

Tying our fate to molecular markings

October 11 2012

(Phys.org)—A Simon Fraser University physicist has helped discover that understanding how a chemical mark on our DNA affects gene expression could be as useful to scientists as fingerprints are to police at a crime scene.

In a new study, Emberly and his colleagues cite proof that variable methylation, a chemical mark on our DNA, is predictive of age, gender, stress, cancer and early-life socioeconomic status within a population. The [Proceedings of the National Academy of Sciences \(PNAS\)](#) has just published the study online.

Working with researchers at the University of British Columbia and Stanford University, Eldon Emberly studied the variation of methylation over a large group of individuals.

DNA that is methylated in our genomes is known to affect whether genes are turned on or off. [Gene expression](#) predicates several attributes linked to our identity, such as gender, ethnicity, age and health.

The trio measured methylation from DNA in the [white blood cells](#) of 92 people aged 24 to 45. Emberly's lab helped to mine the resulting data sets for correlations between variation in the chemical mark and variable social, psychological and [physical traits](#) in the subjects.

The results demonstrated that those who had experienced childhood poverty had a different methylation level from those who hadn't. This was despite the fact everyone in the cohort had achieved the same

[socioeconomic status](#) later in life.

That meant that early-life environment had left a detectable molecular mark on an individual's DNA.

The correlation between methylation and gene expression was complex because it wasn't always predictable but there was one connection of particular note says Emberly, an SFU associate professor.

"Variable methylation correlated with variable expression of the gene DDX4, which is linked to certain cancers."

Emberly says this study's discoveries raise interesting questions, as the connection between methylation and some traits, such as smoking and [alcohol consumption](#), was weaker than expected or non-existent.

"We're now investigating whether methylation variation in different types of tissue is more predictive of some trait," adds Emberly.

Pau Farre, a master's of science student in physics under Emberly's supervision, is doing a statistical analysis of the variability in methylation across tissues.

More information: Factors underlying variable DNA methylation in a human community cohort, [doi: 10.1073/pnas.1121249109](https://doi.org/10.1073/pnas.1121249109)

Provided by Simon Fraser University

Citation: Tying our fate to molecular markings (2012, October 11) retrieved 27 April 2024 from <https://phys.org/news/2012-10-tying-fate-molecular.html>

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