

A new study provides valuable information on DNA methylation and gene expression in children

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Credit: Alex Losada / Barcelona City Council

A new study led by ISGlobal, an institution supported by "la Caixa" Foundation, identifies associations between DNA methylation patterns and gene expression levels in blood samples from children. The findings, published in *eLife*, provide researchers with a powerful tool to better understand the association between early environmental exposures, epigenetic changes and disease.

Cells from the same individual share the same genome but do not express the same [genes](#). Each cell type expresses a different set of genes, which allows it to exert a unique function. This is regulated by the epigenome—chemical modifications of genome (including DNA methylation), which can turn genes on or off. Besides its central role in regulating development, the epigenome also allows cells to respond to environmental factors. Recently, many studies (called epigenome-wide association studies) have tried to link exposure to [environmental factors](#) with altered DNA methylation patterns and disease. However, most analyses do not allow one to determine if and how these methylated sites affect the expression of nearby genes.

"Identifying associations between DNA methylation levels and [gene expression](#) might help us better interpret epigenome-wide association studies and understand the [biological processes](#) leading to disease," says Mariona Bustamante, researcher at ISGlobal, who co-led the investigation together with Carlos Ruiz-Arenas from the Universitat Pompeu Fabra.

In this study, the research team aimed to identify associations between DNA methylation levels at particular positions of the genome with the expression of nearby genes, called expression quantitative trait methylation or eQTM, using [blood samples](#) from 832 children, aged 6-11 years, of the Human Early Life Exposome (HELIX) project. Firstly, methylation and gene expression levels were assessed for each sample. Secondly, each gene was paired with the closest methylation site or sites.

The analysis identified almost 40,000 significant associations between methylation levels and gene expression. In most cases, the methylation site was quite close to the regulated gene, and in 59% of cases, there was an inverse relationship between methylation and [gene expression levels](#) (meaning higher levels of methylation—lower gene expression). Only

13.8% of the associations identified were also found in adults. "This was expected, as it is known that DNA methylation and gene expression change with age, however differences in study designs can also explain this," explains Carlos Ruiz-Arenas, first author of the study.

"Our results provide a catalog of methylation-gene expression associations that could become a powerful tool to help researchers interpret epigenome-wide association studies in children," notes Bustamante. The catalog is publicly available.

More information: Carlos Ruiz-Arenas et al, Identification of autosomal cis expression quantitative trait methylation (cis eQTM) in children's blood, *eLife* (2022). [DOI: 10.7554/eLife.65310](https://doi.org/10.7554/eLife.65310)

Catalog: helixomics.isglobal.org/

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