

Genome-wide transcriptional analysis of cardiovascular-related genes and pathways induced by PM_{2.5} in human myocardial cells

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Abstract

Air pollution has been a major environment-related health threat. Most of the studies on PM_{2.5} toxicity have verified on the cardiovascular system and endothelial cells. However, researches on PM_{2.5}-induced myocardial-related toxicity are limited. This study aims to fully understand the toxic effects of PM_{2.5} on human myocardial cell (AC16) and explore its molecular mechanism based on microarray analysis and bioinformatics analysis. Microarray data analysis manifested that PM_{2.5}-induced toxicity affected expression of 472 genes compared with the control group, including 166 upregulated genes and 306 downregulated genes in human myocardial (AC16) cells. GO analysis showed that cellular processes such as immune response, cell maturation, embryonic heart tube morphogenesis, cellular response to electrical stimulus, skeletal muscle tissue regeneration, and negative regulation of signal transduction were upregulated, while regulation of transcription (DNA-dependent), rhythmic process, protein destabilization apoptotic process, and innate immune response were downregulated. The pathway analysis indicates that cell signaling pathways such as cytokine-cytokine receptor interaction, NF-κB signaling pathway, chemokine signaling pathway, endocrine and other factor-regulated calcium reabsorption, HTLV-I infection, and cell adhesion molecules (CAMs) were

upregulated, while the TGF- β signaling pathway was downregulated. In addition, Signal-net showed that the *TUBA4A*, *ADRBK2*, *BRIX1*, *SMC4*, *EIF5B*, *PRMT1*, *ATG4B*, and *NDC80* genes were significantly decreased, while the expression of the *KRT6B* gene was markedly increased compared with the control group. All the genes were verified by qRT-PCR. This study had provided new bioinformatics evidences in PM_{2.5}-induced myocardial tissue toxicity which is necessary for further cardiovascular system toxicity studies.

Keywords

PM_{2.5} Microarray analysis Bioinformatics analysis Human myocardial cells Signaling pathway Signal-net