

Publication

microRNA expression profiles and personal monitoring of exposure to particulate matter

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An increasing number of findings from epidemiological studies support associations between exposure to air pollution and the onset of several diseases, including pulmonary, cardiovascular and neurodegenerative diseases, and malignancies. However, intermediate, and potentially mediating, biological mechanisms associated with exposure to air pollutants are largely unknown. Previous studies on the human exposome have shown that the expression of certain circulating microRNAs (miRNAs), regulators of gene expression, are altered upon exposure to traffic-related air pollutants. In the present study, we investigated the relationship between particulate matter (PM) smaller than 2.5 μ m (PM; 2.5;), PM; 2.5; absorbance (as a proxy of black carbon and soot), and ultrafine-particles (UFP, smaller than 0.1 μ m), measured in healthy volunteers by 24 h personal monitoring (PEM) sessions and global expression levels of peripheral blood miRNAs. The PEM sessions were conducted in four European countries, namely Switzerland (Basel), United Kingdom (Norwich), Italy (Turin), and The Netherlands (Utrecht). miRNAs expression levels were analysed using microarray technology on blood samples from 143 participants. Seven miRNAs, hsa-miR-24-3p, hsa-miR-4454, hsa-miR-4763-3p, hsa-miR-425-5p, hsa-let-7d-5p, hsamiR-502-5p, and hsa-miR-505-3p were significantly (FDR corrected) expressed in association with PM; 2.5; personal exposure, while no significant association was found between miRNA expression and the other pollutants. The results obtained from this investigation suggest that personal exposure to PM; 2.5; is associated with miRNA expression levels, showing the potential for these circulating miRNAs as novel biomarkers for air pollution health risk assessment.

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