Epigenetic footprints of industrial hazards: discovering methylation markers and their disease associations.

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Environmental pollutants, notably heavy metals, are recognized inducers of epigenetic alterations, which can negatively impact human health. This study aimed to identify methylation markers indicative of environmental hazards by comparing residents living near environmental risk facilities to controls. Utilizing Reduced-representation bisulfite sequencing (RRBS) data, an in-depth Differentially Methylated Regions (DMR) analysis was performed, leading to the identification of precise markers through Meet-in-the-middle analysis. Mendelian Randomization (MR) analysis, supplemented with SNP data, further illuminated diseases associated with these markers. Remarkably, two primary DMRs were pinpointed, each exhibiting a causal relationship with five distinct diseases. Notably, residents in heavy metal-exposed zones, like mines and refineries, manifested specific epigenetic markers. Moreover, findings suggest that these markers might not only signify environmental contamination due to heavy metals but also validate their reliability in future analyses. This study underscores the potential of methylation markers as environmental health indicators and their pivotal role in understanding disease causality.