Science of The Total Environment
Volumes 607–608, 31 December 2017, Pages 795-805

Comprehensive gene and microRNA expression profiling on cardiovascular system in zebrafish co-exposured of SiNPs and MeHg.

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Abstract

Air pollution has been shown to increase cardiovascular diseases. However, little attention has been paid to the combined effects of PM and air pollutants on the cardiovascular system. To explore this, a high-throughput sequencing technology was used to determine combined effects of silica nanoparticles (SiNPs) and MeHg in zebrafish. Our study demonstrated that SiNPs and MeHg co-exposure could cause significant changes in mRNA and miRNA expression patterns in zebrafish. The differentially expressed (DE) genes in profiles 17 and 26 of STC analysis suggest that SiNPs and MeHg co-exposure had more proinflammatory and cardiovascular toxicity in zebrafish than single exposure. Major gene functions associated with cardiovascular system in the co-exposed zebrafish were discerned from the dynamic-gene-network, including stxbp1a, celf4, ahr1b and bai2. In addition, the prominently expressed pathway of cardiac muscle contraction was targeted by 3 DE miRNAs identified by the miRNA-pathway-network (dre-miR-7147, dre-miR-26a and dre-miR-375), which included 23 DE genes. This study presents a global view of the combined SiNPs and MeHg toxicity on the dynamic expression of both mRNAs and

miRNAs in zebrafish, and could serve as fundamental research clues for future studies, especially on cardiovascular system toxicity.

KEYWORDS:

Cardiovascular system; Combined toxicity; MeHg; SiNPs; Transcriptional analysis