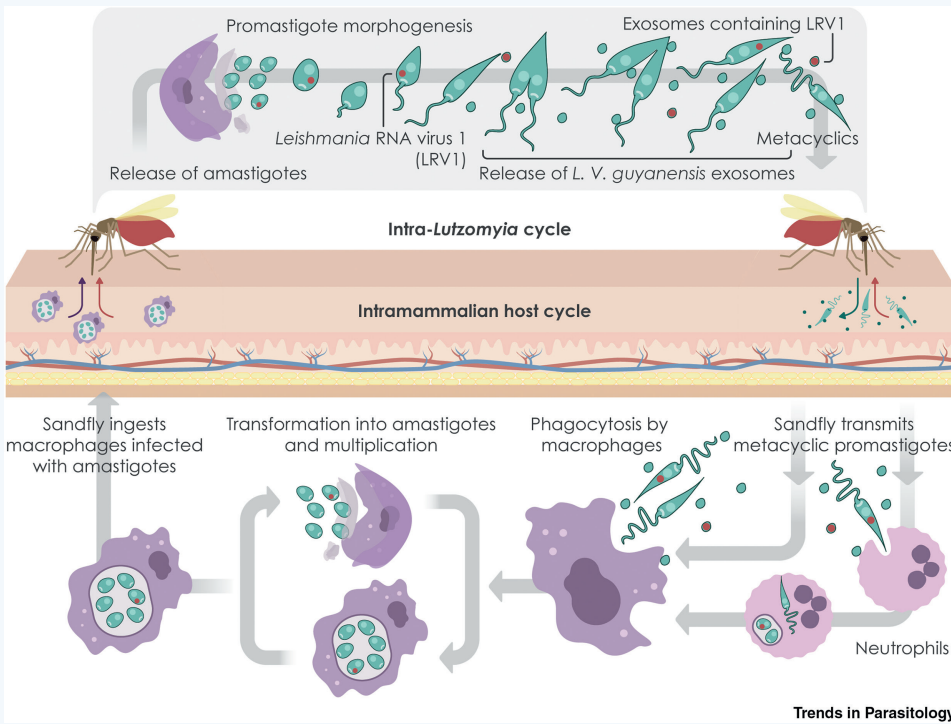


Leishmania Viannia guyanensis

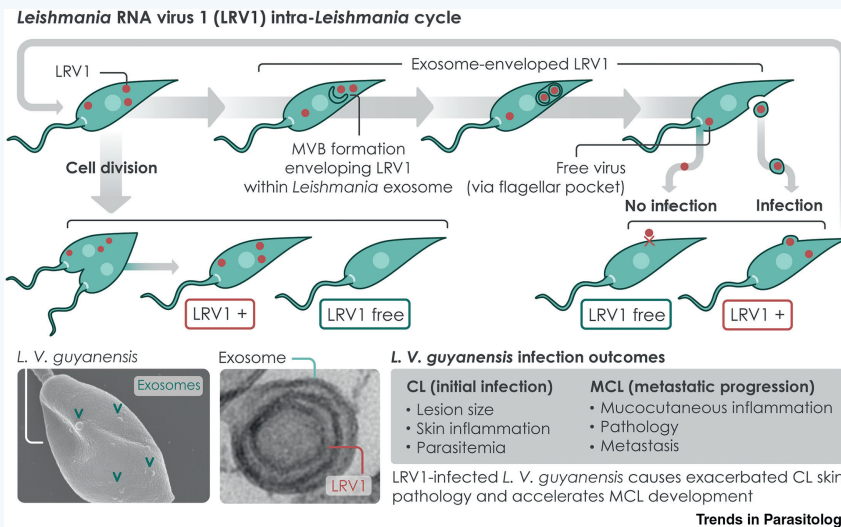
Martin Olivier,^{1,*} Aida Minguez-Menendez,² and Christopher Fernandez-Prada^{2,*}

¹The Research Institute of the McGill University Health Centre, McGill University, Montréal, Canada

²Université de Montréal, Faculty of Veterinary Medicine, St-Hyacinthe, Canada



Leishmania of the Viannia subgenus, including *Leishmania Viannia guyanensis*, is the agent responsible for cutaneous and mucocutaneous leishmaniasis (CL and MCL) in the Americas from the USA to Argentina. 48 000 new cases of CL and MCL are reported yearly, among which 1/10 are associated to *L. V. guyanensis* infection transmitted by female *Lutzomyia* sandflies during the blood meal. Inoculated metacyclic promastigotes, coupled with *Leishmania* exosomes, will infect various inflammatory cells at inoculation sites, where they rapidly transform into amastigotes. Parasites divide and progress in the intramacrophage form, leading to an initial CL skin ulceration. Depending on the inoculation site and host health condition, parasites may metastasize to the nasopharyngeal tissues within a few months. *L. V. guyanensis* is occasionally infected with *Leishmania* RNA virus 1 (LRV1) that can be enveloped by exosomes and is believed to accelerate MCL development.



KEY FACTS:

L. V. guyanensis infection is mainly found in the Amazon basin of South America, including Bolivia, Brazil, and Peru.

The primary hosts are the two-toed sloth, the lesser anteater, and the opossum.

After being inoculated into the skin by female *Lutzomyia* sandflies, the metacyclic promastigotes infect phagocytes at the injection site, leading to localized skin lesions that can evolve to MCL.

Some *guyanensis* strains are infected by LRV1 endovirus, causing a potentially more aggressive form of MCL. LRV1 is not necessary for the development of MCL skin pathology.

LRV1 is maintained in *L. V. guyanensis* by cell division but has been shown to exploit *Leishmania* exosomal pathways to exit promastigotes and infect naive *Leishmania* from the Viannia subgenus.

DISEASE FACTS:

MCL outcomes are influenced by initial CL lesion site, size, and delayed healing.

Disfiguring MCL skin pathology, which affects the mouth and nasopharyngeal tissue, may develop anywhere from several months to 10–20 years after the CL episode.

The nose is mainly affected; however, 1/3 of infected individuals may develop invasive lesions of the pharynx/larynx and upper lip.

Final stages of MCL can lead to major disfigurement, tissue destruction, and nasal obstruction.

While CL can heal spontaneously, MCL never heals by itself.

TAXONOMY AND CLASSIFICATION:

- PHYLUM:** Euglenozoa
- CLASS:** Kinetoplastea
- ORDER:** Kinetoplastida
- FAMILY:** Trypanosomatidae
- GENUS:** *Leishmania*
- SUBGENUS:** *Viannia*
- SPECIES:** *L. V. guyanensis*

*Correspondence:

martin.olivier@mcgill.ca (M. Olivier) and christopher.fernandez.prada@umontreal.ca (C. Fernandez-Prada).



Acknowledgments

This work was supported by the Canadian Institute of Health Research (CIHR) and Natural Sciences and Engineering Research Council (NSERC) grants to Martin Olivier and Christopher Fernandez-Prada.

Resources

www.who.int/news-room/fact-sheets/detail/leishmaniasis
www.cdc.gov/parasites/leishmaniasis/health_professionals/index.html
www.paho.org/leishmaniasis
www.paho.org/hq/dmdocuments/2016/2016-cha-leish-epi-report-americas.pdf

Literature

1. Atayde, V.D. *et al.* (2015) Exosome secretion by the parasitic protozoan *Leishmania* within the sand fly midgut. *Cell Rep.* 13, 957–967
2. Atayde, V.D. *et al.* (2019) Exploitation of the *Leishmania* exosomal pathway by *Leishmania* RNA virus 1. *Nat. Microbiol.* 4, 714–723
3. Coughlan, S. *et al.* (2018) *Leishmania naiffii* and *Leishmania guyanensis* reference genomes highlight genome structure and gene evolution in the *Viannia* subgenus. *R. Soc. Open Sci.* 5, 172212
4. Hartley, M.A. *et al.* (2014) The immunological, environmental, and phylogenetic perpetrators of metastatic leishmaniasis. *Trends Parasitol.* 30, 412–422
5. Ives, I. *et al.* (2011) *Leishmania* RNA virus controls the severity of mucocutaneous leishmaniasis. *Science* 331, 775–778
6. Kariyawasam, R. *et al.* (2019) Virulence factor RNA transcript expression in the *Leishmania Viannia* subgenus: influence of species, isolate source, and *Leishmania* RNA virus-1. *Trop. Med. Health* 47, 25
7. Olivier, M. (2011) Host–pathogen interaction: culprit within a culprit. *Nature* 471, 173–174
8. Soares, R.P. *et al.* (2017) Highlights of the São Paulo ISEV Satellite Meeting on extracellular vesicles in pathogens. *J. Extra. Vesicl.* Published online November 26, 2017. <https://doi.org/10.1080/20013078.2017.1407213>
9. Oliveira Guerra, J.A. *et al.* (2011) Mucosal Leishmaniasis Caused by *Leishmania (Viannia braziliensis)* and *Leishmania (Viannia) guyanensis* in the Brazilian Amazon. *PLoS Negl. Trop. Dis.* 5, e980
10. WHO Expert Committee (2010) *Control of the Leishmaniases*. WHO Technical Report Series no. 949, pp. 1–185, WHO