EPIGENETICS

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Introduction

The epigenetics is the study of how DNA interact with some molecules which can activate and deactivate genes. This molecules in fact don't eliminate the piece of DNA, but inhibit the gene expression of that fragment. This mechanism is the basis of cell differentiation and it is heavily influenced by factors like the diet, the environment where you live, your life experiences and even emotional traumas.

To understand the fact that the gene expression can change, we first have to learn something about transcription.

Transcription is the first step of gene expression, in which a particular segment of DNA is copied into RNA (especially mRNA) by the enzyme RNA polymerase. During transcription, a DNA sequence is read by an RNA polymerase, which produces a complementary, antiparallel RNA strand.



Epigenetic mechanisms

Two factors can result in epigenetics effects: modification of DNA and so the modification of protein, and gene silencing.

Genetic modification is a technique to change the characteristics of a plant, animal or micro-organism by transferring a piece of DNA from one organism to a different organism. This is done through targeted removal of the desired genes from the DNA of one organism and adding them to the other organism.

By inserting or modifying a new piece of DNA, the sequence of the amino acids changes, which leads to different proteins.

Epigenetics modification is a bit different, in fact it results on the phenotype of individuals and not on the genotype. In fact two twins can be extremely different even if their DNA is the same.

The DNA can be affected in different ways. For example, the addition of acetyl groups (acetylation) to DNA histones enhances transcription. In contrast, the addition of methyl groups (methylation) to some regulatory regions of the DNA itself reduces gene transcription. Both of this modifications are not eternal, in fact they are reversible. For example, methyl groups can unchain from the DNA, restoring the transcription of that section of DNA.



Example of epigenetic mutations

Food example: How does green tea influence DNA?

Many studies suggest green tea is a cancer chemopreventive agent. Study leader Weronica Ek, of Uppsala University in Sweden, found that drinking tea appears to trigger epigenetic changes in women that are associated with cancer and the metabolism of the hormone estrogen. Previous research has shown that what we eat and drink can affect the expression of genes. One study published last year, found that a typical Western diet may lead to epigenetic changes by altering gut bacteria. Tea consumption did not lead to any changes in DNA methylation among men. Found in green tea, the polyphenol compound epigallocatechin-3gallate has many biological activities, including the inhibition of DNA methylation. Curcumin, a compound found in turmeric (*Curcuma longa*), can have multiple effects on gene activation, because it inhibits DNA methylation but also modulates histone acetylation.

Overall, the researchers believe that their findings indicate that tea consumption may trigger epigenetic changes in women that are related to cancer, though they caution that further research is needed to determine whether this effect is positive or negative.





Environmental example: How does famine influence DNA?

A study based on the analysis of data collected in the Netherlands over the years of hunger in 1944-45, during which the population there suffered particularly difficult conditions. The population's nutritional intake dropped to fewer than 1000 calories per day. Women continued to conceive and give birth during these hard times, and these children are now adults in their sixties. Recent studies have revealed that these individuals – exposed to calorie restrictions while in their mother's uterus – have a higher rate of chronic conditions such as diabetes, cardiovascular disease and obesity.

The answer appears to lie in the epigenetic adaptations made by the foetus in response to the limited supply of nutrients. It was discovered that people who were exposed to famine in utero have a lower degree of methylation of a gene implicated in insulin metabolism. This has some startling implications: although epigenetic changes are in theory reversible, useful changes that take place during embryonic development can nonetheless persist in adult life, even when they are no longer useful and could even be detrimental. Some of these changes may even persist through generations, affecting the grandchildren of the exposed women.





Nutrition example: How does nutrition influence animals?

Another striking example of how nutrition influences epigenetics during development is found in mice. Individuals with an active agouti gene have a yellow coat and a propensity to become obese. This gene, however, can be switched off by DNA methylation. If a pregnant agouti mouse receives dietary supplements that can release methyl groups – such as folic acid or choline – the pups' agouti genes become methylated and thus inactive. These pups still carry the agouti gene but they lose the agouti phenotype: they have brown fur and no increased tendency towards obesity.

The effects of early diet on epigenetics are also clearly visible among honeybees. What differentiates the sterile worker bees from the fertile queen is not genetics, but the diet that they follow as larvae. Larvae designated to become queens are fed exclusively with royal jelly, a substance secreted by worker bees, which switches on the gene programme that results in the bee becoming fertile.







