

Our epigenome is influenced by our habitat and lifestyle

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Aka Pygmy, Central African Republic. Credit: © Serge BAHUCHET/MNHN/CNRS Photo Library

Research on the genomes of Pygmy hunter-gatherer populations and Bantu farmers in Central Africa, carried out by scientists from the Institut Pasteur and the CNRS in cooperation with French and international teams, has shown for the first time that our habitat and lifestyle can have an impact on our epigenome - the entire system that controls the expression of our genes without affecting their sequence. In this study, the scientists have shown that moving from a forest habitat to an urban environment has a profound impact on the epigenetic patterns of the immune response. Conversely, the different historical lifestyles of these populations - sedentary farming or nomadic hunting and gathering

- are likely to affect more lasting functions, such as those associated with development, by modulating their genetic control via natural selection.

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How do humans adapt to their environment, for example their habitat (forest, rural or urban) and their lifestyle (nomadic hunting and gathering or sedentary farming)? Over the course of human evolution, the environment has exerted selective pressure, resulting in the selection of genetic mutations that are beneficial for our species. Scientists from the Human Evolutionary Genetics Unit (Institut Pasteur/CNRS URA 3012), directed by Lluís Quintana-Murci, CNRS director of research at the Institut Pasteur, have recently proven that the habitat and lifestyle of human populations can also have an epigenetic impact, by bringing about changes that modulate gene expression.

Unlike genetics, which looks at the sequence of the nucleic acids that make up DNA and carry our genes, epigenetics focuses on elements which don't alter the genetic sequence but which may affect gene expression. For this research, the scientists examined epigenetic changes to DNA such as methylation, in which methyl chemical groups are added to the gene sequence (see inset).

To determine the extent to which the environment influences the epigenome, the scientists looked at two populations in Central Africa with different lifestyles and habitats: Pygmies, who are nomadic hunter-gatherers living in forests, and Bantu, sedentary farmers in urban, rural or forest habitats. These two populations separated approximately 60,000 years ago. The scientists also investigated a particular group of Bantu farmers sharing the same forest environment as Pygmies.

The scientists began by comparing the level of genomic methylation in

this specific group of forest-dwelling Bantu with that of urban or rural Bantu. They observed that the recent change in habitat had resulted in changes to the epigenome that mainly affected the functions of the immune system.

At the same time, they compared the methylation of the forest-dwelling Bantu with that of the Pygmies, this time to examine the impact of their lifestyles (the Bantu are farmers, while the Pygmies are hunter-gatherers). The scientists identified differences in the epigenome relating to development (size, bone mineralization, etc.). They observed that these changes affected the physical characteristics that set Bantu apart from Pygmies. They therefore referred to these differences as "historical".

Although epigenetic changes such as DNA methylation can be strongly affected by the environment, they are not passed on from generation to generation. However, they can become hereditary when they are controlled by a mutation in the DNA. The researchers proved that the "recent" changes to the epigenome which affect immunity did not involve genetic control, whereas the "historical" differences did include an element of [genetic control](#), making them hereditary and long-lasting.

These results partly explain why some people are predisposed to certain diseases. "Our research shows that changing lifestyles and habitats have a major influence on our epigenome and that urbanization significantly affects the epigenetic profiles of the immune system. This demonstrates how important it is, alongside more traditional genetic research, to investigate how epigenetic changes could result in an immune system that is more prone to the development of autoimmune diseases, allergies, inflammation and so on," explains Lluís Quintana-Murci.

This type of study, which combines population genetics and epigenetics, may soon be applied to other populations so as to identify which

biological functions are most affected by our increasingly changing environments, lifestyles and habitats.

The [epigenome](#) refers to all the changes in DNA that modulate gene activity without actually changing the genetic sequence. DNA methylation is one of these changes. A methyl group is a molecule bound to the sequence of a gene. Genes with several methyl groups are under-expressed, while genes with virtually no methyl groups are over-expressed. While methylation does not actually change the [genetic sequence](#), it can have a significant impact on gene activity. These [epigenetic changes](#) are much more flexible and occur much more quickly than genetic mutations.

More information: Maud Fagny et al. The epigenomic landscape of African rainforest hunter-gatherers and farmers, *Nature Communications* (2015). [DOI: 10.1038/ncomms10047](https://doi.org/10.1038/ncomms10047)

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