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World Trade Center exposure linked to increased DNA methylation

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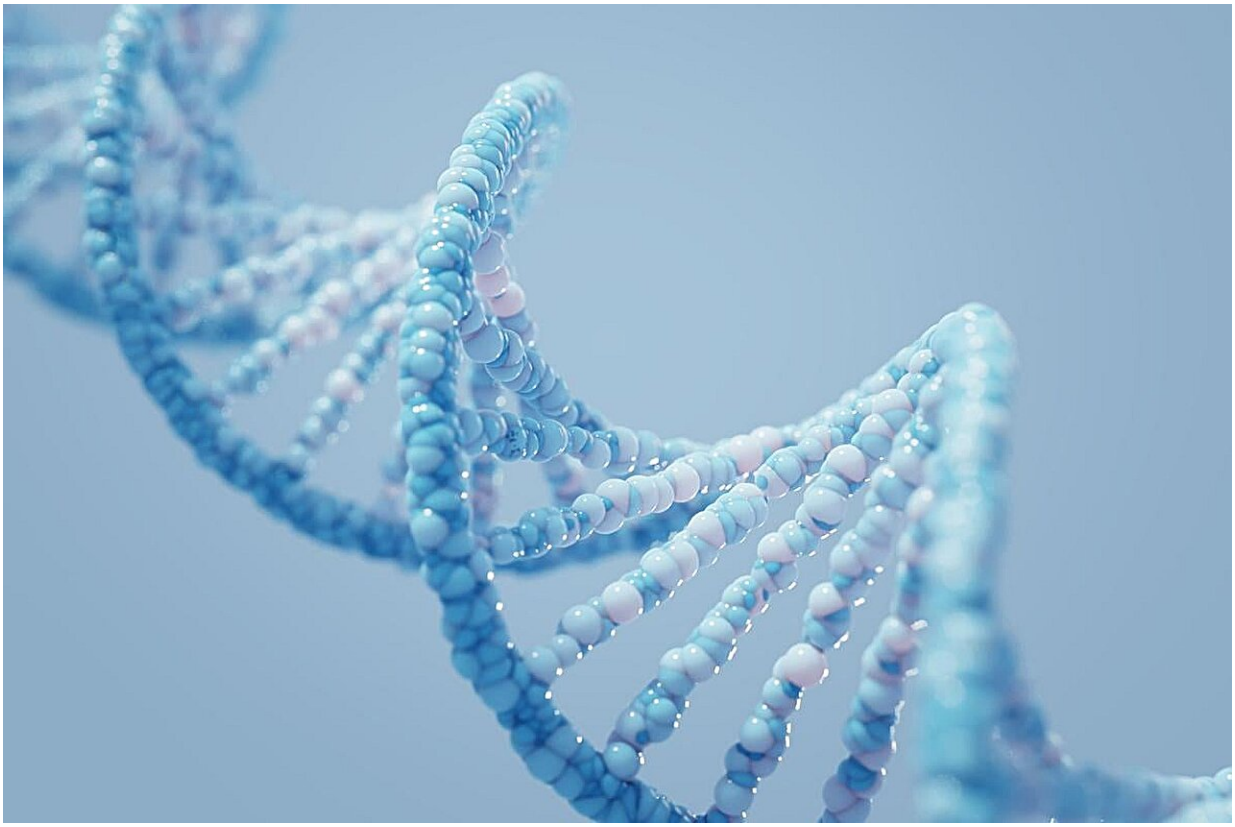

World Trade Center (WTC) exposure is associated with increased DNA methylation, which may contribute to breast cancer, according to a study published in the June issue of *Environmental Epidemiology*.

Stephanie Tuminello, Ph.D., M.P.H., from the NYU Grossman School of Medicine in New York City, and colleagues examined the DNA methylation profiles of WTC-exposed community members who remained cancer-free versus those who developed breast cancer. The study included 64 WTC-exposed women (32 cancer-free, 32 with breast cancer) and 32 WTC-unexposed women from the NYU Women's Health Study (16 cancer-free and 16 with prediagnostic breast cancer).

The researchers found that compared with unexposed participants, WTC-exposed women more often had hypermethylated cytosine-phosphate-guanine probe sites (14.3 versus 4.5 percent). In WTC-exposed groups (breast cancer patients and cancer-free individuals), cancer-related pathways were overrepresented. Forty-seven epigenetically dysregulated genes were identified among WTC-exposed breast cancers compared with the unexposed breast cancer patients. A network was formed from these genes, including Wnt/β-catenin signaling genes *WNT4* and *TCF7L2*; dysregulation of these genes contributed to cancer immune evasion.

"WTC exposure is associated with global and site-specific DNA methylation changes. This was observed among cancer-free WTC-exposed survivors as well as those with breast cancer," the authors write. "Several cancer-related genes and pathways appear to be impacted, and, specifically, WTC exposure may compromise the ability of the immune system to identify and eliminate cancer cells contributing to cancer immune evasion."

More information: Stephanie Tuminello et al, Genome-wide DNA methylation profiles and breast cancer among World Trade Center survivors, *Environmental Epidemiology* (2024). DOI: 10.1097/EE9.0000000000000313