ABSTRACT

Ambient particulate matter (PM) collected in the vicinity of five industries (Cement, Chemical, Thermal power plant, Sponge-iron and Steel) in Tamil Nadu state, India were characterized for size distribution, metals and polycyclic aromatic hydrocarbons (PAHs) content. Genotoxicity of PM and organic matter (OM) extracted from PM was measured in human lung cancer cell-line, A549 and in human liver carcinoma cell-line, HepG2, respectively, using the comet assay. PM values varied from 57.0µg/m³ of air at Cement industry upstream to 561.0µg/m³ of air at Sponge iron industry downstream samples. Their metal content varied from 5.758µg/m³ of air at Chemical industry to 46.144µg/m³ of air at Sponge iron industry and PAH concentration varied from 0.5ng/m³ air in upstream Thermal power plant to 3302.4ng/m³ air in downstream Sponge iron industry samples. While all PM samples induced DNA strand breaks at higher dose levels, downstream samples of Steel and Sponge iron industries which contained relatively higher concentrations of PAHs and metals and exhibited higher levels of pro-oxidant activity as measured by DTT activity induced significantly higher levels of DNA damage in HepG2 and A549 cells. Pretreatment of A549 cells with vitamin C or quercetin significantly reduced PM induced DNA strand breaks. Further proteomic analysis of Steel industry and Sponge iron industry ambient was done by treating A549 cells with PM for 24-hr and the cell lysates were analyzed using quantitative label-free nano LC-MS/MS. A total of 1576 proteins were identified and quantified, with 240 had significantly altered expression in the Steel industry PM treated cells. However, in the sponge iron industry PM treated cells only 27 proteins had shown differential expression. Enrichment analyses revealed that a broad range of cellular and metabolic components were altered upon exposure to steel PM. The 128 up regulated
proteins included mainly of RNA metabolism (73 proteins) like ncRNA metabolism (36 proteins) and RNA splicing (23 proteins). Out of 112 down regulated proteins, 49 are associated with small molecule metabolism (carboxylic acid, carbohydrate, amine, and co-factor metabolism), 20 are with regulation of apoptosis and 12 are with protein ubiquitination. Protein-protein interaction network and biological pathway analysis of these differentially expressed proteins were carried out to obtain a systems level view of proteome changes. Together increased levels of proteins involved in transcription, mRNA processing and translation and lower levels of ubiquitination and proteosomal proteins reflect a rise in the levels of protein synthesis, characteristically proteins associated to redox homeostsis, metabolism and energy generation were inhibited. It could be inferred that PM exposure induced oxidative stress which could have lead into DNA damage and other stresses. However, lowering of cellular metabolism, and energy production could reduce its ability to overcome these stresses.