Observer Z1. Images were acquired in plane scanning mode, and were minimally and equally processed using Carl Zeiss ZEN 2011 software.

Electron Microscopy

Late log-phase promastigotes were fixed with 2% paraformaldehyde plus 2.5% glutaraldehyde in 0.1 M phosphate buffer (pH 7.4) overnight at 4°C. Next, parasites were processed

for Transmission Electron Microscopy (TEM) by post-fixing in 1% osmium tetroxide (OsO₄) plus 0.8% potassium ferricyanide in 0.1 M cacodylate buffer, pH 7.2, then dehydrated in acetone at increasing concentrations of 50, 70, 90, and 100% followed by processing for resin embedding (PolyBed 812, Polysciences). Sections were mounted on uncoated 200-mesh copper grids and viewed under a TEM microscope (JEOL JEM-1230). Alternatively, parasites were processed for Scanning Electron Microscopy (SEM) by first fixing as described above, then adhered on Poly-L-Lysine-coated glass coverslips and post-fixed as described above. Samples were then submitted to critical point-drying under CO₂, coated with a 20 nm-layer of gold particles and examined under SEM (JSM-6390LV, JEOL).

Parasite Growth Curves

Early log-phase promastigotes (1×10^5 /ml) were cultured and the number of viable promastigotes was determined by daily direct counting performed in a Neubauer chamber.

Lipid Droplets Staining and Quantification

Late log-phase promastigotes were fixed with 3.7% formaldehyde and stained with osmium tetroxide. Cell morphology was observed, and LD were counted by light microscopy using a 100X objective lens in 50 consecutively scanned parasites (Araújo-Santos et al., 2014).

Bone Marrow-Derived Macrophages (BMDM) Macrophage and Infection

Bone marrow-derived macrophages (BMDM) were obtained from C57BL/6 mice as previously described. Briefly, cells were collected from femurs and differentiated in RPMI 1640, 20% inactivated FBS, 30% L929 cell-conditioned media (LCCM), 2 mM L-glutamine, 100 U/mL Penicillin, and 100 μ g/mL Streptomycin at 36°C under 5% CO₂. BMDMs were collected after 7 days and seeded on tissue culture plates in RPMI 1640 media, 10% inactivated FBS, 5% LCCM and 2 mM L-glutamine (Araújo-Santos et al., 2014).

Cells (2×10^5) adhered on coverslips were infected with either WT, $\Delta lpg1$, or $\Delta lpg1 + LPG1$ parasites at a 10:1 multiplicity of infection (MOI). After 4 or 72 h of infection, coverslips were fixed and stained with DiffQuik (Wright-Giemsa). Intracellular parasites were counted under light microscopy to determine the infection index under each experimental condition (Araújo-Santos et al., 2014).

RAW 264.7 Cell Line, Culture, and Infection

The mouse macrophage leukemia cell line RAW 264.7 (TIB-71; American Type Culture Collection (ATCC), Manassas, VA, USA) was maintained in DMEM medium with high glucose (Vitrocell Embriolife, Campinas, SP, Brazil) supplemented with 10% heat-inactivated fetal bovine serum (Sigma-Aldrich, St. Louis, MO, USA), 100 U/ml penicillin and 100 μ g/ml streptomycin in an incubator at 37°C under 5% CO₂. RAW 264.7 cells were infected with either WT, $\Delta lpg1$ or $\Delta lpg1 + LPG1$ parasites at a 10:1 multiplicity of infection (MOI). After 4 or 8 h of infection, cells were processed

for quantitative RT-PCR. For the luciferase reporter assay, cultures were washed 2 h post-infection and analyzed 24 h later.

RNA Extraction and RT-qPCR

For real time quantitative polymerase chain reaction analysis, total RNA of control and infected RAW 264.7 cells (1×10^6 cells) was extracted using an Invitrap[®] Spin Cell RNA mini kit (STRACTEC Molecular GmbH, Berlin, Germany). RNA extracts (2 μ g) were reverse transcribed into first-strand cDNA with ImProm-II (Promega) and oligo(dT) primers in accordance with manufacturer instructions. The following primer DNA sequences were used to determine iNOS mRNA levels: Forward 5'-CAGCTGGGCTGTACAAACCTT-3' and Reverse: 5'-CATTGGAAGTGAAGCGTTTCG-3', while GAPDH mRNA levels were quantified using: Forward 5'-TGCACCACCAACTGCTTAGC-3' and Reverse 5'-GGCATGGACTGTGGTCATGAG-3'. Amplicon specificity was carefully verified by the presence of a single melting temperature peak in dissociation curves calculated following RT-qPCR, which was performed via the Applied Biosystems StepOne[™] detection system (Applied Biosystems) using GoTaq[®] qPCR Master Mix (Promega Corp., Madison, WI, USA). All RT-qPCR analyses were performed in triplicate. RT-qPCR data was normalized using GAPDH primers as an endogenous control. All gene expression ratios were calculated by the $\Delta\Delta$ Ct method using StepOne software version 2.0 (Applied Biosystems).

Transient Transfections and Luciferase Assays

To investigate NF- κ B transcriptional activity, RAW 264.7 were plated in 48-well polystyrene plates (1×10^5 cells per well) and transfected with 1 μ g of the p6kB-Luc luciferase reporter construct (kindly provided by Dr. Patrick Baeuerle, Munich University) in the presence of LIPOFECTAMINE 2000 reagent (Invitrogen, Carlsbad, CA, USA). pTK-3XNS luciferase reporter construct was used to measure iNOS promoter activity, provided by Dr. David Geller (University of Pittsburgh, Pennsylvania, EUA). Luciferase activity was normalized using 40 ng of pRL-CMV plasmid (Promega Corp., Madison, WI, USA). Transfected cells were infected with either WT, Δ lpg1 or Δ lpg1+LPG1 parasites at a 10:1 MOI. After 24 h of infection, cells were washed with PBS, lysed according to the Dual Luciferase System protocol (Promega Corp.), and analyzed in a GloMax[®]-Multi detection system (Promega Corp.). Positive controls consisting of cells stimulated with 1 μ g/mL of LPS (Sigma-Aldrich) were used to induce the activation of iNOS gene expression.

Statistical Analysis

BMDM and RAW 264.7 cell infection assays were performed in triplicate, and each experiment was repeated at least three times. Data are presented as the mean and SE (standard error) of representative experiments, and GraphPad Prism 5.0 software (GraphPad Software) was used for data analysis.

Means from different groups were compared by One-way ANOVA and comparisons between two groups were performed using the Student Newman-Keuls post-test. Differences were considered statistically significant when $p \leq 0.05$.

RESULTS

Generation of a *L. infantum* Lpg1-Null Δ lpg1 Mutant

To generate a *L. infantum* LPG-defective (Δ lpg1) mutant, WT *L. infantum* BA262 promastigotes were transfected with the LPG1 targeting constructs (Figures 1A,B). The resulting HYG- and NEO-resistant Δ lpg1 parasites were transfected with a LPG1 expression vector to generate add-back LPG-expressing parasites (Δ lpg1 + LPG1). Loss of LPG expression in the Δ lpg1, was determined by comparing LPG levels in WT, Δ lpg1, and Δ lpg1 + LPG1 *L. infantum* promastigotes by Western blot and by confocal immunofluorescence microscopy (Figures 1C,D). Together, these data indicate that the LPG1 gene was successfully deleted in the Δ lpg1 mutants, resulting in the generation of a LPG-defective *L. infantum* mutant.

LPG1-Null Mutants Retain *L. infantum* Viability and Morphology

To determine the effect of deleting LPG1 on parasite growth and morphology, axenic cultures of the three isolates were monitored and counted daily for 10 days until reaching late log phase. A delayed replication capability of the Δ lpg1 mutant parasites was noted in comparison to the WT and Δ lpg1 + LPG1 parasites (Figure 2A). Wild-type *L. infantum* presented regular growth for 7 days until reaching stationary phase, with a cell density of approximately $3\text{--}4 \times 10^7$ parasites/ml, while the Δ lpg1 mutant reached the same phase approximately 3 days later, with a cell density of $1\text{--}2 \times 10^7$ parasites/ml (Figure 2A). The Δ lpg1 + LPG1 mutants presented an intermediate growth profile, reaching stationary phase shortly after the WT parasites. Area Under the Curve (AUC) analysis of the growth curve revealed a significant difference only when comparing WT and Δ lpg1 parasites ($p < 0.05$), yet no differences were observed between WT and Δ lpg1 + LPG1 mutants (Figure 2B). Upon reaching stationary phase, parasites were examined by electron microscopy to assess the presence of morphological alterations. Under both SEM and TEM, no alterations in morphology (Figure 2C) or in ultrastructural characteristics (Figure 3A) were detected among WT, Δ lpg1, and Δ lpg1 + LPG1 promastigotes. In addition, the absence of LPG1 had no impact on the number of lipid bodies present within the parasites (Figure 3A). Hence, whereas the LPG1 gene had a limited impact on *L. infantum* promastigotes proliferation, it did not significantly alter morphological features of these parasites (Figure 3).

Lpg1-Null Mutants Exhibit Limited Survival in Macrophages

To evaluate differences in parasite survival among WT and transgenic parasites *in vitro*, BMDMs were infected for 4 or

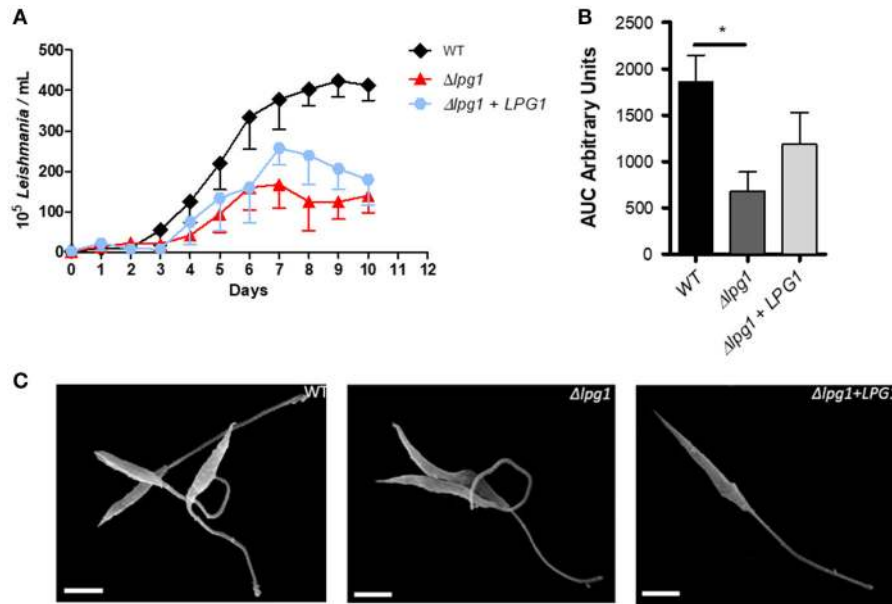


FIGURE 2 | Growth curve and morphology of the $\Delta lpg1$ mutant. WT, $\Delta lpg1$ and $\Delta lpg1 + LPG1$ parasites were cultured at initial concentrations of 1×10^5 /ml in HOMEM medium. **(A)** Axenic growth curve of late log-phase WT, $\Delta lpg1$ and $\Delta lpg1 + LPG1$ parasites, as showed by the area under the curve (AUC) **(B)**. The number of viable parasites was evaluated by direct counting. Each point represents mean and SE. Data are representative of at least three independent assays and were collected in triplicate for each condition. * $p < 0.05$. **(C)** Parasites were processed for scanning electron microscopy (SEM) and photographed under a JEOL JSM-6390LV microscope at 6000x magnification **(C)**. Scale bar, 2 μ m.

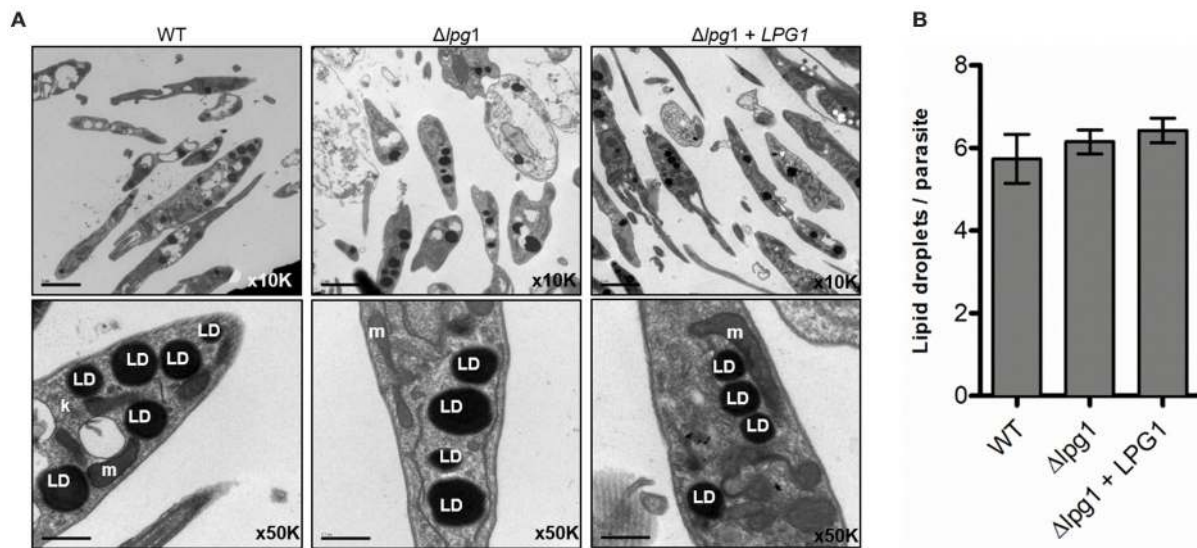
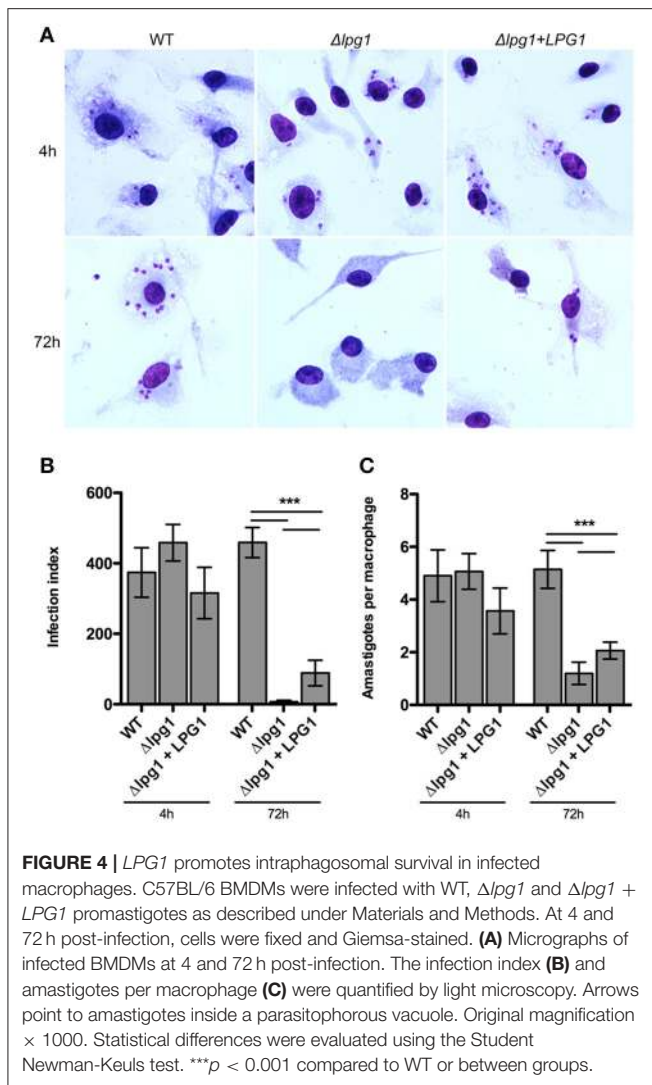


FIGURE 3 | Deletion of *LPG1* does not alter LD formation in *Leishmania infantum*. **(A)** Panels show stationary phase WT, $\Delta lpg1$ and $\Delta lpg1 + LPG1$ promastigotes analyzed by transmission electron microscopy (TEM) and photographed under a JEOL 1230 microscope. **(B)** Bars represent the mean number of LD \pm SE in WT, $\Delta lpg1$ or $\Delta lpg1 + LPG1$ parasites stained with osmium tetroxide. k, kinetoplast; LD, lipid droplets; m, mitochondrion. Scale bar, 0.5 μ m.

72 h. No differences were observed between the *Leishmania* parasites after 4 h of infection (**Figure 4**). However, at 72 h post-infection, WT parasites survived more efficiently than the $\Delta lpg1$ mutant. Expression of *LPG1* in the $\Delta lpg1$ mutant partially

restored its capacity to survive and replicate within macrophages. These data reinforce the importance of *LPG* as a virulence factor in the successful maintenance of *Leishmania infantum* infection.



LPG1-Null Mutants Induce NF- κ B-Dependent iNOS Expression in Macrophages

To assess the impact of LPG on the expression of inducible nitric oxide synthase by host cells, we first analyzed iNOS transcript levels in RAW 264.7 cells infected with WT or transgenic parasites. The $\Delta lpg1$ mutant induced a robust (3.5-fold increase) expression of iNOS compared to WT and $\Delta lpg1 + LPG1$ promastigotes (Figure 5A). We next performed luciferase reporter assays to characterize the modulation of the iNOS promoter by *L. infantum* promastigotes. RAW 264.7 cells were transiently transfected with either the iNOS promoter reporter construct pTK-3XNS or the NF- κ B consensus luciferase reporter construct (p κ B-Luc) prior to infection with either *L. infantum* WT, $\Delta lpg1$ or $\Delta lpg1 + LPG1$, or stimulation with LPS. As shown in Figures 5B,C, LPG-deficient promastigotes induced stronger activation of the iNOS promoter and of the NF- κ B reporter. Collectively, these findings indicate that LPG contributes to the evasion of iNOS expression by *L. infantum* promastigotes.

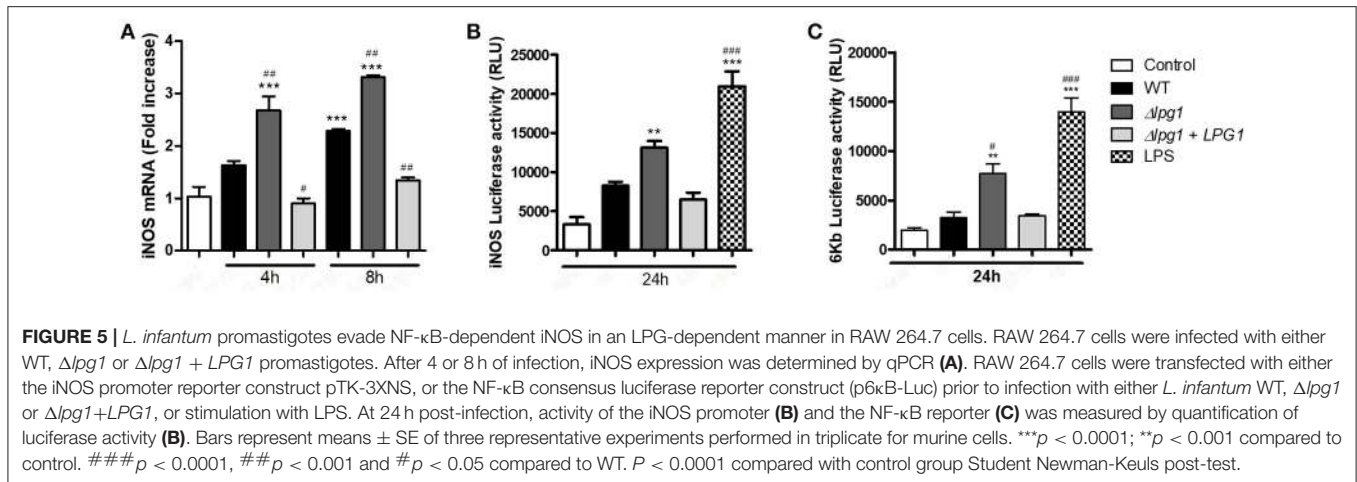
DISCUSSION

Previous studies using purified LPG were important to unravel its impact on the activation of the immune system. Although purified LPG from different species can activate the release of inflammatory mediators, understanding the role of this response in the context of infection remains a challenge. While some groups have characterized Old World *LPG1*-defective *Leishmania* species, the behavior of these parasites when compared to their WT counterparts varies depending on the species under study (Spath et al., 2003; Capul et al., 2007; Forestier et al., 2014). Here, we generated for the first time a LPG-deficient mutant of *L. infantum*, a New World species cluster.

A comparison of parasite growth between axenic cultures containing each of the three isolates showed that the deletion of *LPG1* resulted in a delayed capability of the $\Delta lpg1$ mutant parasites to replicate in comparison to cultures of WT and $\Delta lpg1 + LPG1$ parasites. While the deletion of the *LPG1* gene had a limited impact on *L. infantum* promastigote proliferation, no significant morphological or ultrastructural alterations were seen in these parasites, indicating that targeting the *LPG1* gene does not interfere with the intrinsic cell biology of *L. infantum*.

Recently, we have demonstrated that intact LPG from *L. infantum* promastigotes, but not its glycan and lipid moieties, induced a range of pro-inflammatory responses, including prostaglandin E₂ (PGE₂) and nitric oxide (NO) release, increased LD formation, and inducible nitric oxide synthase (iNOS) and cyclooxygenase-2 expression (Lima et al., 2017). Consequently, a limitation of using purified LPG is that the physiological conditions present in host cell-parasite interactions are not accurately replicated. LDs are key cytoplasmic organelles involved in production of lipid mediators and pro-inflammatory cytokines in mammalian cells (Bozza et al., 2011). Several intracellular pathogens, including *Leishmania*, take advantage of LD formation in host cells (Rabhi et al., 2016). Moreover, LDs have also been described in trypanosomatids in association with arachidonic acid metabolism (Araújo-Santos et al., 2014). Our group previously reported an increase in LD formation during *L. infantum* metacyclogenesis, as well as in the intracellular amastigote form (Araújo-Santos et al., 2014). Here, we showed that the absence of the *LPG1* gene in *L. infantum* did not alter the biogenesis of LDs. In addition, our previous findings showed that parasite-derived PGF_{2 α} produced inside LDs plays a critical role during macrophage infection (Araújo-Santos et al., 2014). We fully intend to comprehensively investigate the potential influence of *LPG1* on the release of PGF_{2 α} in infected macrophages using this novel *L. infantum* $\Delta lpg1$ mutant.

In *L. major* and *L. donovani*, the specific loss of LPG through the ablation of *LPG1* galactofuranosyl transferase strongly impairs the ability of parasites to survive within the sandfly host, as well as to establish infection in mammalian macrophages and in mice (Sacks et al., 2000; Spath et al., 2003; Secundino et al., 2010). Hence, in these species, LPG impairs the microbicidal mechanisms associated with the biogenesis of phagolysosomes, including assembly of the NADPH oxidase and recruitment of the v-ATPase (Lodge et al.,



2006; Vinet et al., 2009). Our results indicate that, similarly to these species, *L. infantum* LPG1 is required for replication within macrophages. Whether LPG contributes to the ability of *L. infantum* to successfully infect macrophages through the impairment of phagolysosomal biogenesis remains to be investigated. Interestingly, we observed that our Δ lpg1 mutant parasites induced robust NF- κ B-dependent iNOS expression compared to parental WT *L. infantum* promastigotes. This seems to suggest that the reduced survival of Δ lpg1 mutants in mouse macrophages may be related to higher levels of iNOS, which is responsible for the generation of leishmanicidal nitric oxide (Coelho-Finamore et al., 2011; Passero et al., 2015). Further study will involve investigating the contribution of nitric oxide production with respect to the reduced ability of Δ lpg1 mutants to survive within macrophages. The underlying mechanism by which Δ lpg1 mutant parasites induce high levels of NF- κ B activation remains unknown, and thus represents an additional aspect of host cell-parasite interplay that we intend to further investigate.

With regard to the partial restoration of the WT phenotype observed in Δ lpg1 + LPG1 parasites, it has been well-documented that complemented parasites commonly do not fully recover virulence. The inappropriate regulation of LPG1 expression by the episomal vector may be a possible explanation for this observation (Späth et al., 2000; Späth et al., 2003; Joshi et al., 2002). A previous study demonstrated that *L. major* LPG1-deficient mutant promastigotes present an attenuated virulence phenotype, as evidenced by the delayed formation of lesions *in vivo* (Späth et al., 2000). In addition, this delay was associated with a 100-fold decrease in parasite survival within macrophages *in vitro*. The data presented herein are consistent with these results, as well as with other reports in the literature (Privé and Descoteaux, 2000; Sacks et al., 2000; Zhang et al., 2004) propounding LPG as a virulence factor.

Taken together, the present findings support the importance of creating LPG-deficient mutants in various *Leishmania* spp. as a unique tool to investigate the specific impact and contribution of this abundant virulence factor in the complex host cell-*Leishmania* interplay. Hence, we are currently conducting studies

to compare the responses of various immune cells to live *L. infantum* promastigotes in the presence or absence of surface-expressed LPG, since we feel it is important to thoroughly characterize these isolates to obtain a more comprehensive understanding regarding the role of *L. infantum* LPG1 in future *in vitro* and *in vivo* studies.

AUTHOR CONTRIBUTIONS

ML-S, CM, JL, GA, GQ-C, AC, SM-P, UG, LF, TA-S, AD, and VB conceived and designed the study, contributed to the data analysis, drafted, and revised the manuscript. ML-S, CM, JL, GA, GQ-C, AC, SM-P, CF, FJ-S, and TA-S performed the experiments. ML-S, CM, JL, LF, TA-S, AD, and VB wrote and revised the manuscript. All authors read and approved the final version of this manuscript.

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