

Your DNA may carry a 'memory' of your living conditions in childhood

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(Medical Xpress) -- Family living conditions in childhood are associated with significant effects in DNA that persist well into middle age, according to new research by Canadian and British scientists.

The team, based at McGill University in Montreal, University of British Columbia in Vancouver and the UCL Institute of [Child Health](#) in London looked for gene methylation associated with social and [economic factors](#) in early life. They found clear differences in gene methylation between those brought up in families with very high and very low standards of living. More than twice as many methylation differences were associated with the combined effect of the wealth,

housing conditions and occupation of parents (that is, early upbringing) than were associated with the current socio-economic circumstances in adulthood. (1252 differences as opposed to 545).

The findings, published online today in the [International Journal of Epidemiology](#), could provide major evidence as to why the health disadvantages known to be associated with low socio-economic position can remain for life, despite later improvement in living conditions. The study set out to explore the way early life conditions might become ‘biologically-embedded’ and so continue to influence health, for better or worse, throughout life. The scientists decided to look at [DNA](#) methylation, a so-called epigenetic modification that is linked to enduring changes in gene activity and hence potential health risks. (Broadly, methylation of a gene at a significant point in the DNA reduces the activity of the gene.)

Researchers focussed on 40 UK participants in an ongoing study that has documented many aspects of the lives of over 10,000 people born in March 1958 from birth onwards.

The researchers studied DNA that was prepared from blood samples taken when the participants were 45 years old. They chose people who experienced either very high or very low standards of living as children or adults, to study any differences in DNA methylation that might exist between people with very different living conditions. The analysis measured DNA methylation differences between socio-economic groups at the control regions of over 20,000 genes.

“This is the first time we’ve been able to make the link between the economics of early life and the biochemistry of DNA,” says Moshe Szyf, McGill professor of Pharmacology.

“If we think of the genome as sentences, your DNA, or letters are what

is inherited from your father and mother. The DNA methylation is like the punctuation marks that determine how the letters should be combined into sentences and paragraphs that are read differently in the different organs of the body the heart, the brain, and so on,” Szyf explains. “What we’ve learned is that these punctuation marks are attentive to signals that come from the environment, and that they take cues from living conditions in childhood. Essentially, they act as a mechanism, we believe, for adapting the DNA to the fast changing world.”

“We found a surprising amount of variation in DNA methylation – over 6000 gene control regions showed clear differences between the 40 research participants” said author Emeritus Professor Marcus Pembrey, UCL Institute of Child Health. “Within this widespread variation, there was a distinct DNA methylation profile associated with high living standards in both childhood and as an adult. Even more surprising, given the DNA was obtained at 45years, methylation levels for 1252 gene promoters were associated with childhood living conditions compared to 545 promoters for living conditions in adulthood.”

The methylation profiles associated with childhood family living conditions were clustered together in large stretches of DNA, which suggests that a well-defined epigenetic pattern is linked to early socio-economic environment. “The adult diseases already known to be associated with early life disadvantage include coronary heart disease, type 2 diabetes and respiratory disorders,” said author, Chris Power, Professor of Epidemiology and Public Health at the UCL Institute of Child Health, “so it is hoped that future research will define which network of genes showing methylation differences are in turn associated with particular diseases.”

“The current research represents just a beginning because it cannot tell us precisely when in [early life](#) these epigenetic patterns arose or what the

long-term health effects will be” said Prof Power. “This knowledge will be needed before useful interventions can be considered, but that must be the long term aim”.

The study did not show:

- specific disease effects linked to these areas of DNA methylation differences
- or indeed whether there were positive or protective effects
- or whether these changes might be passed on to offspring.

The study was not designed to look at these areas.

Provided by McGill University

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