# EGR1

EGR1 (Early growth response protein 1) also known as Zif268 (zinc finger protein 225) or NGFI-A (nerve growth factor-induced protein A) is a protein that in humans is encoded by the EGR1 gene.

EGR-1 is a mammalian transcription factor. It was also named Krox-24, TIS8, and ZENK. It was originally discovered in mice.

---

A study aims to explore the molecular mechanism of Egr1 and Phlda1 in regulating hemin-induced neuronal pyroptosis, and hope to provide novel therapeutic targets for ICH treatment. Mouse hippocampal neuron cells treated with hemin were used to simulate an in-vitro ICH model. Using qRT-PCR and western blot to evaluate mRNA and protein concentrations. MTT assay was utilized to assess cell viability. LDH levels were determined by lactate Dehydrogenase Activity Assay Kit. IL-1β and IL-18 levels were examined by ELISA. The interaction of Egr1 and Phlda1 promoter was evaluated using chromatin immunoprecipitation and dual-luciferase reporter assays. Egr1 and Phlda1 were both upregulated in HT22 cells following hemin treatment. Hemin treatment caused a significant reduction in HT22 cell viability, an increase in Nlrc4 and HT22 cell pyroptosis, and heightened inflammation. However, knocking down Egr1 neutralized hemin-induced effects on HT22 cells. Egr1 bound to the promoter of Phlda1 and transcriptionally activated Phlda1. Silencing Phlda1 significantly reduced Nlrc4-dependent neuronal pyroptosis. Conversely, overexpressing Phlda1 mitigated the inhibitory effects of Egr1 knockdown on Nlrc4 and neuronal pyroptosis during ICH. Egr1 enhanced neuronal pyroptosis mediated by Nlrc4 under ICH via transcriptionally activating Phlda1 [1)].

---

---

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 [2].

1)
Wang J, Gu D, Jin K, Shen H, Qian Y. Egr1 promotes Nlrc4-dependent neuronal pyroptosis through phlda1 in an in-vitro model of intracerebral hemorrhage. Neuroreport. 2024 Apr 17. doi: 10.1097/WNR.0000000000002035. Epub ahead of print. PMID: 38652514.
2)
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.