

# Exposure to metals changes gene regulation in wild great tit populations

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Epigenetic changes are one of the less studied mechanisms via which organisms adapt to environmental changes. Epigenetic changes, such as DNA methylation, do not alter DNA sequence, but regulate gene

expression. Two new studies showed that nestling exposure to metals, lead and arsenic, alters great tit DNA methylation patterns. This could influence gene expression, and either help to adapt to polluted environments or lead to detrimental, even long-lasting, consequences.

Genes code life. Gene expression is regulated by epigenetic markers, which attach to DNA and can increase or decrease [gene expression](#). Methyl groups that bind to DNA are one of the most studied epigenetic markers. Many [environmental factors](#) are known to influence DNA methylation, ie. binding of methyl groups to DNA.

Metal pollution has increased because of emissions from traffic, industry and mining activities. Metals are stable pollutants, and therefore present long after emissions have ceased. One of the studied metals, arsenic, has been classified as one of the most harmful environmental toxins.

Laboratory animals are most often used to study the effects of metals on organisms, including also DNA methylation. The concentrations in these studies are however often higher than environmentally relevant levels in wild populations. Species also respond to pollutants very differently, and therefore results from laboratory animals are not always applicable to other taxa.

"We know that developing individuals are especially sensitive to environmental pollutants, and that these effects can be long-lasting. Yet we don't fully understand why this is. Epigenetic changes are one potential mechanism", says Assistant Professor Suvi Ruuskanen from the Department of Biological and Environmental Sciences at the University of Jyväskylä.

The international research team studied experimentally, whether exposure to environmentally relevant levels of arsenic or lead influences DNA methylation in nestlings.

"We compared these new results to similar data collected from birds at Harjavalta, Finland, copper smelter. In this area, birds are exposed to different types of metals but also poorer food quality and availability of food" says Tapio Eeva, University Lecturer from the Department of Biology at the University of Turku.

The researchers report that exposure to arsenic influenced DNA methylation in genes associated with development. Exposure to lead affected especially genes related to neural development. Nestlings from the polluted area in Harjavalta showed the largest changes. These changes could be related to the direct effects of metals or effects of metals on the environment, such as food quantity and quality.

"Many previous studies have concentrated on prenatal changes in DNA methylation, but our results confirm that the environment alters epigenetic code also at later life-stages. The future will tell how stable these changes are", says researcher Veronika Laine from the Natural history museum at the University of Helsinki.

**More information:** Hannu Mäkinen et al, The effect of experimental lead pollution on DNA methylation in a wild bird population, *Epigenetics* (2021). [DOI: 10.1080/15592294.2021.1943863](https://doi.org/10.1080/15592294.2021.1943863)

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