

# 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/ $\beta$ -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](#)



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