Epigenetic Footprints of Pollutant Exposure: DNA Methylation Changes Reflecting Sewage-Worker Analog Conditions

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Abstract

Sewage workers all around the world have been subjected to hazardous working conditions daily. The continuous exposure to toxins like heavy metals, industrial chemicals, and pharmaceuticals can cause oxidative stress, which disrupts normal gene regulation and, in turn, triggers epigenetic changes like DNA methylation. Thus, this study investigates epigenomic footprints in sewage workers through the analysis of datasets from individuals exposed to environmental pollutants or infectious agents present in sewage. The bioinformatics approach was used, utilizing various websites and software like NCBI Pubmed, GEO, EWAS, STRING database, Cytoscape, bioDBnet, and Google Sheets for data collection and processing. Analysis of the expression dataset generated a list of 411 differentially expressed genes. From network and pathway analysis and comparing top ten key hub genes were identified. From trend scoring, network, and EWAS study, 3 topmost methylation scar genes were identified, which were: Aconitase 2 (ACO2), Erb-B2 Receptor Tyrosine Kinase 2 (ERBB2), and Heme Oxygenase 1 (HMOX1). The future scope of the study includes the development of better and more advanced technology, which can make the work of these sanitation workers safer. Moreover, it helps in creating awareness as to how the sewage workers might not only be falling sick very frequently due to these infectious substances but also falling victim to chronic diseases due to DNA methylation, which remains unidentified. Thus, more research can be conducted on how these can be easily identified and treated, if possible, so that future generations do not have to face the consequences.