

Structure and Evolution of Protozoan Leishmania

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Opinion Article

Received: 05-Aug-2022, Manuscript No. JZS-22-99164; **Editor assigned:** 08- Aug-2022, Pre QC No. JZS-22-99164; **Reviewed:** 22- Aug-2022, QC No. JZS-22-99164; **Revised:** 29- Aug-2022, Manuscript No. JZS-22-99164(R); **Published:** 05-Sep-2022, DOI: 10.4172/2321-6190.10.S6.004

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DESCRIPTION

Leishmania is a parasitic protozoan, a single-celled organism of the genus Leishmania that are responsible for the disease leishmaniasis. They are spread by sandflies of the genus Phlebotomus in the Old World, and of the genus Lutzomyia in the New World. At least 93 sandfly species are proven or probable vectors worldwide. Their primary hosts are vertebrates; Leishmania commonly infects hyraxes, canids, rodents, and humans.

Structure

Leishmania species are unicellular eukaryotes having a well-defined nucleus and other cell organelles including kinetoplasts and flagella. Depending on the stage of their life cycle, they exist in two structural variants, as:

- The amastigote form is found in the mononuclear phagocytes and circulatory systems of humans. It is an intracellular and nonmotile form, being devoid of external flagella. The short flagellum is embedded at the anterior end without projecting out. It is oval in shape, and measures 3 μm –6 μm in length and 1 μm –3 μm in breadth. The kinetoplast and basal body lie towards the anterior end.
- The promastigote form is found in the alimentary tract of sandflies. It is an extracellular and motile form. It is considerably larger and highly elongated, measuring 15 μm –30 μm in length and 5 μm in width. It is spindle-shaped, tapering at both ends. A long flagellum (about the body length) is projected externally at the anterior end. The nucleus lies at the centre, and in front of it are the kinetoplast and the basal body.

Evolution

The details of the evolution of this genus are debated, but Leishmania apparently evolved from an ancestral trypanosome lineage. The oldest lineage is that of the Bodonidae, followed by Trypanosoma brucei, the latter being

confined to the African continent. *Trypanosoma cruzi* groups with trypanosomes from bats, South American mammals, and kangaroos suggest an origin in the Southern Hemisphere. These clades are only distantly related. The remaining clades in this tree are *Blastocrithidia*, *Herpetomonas*, and *Phytomonas*. The four genera *Leptomonas*, *Crithidia*, *Leishmania*, and *Endotrypanum* form the terminal branches, suggesting a relatively recent origin. Several of these genera may be polyphyletic and may need further division.

The origins of genus *Leishmania* itself are unclear. One theory proposes an African origin, with migration to the Americas. Another proposes migration from the Americas to the Old World via the Bering Strait land bridge around 15 million years ago. A third theory proposes a Palearctic origin. Such migrations would entail subsequent migration of vector and reservoir or successive adaptations along the way. A more recent migration is that of *L. infantum* from Mediterranean countries to Latin America (known as *L. chagasi*), since European colonization of the New World, where the parasites picked up their current New World vectors in their respective ecosystems. This is the cause of the epidemics now evident. One recent New World epidemic concerns foxhounds in the USA.

Although it was suggested that *Leishmania* might have evolved in the Neotropics. This is probably true for species belonging to the subgenera *Viannia* and *Endotrypanum*. However, there is evidence that the primary evolution of the subgenera *Leishmania* and *Sauroleishmania* is the Old world. While the *Mundinia* species appear to be more universal in their evolution. One theory is that different lineages became isolated geographically during different periods and it is this that gave rise to this evolutionary mosaicism. But there is no doubt that the *Leishmaniinae* are a monophyletic group. A large data set analysis suggests that *Leishmania* evolved 90 to 100 million years ago in Gondwana. The reptile infecting species originated in mammalian clades. *Sauroleishmania* species were originally defined on the basis that they infected reptiles (lizards) rather than mammals. Based on molecular evidences, they have been moved to subgenus status within *Leishmania*. This subgenus probably evolved from a group that originally infected mammals.