Publication

Genome-wide DNA methylation in peripheral blood and long-term exposure to source-specific transportation noise and air pollution: the SAPALDIA study

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Few epigenome-wide association studies (EWAS) on air pollutants exist, and none have been done on transportation noise exposures, which also contribute to environmental burden of disease.; We performed mutually independent EWAS on transportation noise and air pollution exposures.; We used data from two time points of the Swiss Cohort Study on Air Pollution and Lung and Heart Diseases in Adults (SAPALDIA) from 1,389 participants contributing 2,542 observations. We applied multiexposure linear mixed-effects regressions with participant-level random intercept to identify significant Cytosine-phosphate-Guanine (CpG) sites and differentially methylated regions (DMRs) in relation to 1-y average aircraft, railway, and road traffic day-evening-night noise (Lden); nitrogen dioxide (; NO; 2;); and particulate matter (PM) with aerodynamic diameter; <; 2.5; μ; m; (; PM; 2.5;). We performed candidate (CpG-based; cross-systemic phenotypes, combined into ”allostatic load”) and agnostic (DMR-based) pathway enrichment tests, and replicated previously reported air pollution EWAS signals.; We found no statistically significant CpGs at false discovery rate; <; 0.05; . However, 14, 48, 183, 8, and 71 DMRs independently associated with aircraft, railway, and road traffic Lden;; NO; 2; ; and; PM; 2.5; , respectively, with minimally overlapping signals. Transportation Lden and air pollutants tendentially associated with decreased and increased methylation, respectively. We observed significant enrichment of candidate DNA methylation related to C-reactive protein and body mass index (aircraft, road traffic Lden, and; PM; 2.5;), renal function and ”allostatic load” (all exposures). Agnostic functional networks related to cellular immunity, gene expression, cell growth/proliferation, cardiovascular, auditory, embryonic, and neurological systems development were enriched. We replicated increased methylation in cg08500171 (; NO; 2;) and decreased methylation in cg17629796 (; PM; 2.5;).; Mutually independent DNA methylation was associated with source-specific transportation noise and air pollution exposures, with distinct and shared enrichments for pathways related to inflammation, cellular development, and immune responses. These findings contribute in clarifying the pathways linking these exposures and age-related diseases but need further confirmation in the context of mediation analyses. https://doi.org/10.1289/EHP6174.
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