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Leishmaniasis Analysis of Circular Ribosome Expression Profiles

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Introduction

The tropical disease leishmaniasis has a significant effect on global public health. After malaria and schistosomiasis, leishmaniasis ranks third among parasitic diseases in terms of morbidity. A new class of noncoding RNAs known as circular RNAs (circRNAs) control biological and developmental processes. However, there has been no published research on the role that circRNAs play in leishmaniasis. Leishmaniasis circRNA expression profiles are the subject of this first study. GO and KEGG analyses were used to determine the differentially expressed circRNAs' potential function in the host genes. The circRNA-miRNA-mRNA regulatory network and the protein-protein interaction (PPI) network were analyzed using R software and the STRING database, respectively. 4664 significant circRNAs with differential expression were found and compared to controls; 2733 were down-regulated, while 1931 were up-regulated. In differentially expressed circRNAs, host genes enriched in ubiquitin-mediated proteolysis, endocytosis, the MAPK signaling pathway, renal cell carcinoma, autophagy, and the ErbB signaling pathway were found.

Description

A parasitic disease characterized by an obligate intracellular pathogen is leishmaniasis. After malaria and schistosomiasis, leishmaniasis is the third most common cause of morbidity in terms of disability adjusted life years (DALYs). However, after malaria, it is the second leading cause of death. Leishmaniasis-endemic regions include 101 nations and approximately 350 million people, according to published reports. Prevention, diagnosis, and treatment are difficult for leishmaniasis patients because most live in impoverished areas. Consequently, leishmaniasis kills 40,000 people annually and affects over 2 million people worldwide. Additionally, this parasite is highly recurrent; Six to twelve months after receiving treatment, patients may relapse. Patients may also contract a secondary infection or multisystem disease, both of which can result in death if left untreated. The most common way to diagnose leishmaniasis is to look for pathogens in smears or cultures of bone marrow.

However, not only is bone marrow aspiration painful, but the extremely low protozoa density also makes it difficult to diagnose. In addition, it is simple to confuse visceral leishmaniasis with other diseases, particularly in areas where it is endemic, due to the absence of distinct clinical symptoms. As a consequence of this, epidemiological studies are also required. Additionally, clinicians must identify additional leishmaniasis epidemiological characteristics because the occurrence of minimally symptomatic, completely asymptomatic, and subclinical disease is considered an important aspect of the epidemiology of visceral leishmaniasis. In order to develop effective diagnostic biomarkers, it is crucial to investigate the mechanism of visceral leishmaniasis. In 1976, the first circular RNAs (circRNAs) were found in RNA viruses. The development of high-throughput sequencing technology has led to the identification of thousands of circRNA species, and this number is still rising. Despite the fact that circRNAs are a novel type of non-coding RNA with covalent closed-loop structures, some circRNAs can encode proteins [1-3].

Due to their impact on animals and the environment, zoonotic diseases have a significant impact on human health. Based on the various expressions of circRNAs in patients, this study discovered biomarkers of leishmaniasis to help reduce the harm caused by zoonotic diseases. High-throughput sequencing was used to identify the circRNAs and miRNAs with differential expression. The functionals and pathways of host genes were also investigated using gene ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes. CircRNAs are more stable as a result. They have been linked to many diseases, including cancer, cerebrovascular disease, systemic lupus erythematosus, and others, according to numerous studies. However, there has been no published research on the molecular mechanisms and functions of circRNAs in leishmaniasis [4,5].

Conclusion

The results of the GO enrichment analysis suggest that host genes may be involved in the development of leishmaniasis. The main five huge sign pathways recognized by KEGG pathway investigation are ubiquitin-interceded proteolysis, endocytosis, the MAPK flagging pathway, renal cell carcinoma, autophagy, and the ErbB flagging pathway. Leishmaniasis has been linked to three of these five important signaling pathways.

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