

Twin study highlights importance of both genetics and environment on gene activity

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New research highlights the extent to which epigenetic variation is influenced by both inherited and environmental factors.

Epigenetic processes affect the expression or activity of genes without changing the underlying DNA sequence and are believed to be one mechanism by which the environment can interact with the genome.

Now, an international group of researchers including teams from the University of Exeter, King's College London, and Duke University in the USA have published a study in *PLOS Genetics*, using a unique cohort of over 700 pairs of twins to identify the factors influencing chemical modifications to DNA across the genome. In the study, funded by the Medical Research Council, the team compared the similarities between identical and non-identical twins, and found that [epigenetic marks](#) are more similar between identical twins—highlighting the role of DNA sequence variation in regulating gene activity. They also found that sites at which epigenetic variation is strongly linked to environmental exposures—such as smoking and obesity—are also partly under genetic control.

Professor Jonathan Mill, of the University of Exeter Medical School, led the study. He said: "These results highlight how both heritable and [environmental factors](#) can influence the way in which [genes](#) are expressed and function, with important implications for studies of health and disease."

Dr. Eilis Hannon, of the University of Exeter Medical School, was first author on the paper. She commented "Our study provides a useful framework for interpreting the results of epigenetic epidemiological studies and shows that epigenetic differences are a potential mechanism linking genetic variation to gene regulation."

The paper, "Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins", is published in *PLOS Genetics*.

More information: Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. / Hannon, Eilis; Knox, Olivia; Sugden, Karen; Burrage, Joe; Wong, Chloe Chung Yi; Belsky, Daniel; Corcoran, David L.;

Arseneault, Louise; Moffitt, Terrie Edith; Caspi, Avshalom; Mill, Jonathan. In: *PLoS genetics*, 06.07.2018.

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