

Researchers discover key role of DNA methylation in Alzheimer's disease

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Mount Sinai researchers have published a study in *Alzheimer's & Dementia: The Journal of the Alzheimer's Association* that sheds new light on the role of DNA methylation in Alzheimer's disease (AD). The study

found that DNA methylation has a profound impact on gene and protein co-expression networks associated with AD and could lead to the discovery of new neuropathological processes and molecular mechanisms for developing novel treatments for the disease.

The study was conducted using a novel analytical approach to quantify the impact of DNA methylation on gene and protein expression and a large cohort of post-mortem control, mild cognitive impaired (MCI), and AD brains from the Mount Sinai Brain Bank. The researchers profiled genome-wide methylomic variations in the [parahippocampal gyrus](#), a region of the brain involved in a variety of functions including memory processing, and investigated the influence of these changes on mRNA and protein co-expression networks. They discovered 270 distinct differentially methylated regions (DMRs) in AD compared to normal controls and validated their key findings using an independent cohort (Religious Orders Study and Memory Assessment Project, ROSMAP).

"Our study represents the first comprehensive effort to integrate high-throughput profiling of multi-omics in Alzheimer's disease," said senior author, Bin Zhang, Ph.D., Willard T.C. Johnson Research Professor of Neurogenetics and Director of the Mount Sinai Center for Transformative Disease Modeling. "It provides a framework for future data integration at the multi-scale network level and could lead to the discovery of new targets for [drug discovery](#) in Alzheimer's disease."

The results of this study offer a novel approach to investigating the relationship between DNA methylation and gene/[protein expression](#), and highlight the importance of epigenetic mechanisms in human diseases such as AD. The researchers plan to extend their methods to study the methylomic variation and impacts on multiscale networks at the single-cell level, which could provide new insights into the DNA methylation profiles of individual cell types.

More information: Genome-wide methylomic regulation of multiscale gene networks in Alzheimer's disease, *Alzheimer's & Dementia* (2023). [DOI: 10.1002/alz.12969](https://doi.org/10.1002/alz.12969)

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