hsa_circ_0001445

hsa_circ_0001445 is a circular RNA molecule found in humans.

hsa_circ_0001445 has been found to be involved in various biological processes, including the regulation of gene expression and the development of certain diseases. For example, studies have shown that hsa_circ_0001445 is upregulated in cancer cells and may play a role in promoting cancer progression by regulating key signaling pathways.

In addition, hsa_circ_0001445 has been found to be involved in the regulation of immune responses, with some studies suggesting that it may play a role in the development of autoimmune diseases.

Overall, the exact function of hsa_circ_0001445 is still being investigated, and further research is needed to fully understand its role in human biology and disease.

To evaluate the hsa_circ_0001445 level in peripheral blood leukocytes of patients with coronary heart disease (CHD) and its related clinical factors, and predict its circRNA-miRNA-mRNA regulatory network in CHD pathogenesis via bioinformatics analysis.

Methods: Peripheral blood leukocytes were isolated from the whole blood samples of 94 CHD patients (aged 65.96 ± 9.78 years old) and 126 healthy controls (aged 60.75 ± 8.81 years old). qRT-PCR was used to quantify the expression level of circRNA and subsequently analyze its association with CHD clinical parameters. Via bioinformatics algorithm and GEO datasets, differential miRNA expression was evaluated using the Limma package. A miRNA-mRNA regulatory network was predicted by cyTargetLinker. ClusterProfiler was employed to perform functional enrichment analysis of the circRNA network to investigate its role in CHD pathogenesis.

Results: The expression of hsa_circ_0001445 in peripheral blood leukocytes of CHD patients was downregulated compared with that of healthy controls. Positive correlations were evident between hsa_circ_0001445 expression level and the levels of hemoglobin, triglycerides, high- and low-density lipoprotein cholesterol. A significant negative correlation was also found between hsa_circ_0001445 expression level and age and the neutrophil level. Low expression of hsa_circ_0001445 exhibited a discriminatory ability between CHD patients and healthy controls with a sensitivity of 67.5% and a specificity of 76.6% ($p < 0.05$). By bioinformatics analysis, 405 gene ontology terms were identified. The Kyoto Encyclopedia of Genes and Genomes terms focused principally on the PI3K-Akt signaling pathway. hsa_circ_0001445 was associated with the expression of three miRNAs that may regulate 18 genes involved in KEGG processes: hsa-miR-507, hsa-miR-375-3p, and hsa-miR-942-5p.

Conclusion: The hsa_circ_0001445 level in peripheral blood leukocytes may serve as a biomarker for CHD diagnosis. Our work on circRNA-miRNA-mRNA networks suggests a potential role for hsa_circ_0001445 in CHD development 1).

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Dinh P, Peng J, Tran T, Wu D, Tran C, Dinh T, Pan S. Identification of hsa_circ_0001445 of a novel circRNA-miRNA-mRNA regulatory network as potential biomarker for coronary heart disease. Front Cardiovasc Med. 2023 Mar 14;10:1104223. doi: 10.3389/fcvm.2023.1104223. PMID: 36998978; PMCID: PMC10043405.