METAGENOMIC ANALYSIS OF INTESTINAL MICROBIOTA CHANGES IN MICE INFECTED WITH *TRICHURIS MURIS* DURING ACUTE AND CHRONIC PHASES

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The nematode experimental model *Trichuris muris* is frequently used to study infection processes in soil-transmitted helminths (STH) and host-parasite interactions. However, the associations between helminths and bacteria remains poorly known, particularly regarding the impact of this interaction on the pathophysiology of intestinal infections. In this study, we highlight bacterial virulence in the context of an altered host microbiota. During chronic trichuriasis, a inflammatory process occurs due to lesions caused by adult worms onthe intestinal epithelium. Our group has previously demonstrated that *T. muris* alters gut microbiota composition, and the resulting tissue damage facilitates bacterial invasion into the submucosal layer, leading to dysbiosis and bacterial translocation from the acute to the chronic phase of infection. The aim of the present study is to identify the main bacterial groups present in the microbiota of C57BL/6 mice infected with low doses of *T. muris* at different stages of infection and compare them with a control group. Fecal samples were collected from infected and control mice at 90 minutes and at 10, 17, 22, and 35 days post-infection. Microbiome analysis was performed using 16S rRNA sequencing on the Illumina MiSeq platform. Results showed that the control group exhibited a higher abundance of *Lactobacillales* compared to infected mice, where this abundance was markedly reduced. The *Clostridiales* order increased during the acute phase but declined in the chronic phase, although it remained more abundant in the chronic phase compared to the control group. The *Bacteroidales* order showed an initial increase during the acute phase, followed by a significant rise in the chronic phase compared to both the controls and the acute phase. In conclusion, trichuriasis induces significant alterations in gut microbiota composition, reducing beneficial bacteria while promoting the proliferation of pathogenic ones, which directly impacts host health.

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