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Analysis of Circular Ribosome Expression Profiles in Leishmaniasis

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Introduction

Leishmaniasis is a tropical disease that has a significant impact on global public health. Leishmaniasis is the third most common cause of morbidity among parasitic diseases, following malaria and schistosomiasis. Circular RNAs (circRNAs) are a new class of noncoding RNAs that regulate biological and developmental processes. However, no research on the function of circRNAs in leishmaniasis has been published. This is the first study to look at the circRNA expression profiles in leishmaniasis. The potential function of the host genes of differentially expressed circRNAs was determined using GO and KEGG analyses. R software and the STRING database were used to analyse the circRNA-miRNA-mRNA regulatory network and protein-protein interaction (PPI) networks, respectively. A total of 4664 significant differentially expressed circRNAs were identified and compared to controls; 1931 were up-regulated and 2733 were down-regulated. Host genes enriched in ubiquitin-mediated proteolysis, endocytosis, the MAPK signalling pathway, renal cell carcinoma, autophagy, and the ErbB signalling pathway were found in differentially expressed circRNAs.

Description

Leishmaniasis is a parasitic disease that is caused by an obligate intracellular pathogen. In terms of disability adjusted life years, leishmaniasis is the third leading cause of morbidity after malaria and schistosomiasis (DALYs). However, it is the second leading cause of death after malaria. According to published reports, leishmaniasis-endemic areas include 101 countries and approximately 350 million people. The majority of leishmaniasis patients live in impoverished areas, making prevention, diagnosis, and treatment difficult [1-3]. As a result, leishmaniasis affects over 2 million people worldwide each year, resulting in an estimated 40,000 deaths. This parasite also has a high recurrence rate; patients may relapse 6-12 months after receiving treatment. Furthermore, if left untreated, patients can develop multisystem disease or a secondary infection, which can lead to death. Detecting pathogens in bone marrow aspirate smears or cultures is the traditional method of diagnosing leishmaniasis.

However, bone marrow aspiration is not only painful, but the protozoa density is extremely low, making the diagnosis difficult. Furthermore, because visceral leishmaniasis has no distinct clinical symptoms, it is easy to confuse it with other diseases, particularly in endemic areas. As a result, epidemiological investigations are also required. Furthermore, the occurrence of minimally symptomatic, completely asymptomatic, and subclinical disease is regarded as an important aspect of the epidemiology of visceral leishmaniasis, necessitating clinicians to identify additional leishmaniasis epidemiological characteristics. As a result, it is critical to investigate the mechanism of visceral leishmaniasis in order to develop effective diagnostic biomarkers. Circular RNAs (circRNAs) were discovered in RNA viruses for the first time in 1976. Thousands of circRNA species have been identified as a result of the advancement of high-throughput sequencing technology, and the number is still growing. Although circRNAs are a new type of non-coding RNA with covalent closed-loop structures, some circRNAs have the ability to code for proteins.

Zoonotic diseases have a significant impact on human health as a result of their impact on animals and the environment. In order to reduce the harm caused by zoonotic diseases, this study discovered biomarkers of leishmaniasis based on the different expressions of circRNAs in patients. As a result, high-throughput sequencing was used to identify the differentially expressed circRNAs and miRNAs. Furthermore, gene ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes were used to examine the functionals and pathways of host genes [4,5]. As a result, circRNAs are more stable. Many studies have shown that they are linked to a variety of diseases such as cancer, cerebrovascular disease, systemic lupus erythematosus, and others. However, no research on the function and molecular mechanisms of circRNAs in leishmaniasis has been published.

Conclusion

According to the GO enrichment analysis results, host genes may play an important role in the occurrence of leishmaniasis. The top five significant signal pathways identified by KEGG pathway analysis are ubiquitin-mediated proteolysis, endocytosis, the MAPK signalling pathway, renal cell carcinoma, autophagy, and the ErbB signalling pathway. Three of these five significant signalling pathways have been linked to leishmaniasis.

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