Atherogenesis

Atherogenesis is the process of forming plaques in the intima layer of arteries. Atherosclerosis is developed progressively with inflammation and lipid accumulation varying significantly among individuals.

In an atherosclerotic artery wall, monocyte-derived macrophages are the principal mediators that respond to pathogens and inflammation.

Wang et al. aimed to investigate potential genetic changes in gene expression between normal tissue-resident macrophages and atherosclerotic macrophages in the human body.

The expression profile data of GSE7074 acquired from the Gene Expression Omnibus (GEO) database, which includes the transcriptome of 4 types of macrophages, was downloaded. Differentially expressed genes (DEGs) were identified using R software, then we performed functional enrichment, protein-protein interaction (PPI) network construction, key node, and module analysis, and prediction of microRNAs (MicroRNAs)/transcription factors (TFs) targeting genes. RESULTS After data processing, 236 DEGs were identified, including 21 upregulated genes and 215 downregulated genes. The DEG set was enriched in 22 significant Gene Ontology (GO) terms and 25 Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, and the PPI network constructed with these DEGs comprised 6 key nodes with degrees ≥8. Key nodes in the PPI network and simultaneously involved in the prime modules, including rhodopsin (RHO), coagulation factor V (F5), and bestrophin-1 (BEST1), are promising for the prediction of atherosclerotic plaque formation. Furthermore, in the MicroRNA/TF-target network, hsa-miR-3177-5p might be involved in the pathogenesis of -atherosclerosis via regulating BEST1, and the transcription factor early growth response-1 (EGR1) was found to be a potential promoter in atherogenesis.

The identified key hub genes, predicted MicroRNAs/TFs, and underlying molecular mechanisms may be involved in atherogenesis, thus potentially contributing to the treatment and diagnosis of patients with atherosclerotic disease [1)].

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Wang W, Zhang K, Zhang H, Li M, Zhao Y, Wang B, Xin W, Yang W, Zhang J, Yue S, Yang X. Underlying Genes Involved in Atherosclerotic Macrophages: Insights from Microarray Data Mining. Med Sci Monit. 2019 Dec 25;25:9949-9962. doi: 10.12659/MSM.917068. PubMed PMID: 31875420.