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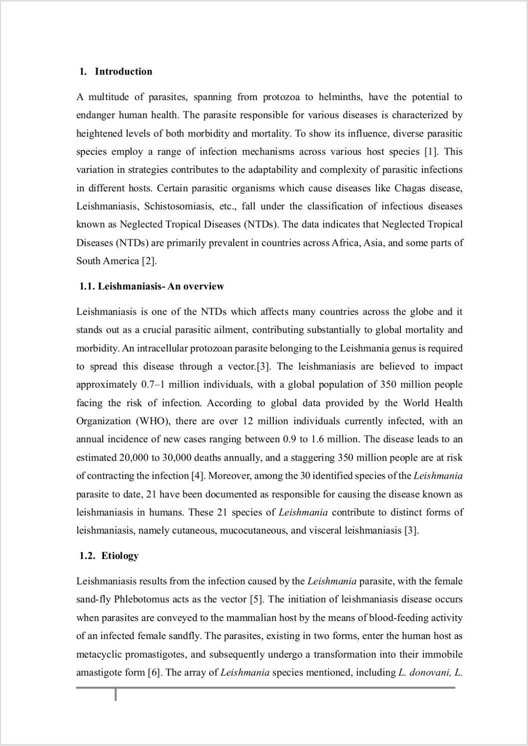

1. Introduction

A multitude of parasites, spanning from protozoa to helminths, have the potential to endanger human health. The parasite responsible for various diseases is characterized by heightened levels of both morbidity and mortality. To show its influence, diverse parasitic species employ a range of infection mechanisms across various host species [1]. This variation in strategies contributes to the adaptability and complexity of parasitic infections in different hosts. Certain parasitic organisms which cause diseases like Chagas disease, Leishmaniasis, Schistosomiasis, etc., fall under the classification of infectious diseases known as Neglected Tropical Diseases (NTDs). The data indicates that Neglected Tropical Diseases (NTDs) are primarily prevalent in countries across Africa, Asia, and some parts of South America [2].

1.1. Leishmaniasis- An overview

Leishmaniasis is one of the NTDs which affects many countries across the globe and it stands out as a crucial parasitic ailment, contributing substantially to global mortality and morbidity. An intracellular protozoan parasite belonging to the Leishmania genus is required to spread this disease through a vector.[3]. The leishmaniasis are believed to impact approximately 0.7–1 million individuals, with a global population of 350 million people facing the risk of infection. According to global data provided by the World Health Organization (WHO), there are over 12 million individuals currently infected, with an annual incidence of new cases ranging between 0.9 to 1.6 million. The disease leads to an estimated 20,000 to 30,000 deaths annually, and a staggering 350 million people are at risk of contracting the infection [4]. Moreover, among the 30 identified species of the *Leishmania* parasite to date, 21 have been documented as responsible for causing the disease known as leishmaniasis in humans. These 21 species of *Leishmania* contribute to distinct forms of leishmaniasis, namely cutaneous, mucocutaneous, and visceral leishmaniasis [3].

1.2. Etiology

Leishmaniasis results from the infection caused by the *Leishmania* parasite, with the female sand-fly Phlebotomus acts as the vector [5]. The initiation of leishmaniasis disease occurs when parasites are conveyed to the mammalian host by the means of blood-feeding activity of an infected female sandfly. The parasites, existing in two forms, enter the human host as metacyclic promastigotes, and subsequently undergo a transformation into their immobile amastigote form [6]. The array of *Leishmania* species mentioned, including *L. donovani, L.*

Study on genomic sequences and proteins of Leishmania donovani by sequence and structure-based approach

by Debanjan Saha

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