Acute changes in DNA methylation in relation to 24/h personal air pollution exposure measurements : a panel study in four European countries

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 4482665
Author(s) Mostafavi, Nahid; Vermeulen, Roel; Ghantous, Akram; Hoek, Gerard; Probst-Hensch, Nicole; Herceg, Zdenko; Tarallo, Sonia; Naccarati, Alessio; Kleinjans, Jos C. S.; Imboden, Medea; Jeong, Ayoung; Morley, David; Amaral, Andre F. S.; van Nunen, Erik; Gulliver, John; Chadeau-Hyam, Marc; Vineis, Paolo; Vlaanderen, Jelle

Author(s) at UniBasel Probst Hensch, Nicole ; Imboden, Medea ; Jeong, Ayoung ;
Year 2018

Title Acute changes in DNA methylation in relation to 24/h personal air pollution exposure measurements : a panel study in four European countries

Journal Environment international

Volume 120

Pages / **Article-Number** 11-21
One of the potential mechanisms linking air pollution to health effects is through changes in DNA-methylation, which so far has mainly been analyzed globally or at candidate sites.; We investigated the association of personal and ambient air pollution exposure measures with genome-wide DNA-methylation changes.; We collected repeated 24-hour personal and ambient exposure measurements of particulate matter (PM; 2.5;), PM; 2.5; absorbance, and ultrafine particles (UFP) and peripheral blood samples from a panel of 157 healthy non-smoking adults living in four European countries. We applied univariate mixed-effects models to investigate the association between air pollution and genome-wide DNA-methylation perturbations at single CpG (cytosine-guanine dinucleotide) sites and in Differentially Methylated Regions (DMRs). Subsequently, we explored the association of air pollution-induced methylation alterations with gene expression and serum immune marker levels measured in the same subjects.; Personal exposure to PM; 2.5; was associated with methylation changes at 13 CpG sites and 69 DMRs. Two of the 13 identified CpG sites (mapped to genes KNDC1 and FAM50B) were located within these DMRs. In addition, 42 DMRs were associated with personal PM; 2.5; absorbance exposure, 16 DMRs with personal exposure to UFP, 4 DMRs with ambient exposure to PM; 2.5; , 16 DMRs with ambient PM; 2.5; absorbance exposure, and 15 DMRs with ambient UFP exposure. Correlation between methylation levels at identified CpG sites and gene expression and immune markers was generally moderate.; This study provides evidence for an association between 24-hour exposure to air pollution and DNA-methylation at single sites and regional clusters of CpGs. Analysis of differentially methylated regions provides a promising avenue to further explore the subtle impact of environmental exposures on DNA-methylation.
Publisher Elsevier

ISSN/ISBN 0160-4120

edoc-URL https://edoc.unibas.ch/65071/

Full Text on edoc No;

Digital Object Identifier DOI 10.1016/j.envint.2018.07.026

PubMed ID http://www.ncbi.nlm.nih.gov/pubmed/30055357