

# Environmental change leaves its footprint in the epigenome

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The experiment was carried out with wild-caught mice that were kept in enclosures instead of the usual cages. In this setup the mice build nests, populate them with family groups and females may practice communal rearing of the young. Credit: A. Börsch-Haubold

(Phys.org) —Monozygotic twins look more similar when they are young than later in life. One of the reasons for this is epigenetic change in the

form of chemical modifications of the DNA or its packaging proteins. Environmental factors can influence these modifications over a lifetime. Scientists at the Max Planck Institute for Evolutionary Biology in Plön have now for the first time investigated one such epigenetic mark in wild mice and found that it changes in response to a switch to an energy-rich diet and longer daylight hours. This activates genes in the liver involved in metabolizing the energy-rich diet. However, these adaptations to mild environmental variation are not passed on to the next generation. Similar environmental change may also influence epigenetic marks in humans.

Epigenetic change can affect DNA and its histone packaging proteins. It may be caused by any number of [environmental factors](#) including diet, population density, and stress. The specific modification investigated by the scientists from Plön is the triple methylation of a specific lysine in one of the [histone proteins](#). This activates genes located next to the modified histone protein.

To ensure reproducibility, most epigenetic studies are carried out on inbred mouse strains or cell lines. However, this makes it difficult to study the epigenetic consequences of natural environmental change in connection with individual genomic diversity. The scientists at the Max-Planck-Institute in Plön have therefore used wild-caught house mice (*Mus musculus*) to investigate the effect of diet and day length on epigenetic changes of histone proteins.

They raised two mouse populations in semi-natural enclosures with different food and day lengths. Instead of the standard chow containing eleven percent fat, the treatment group was given a chow containing 22 percent fat. This group was also exposed to 18-hour days instead of the standard 12 hours to mimic the rich food and long days of summer.

The Max Planck scientists observed the two populations over several generations for eight months. They measured genome-wide histone tri-

methylation in the livers of young animals whose parents were already born under the experimental conditions.

The shift in fat, carbohydrate and protein content of the diet did not lead to the addition or deletion of marked positions in the genome. "A healthy liver cell remains a healthy liver cell; a change in the number of marked positions would probably indicate the onset of disease", explains Angelika Börsch-Haubold from the Max-Planck Institute for Evolutionary Biology the absence of qualitative changes in the epigenome.

Using custom-made databases and software, the scientists discovered that the histone modifications changed quantitatively in response to the new conditions. This led to the activation of genes for fat and cholesterol metabolism, as well as bile production. "These changes enable the animals to better digest the fat-rich diet", says Börsch-Haubold.

The changes were not passed on to the offspring. In contrast, it is known that catastrophic events like famine or trauma may cause epigenetic change that is heritable over several generations. But epigenetic changes in response to milder environmental variation remain confined to a single generation. "Our study shows for the first time that a natural [environmental change](#) influences the epigenome of wild animals", says Börsch-Haubold. Next the scientists plan to investigate at what stage in the lifecycle of an animal the environment influences [epigenetic changes](#)

**More information:** Börsch-Haubold AG, Montero I, Konrad K, Haubold B (2014) "Genome-Wide Quantitative Analysis of Histone H3 Lysine 4 Trimethylation in Wild House Mouse Liver: Environmental Change Causes Epigenetic Plasticity." *PLoS ONE* 9(5): e97568. [DOI: 10.1371/journal.pone.0097568](https://doi.org/10.1371/journal.pone.0097568)

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