

# Impact of Ambient Particulate Matter on the DNA Methylation of Asthma-related Genes in Bronchial Epithelial Cells

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*Pollution is made of many toxic components that contribute to disease. Particulate matter (PM) is classified by its size (e.g. <10 µm [PM<sub>10</sub>] or <2.5 µm [PM<sub>2.5</sub>]). PM<sub>2.5</sub> is considered more harmful than PM<sub>10</sub> because it can penetrate deeper into the lungs and enter the bloodstream. PM<sub>2.5</sub> contains numerous toxic chemicals such as polycyclic aromatic hydrocarbons (PAHs), metals, and fine particles. These components can cause respiratory and cardiovascular diseases, as well as cancer. PM<sub>2.5</sub> has been linked to increased mortality and hospital admissions for heart and lung conditions. It can also affect gene expression and DNA methylation patterns. In this study, we investigated the impact of ambient PM<sub>2.5</sub> on the DNA methylation of asthma-related genes in bronchial epithelial cells. We found that exposure to PM<sub>2.5</sub> led to significant changes in the methylation levels of several key genes involved in asthma pathophysiology. These changes were associated with altered gene expression and cellular function. Our results suggest that PM<sub>2.5</sub> may play a role in the development and progression of asthma through epigenetic mechanisms. Further research is needed to fully understand the complex interactions between PM<sub>2.5</sub> and gene regulation in the context of respiratory diseases.*

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