

Heterogeneous Ozone Effects on the DNA Methylome of Bronchial Cells Observed In a Crossover Study

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Abstract

We used a randomized crossover experiment to estimate the effects of ozone (vs. clean air) exposure on genome-wide DNA methylation of target bronchial epithelial cells, using 17 volunteers, each randomly exposed on two separated occasions to clean air or 0.3-ppm ozone for two hours. Twenty-four hours after exposure, participants underwent bronchoscopy to collect epithelial cells whose DNA methylation was measured using the Illumina 450 K platform. We performed global and regional tests examining the ozone versus clean air effect on the DNA methylome and calculated Fisher-exact p-values for a series of univariate tests. We found little evidence of an overall effect of ozone on the DNA methylome but some suggestive changes in PLSCR1, HCAR1, and LINC00336 DNA methylation after ozone exposure relative to clean air. We observed some participant-to-participant heterogeneity in ozone responses.