CHANGES IN GUT MICROBIOTA COMPOSITION IN HAMSTERS INFECTED WITH *Leishmania chagasi*

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**ABSTRACT**

**Introduction:** Intestinal microbiota has an important role in providing nutrients, resistance against pathogenic bacteria and interaction with immune system. Changes in gut microbiota composition and function have been associated with many diseases. Visceral leishmaniasis (VL) is a parasitic disease with clinical manifestations such as fever, hepatomegaly, splenomegaly and weight loss. If untreated can lead to death.

**Objectives:** In this study we used an experimental model of VL to evaluate changes in gut microbiota composition during infection and to determinate association among microbiota, parasite load and biochemical markers.

**Material and Methods:** Golden hamster (*Mesocricetus auratus*) males were infected with *L. chagasi* \((10^5\) parasites injected in the ear), and euthanized after 4 (n=9) and 8 (n=9) months. Parasite load in spleen and liver was evaluated by the limiting dilution technique. Histological analysis of intestinal mucosa was carried out through microscopy of gut sections stained with haematoxylin-eosin. Real-time quantitative PCR (qPCR) was used to quantify two groups of bacteria: *Bifidobacterium* spp and *Lactobacillus* spp.

**Results:** There were no histological differences in the intestinal mucosa from the animals. Infected hamsters exhibit less *Bifidobacterium* spp than control hamsters after 4 months of infection (mean±SD=25.13 ± 2.87 and 22.36 ± 1.85 cycle threshold (CT); \(P=0.2\)) and more after 8 months (mean±SD=21.97 ± 0.48 and 23.51 ± 2.71 CT for infected and controls respectively; \(P=0.5\)). There were no differences in the number of *Lactobacillus* spp in both infected and control hamsters groups, after 4 (means±SD=23.65 ± 2.183 and 23.85 ± 5.397 CT, respectively; \(P=0.5\)) and 8 months of infection (means±SD=25.15 ± 1.782 and 29.77 ± 2.786 CT, respectively; \(P=0.2\)).

**Conclusions:** These results indicate that there were changes in the gut microbiota composition during experimental leishmaniasis, which could be involved in the pathogenesis of this disease.

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**KEY WORDS:** Visceral Leishmaniasis, *Bifidobacterium* spp, *Lactobacillus* spp.