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Biomarkers of DNA methylation can be a predictor of breast cancer risk

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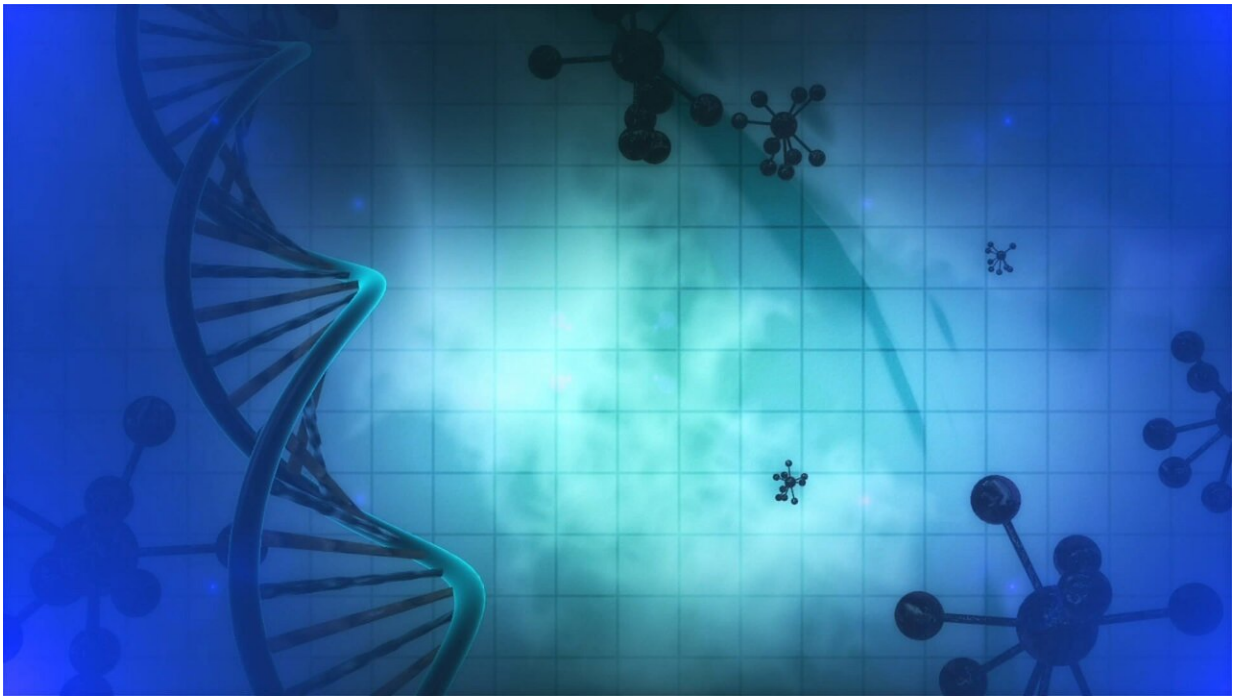

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Biomarkers of DNA methylation, which regulate gene expression, can be a predictor of breast cancer risk, according to a study published in *Journal of the National Cancer Institute*.

Vanderbilt's Jirong Long, Ph.D., associate professor of Medicine, Division of Epidemiology, and colleagues conducted a methylation-wide

association (MeWAS) study of data from 228,951 women of European descent with the goal of identifying new genes and methylation markers associated with breast cancer risk. They discovered 450 DNA methylation sites associated with breast cancer, including 45 sites located in novel chromosome regions that had not been previously reported for breast cancer.

Integrative analyses of genetic DNA methylation and gene expression data found that 38CpGs may affect breast cancer risk through regulating expression of 21 genes.

"This study used a novel approach to investigate DNA methylation in hundreds of thousands of participants," Long said.

In conducting the MeWAS study, Long and colleagues came up with a new methodology for identifying novel DNA methylation biomarkers that can be applied to other diseases. They first built statistical models to predict DNA methylation levels via multiple genetic variants in a reference dataset, then validated the models in independent samples, and then applied the prediction models to a large genetic dataset to test the genetically-determined methylation level with disease risk.

"Our novel methodology overcomes limitations of traditional epidemiological studies and is more accurate and powerful than studies based on a single meQTL approach," the researchers wrote.

Provided by Vanderbilt University

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