

To Reduced DNA Methylation Study Finds High Intake of Ultra-Processed Foods is Important

Researchers explored how consuming ultra-processed foods (UPFs) affects epigenetic regulation, specifically in peripheral [blood leukocytes](#) of women, through a process called deoxyribonucleic acid (DNA) methylation.

They found that women who consumed more UPFs showed 80 differentially methylated regions (DMRs) at nominal $p < 0.05$ (uncorrected for multiple testing) compared with those who consumed less. In most cases, [DNA methylation](#) activity was reduced (hypomethylated). Since this process is crucial to many biological functions, these exploratory results suggest a potential epigenetic link between UPF intake and health outcomes, though causality cannot be inferred.



Study

According to the NOVA system, UPFs include ready-made meals, packaged snacks, and soft drinks. These foods are highly processed and contain preservatives, [flavorings](#), colorings, and additives. They are designed to be convenient, tasty, and have a long shelf life.

The global rise in UPF consumption parallels increases in [obesity](#) and chronic diseases, with UPFs now contributing up to half of total calorie intake in high-income countries. They are often energy-dense, low in essential nutrients, and contain high levels of unhealthy fats, sugar, and salt.

Beyond their poor nutritional profile, UPFs may also harm health through non-nutritional factors such as altered food structure, contaminants, and additives. High consumption has been linked to mental health and cardiovascular conditions, weight gain, [metabolic disorders](#), and even accelerated biological aging.

Researchers conducted a cross-sectional exploratory pilot study that included 30 women between 20 and 40 years old, with a [body mass index](#) (BMI) between 18.5 and 39.9 kg/m², recruited from a previous project.

Participants were excluded if they had conditions or behaviors affecting metabolism, such as over-exercising, amenorrhea, infectious diseases, [cancer](#), breastfeeding, or medication use that could affect weight or eating behavior, as well as eating disorders, chronic illness, pregnancy, smoking, or drug dependence. The study received ethical approval, and all participants provided written consent.

Results

Participants were grouped according to their intake of UPFs. The low-UPF group consumed an average of 14% of total energy from UPFs, while the high-UPF group consumed 45%. Of 20 DNA samples analyzed, five were excluded due to [poor sequencing quality](#), leaving 15 valid samples (7 low-UPF and eight high-UPF participants).

The women had a median age of 31 years and an average BMI of 24.7 kg/m², with no significant differences in body composition or [anthropometric measurements](#) between the two groups.

Biochemical tests showed unexpectedly higher total, low-density lipoprotein (LDL), and non-high-density lipoprotein (HDL) cholesterol levels in the low-UPF group. This finding aligns with previous research, including that of Dicken et al. (2025), which suggests that short-term UPF intake may not always elevate [blood lipids](#), underscoring the complexity of UPF-lipid relationships. Diet comparisons revealed that the low-UPF group consumed more unprocessed foods, protein, and polyunsaturated fats.

[Genome-wide DNA methylation](#) analysis identified 80 differentially methylated regions (DMRs), primarily located in gene promoter areas.

After filtering for regions with greater than fourfold differences, seven regions, RNA5S7, RNA5S9, RNA5S13, LINC00396, FOXP1-AS1, LOC124902961, and REPIN1-AS1, showed the largest [methylation differences](#). These regions were emphasized for visualization rather than being considered the only statistically significant sites.

Most DMRs were hypomethylated in the high-UPF group, indicating that higher UPF intake is associated with lower DNA methylation levels across [multiple genomic regions](#).

Conclusion

This pilot study was the first to utilize NGS to assess genome-wide DNA methylation changes associated with [UPF consumption](#). The results revealed 80 regions with differential methylation, mainly hypomethylated in women with high UPF intake.

Some of the most affected genes, such as FOXP1-AS1 and REPIN1-AS1, are involved in metabolic regulation and cancer-related pathways, suggesting possible [biological links](#) between UPF intake and adverse health effects.

Key strengths include the use of a high-resolution NGS approach, unbiased genome-wide analysis, and accurate [dietary assessment](#) using three-day food records.

However, the small sample size limited statistical power, and the cross-sectional design prevents causal interpretation. P values were nominal, unadjusted for multiple comparisons, and reflect exploratory analysis in a small sample, increasing the possibility of false-positive results. DNA methylation patterns were assessed in blood, which may not reflect methylation in other tissues, and [micronutrient](#) data were lacking. Confounder adjustment (for factors such as BMI or age) was not possible due to the limited sample size.

Despite these limitations, the study indicates that UPF consumption may influence gene regulation through [epigenetic modifications](#), representing a hypothesis-generating step that warrants replication in larger, longitudinal cohorts.

Source:

<https://www.news-medical.net/news/20251104/Study-finds-high-intake-of-ultra-processed-foods-tied-to-reduced-DNA-methylation.aspx>