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Gene profiles to characterize the combined toxicity induced by low level co-exposure of silica nanoparticles and benzo[a]pyrene using whole genome microarrays in zebrafish embryos.

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Abstract

Several studies have suggested that air pollutants combine exposure have greater adverse effects. However, limited studies were available on the combined toxicity of silica nanoparticles (SiNPs) and benzo[a]pyrene (B[a]P). The study was to evaluate the toxic effect and mechanisms of low-dose exposure of SiNPs, B[a]P and co-exposure in zebrafish embryos. In this study, zebrafish embryos received intravenous microinjection of SiNPs and B[a]P, and then was used to select differentially expressed genes by microarray analysis. Multiple bioinformatics analyses and STC analysis were done to identify key genes, pathways and biological processes and the expression trend of genes in each group. 1) 3065 differentially expressed genes were identified in zebrafish embryos. 2) These differentially expressed genes were involved in multiple biological processes and cellular processes such as immunity, response to stimuli, cell proliferation, adhesion, signaling transduction, and embryonic development. 3) Dynamic Gene Network analysis was used to identify a subgroup of 26 core genes that involved in multiple biological processes and cellular processes. 4) Pathway analysis and Signal-net analysis indicated that the MAPK signaling pathway, calcium signaling pathway, p53 signaling pathway, PI3k/Akt signaling pathway, and several pathways associated with immune response were the most prominent significant pathways induced by co-exposure of SiNPs and B[a]P in zebrafish embryos. Our study demonstrated that the molecular actions of co-treated

with SiNPs and B[a]P on the immune system, inflammatory process and cardiovascular development had more severe toxicity than single exposure.

KEYWORDS:

Benzo[a]pyrene; Combined toxicity; Genome microarrays; Silica nanoparticles; Zebrafish embryos