
IS18. EPIGENETIC ALTERATIONS BY OCCUPATIONAL EXPOSURE

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Occupational factors contribute significantly to global burden of chronic diseases like cancer and neurobehavioural disorders. A clear understanding of underlying mechanisms is crucial for prevention. Epigenetics is currently of major interest, as it provides insight in how cells respond to environmental stimuli. In order to investigate whether occupational exposure induces epigenetic alterations similar as observed in chronic diseases, we carried out several translation studies in workers exposed to solvents and carbon nanotubes to validate DNA methylation alterations observed in *in vitro* and animal studies.

Global DNA methylation and demethylation patterns were studied using LC-MS/MS. Genome-wide assessment of DNA methylation was performed with Infinium HumanMethylation450 BeadChip Array. Levels of methylation of specific genes were measured by pyrosequencing.

We observed in lab settings, global DNA hypomethylation in TK6 cells after exposure to several solvents. DNA hypermethylation was observed in blood DNA of individuals working with solvents. Carbon nanotubes altered *in vitro* methylation and gene expression levels of 17 genes involved in the regulation of transcription, cell development and other cellular processes. In mice, nanoparticles affected methylation of ATM gene but not the global DNA methylation and hydroxymethylation levels. In exposed workers a significant hypermethylation was observed for DNMT1 in bloodcells.

Occupational exposure to solvents and particles induce global and gene specific DNA methylation alterations. It remains to be investigated which epigenetic response to occupational stressors leads to pathological signalling events initiating the disease process.

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