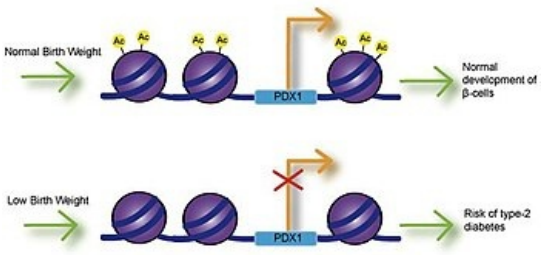
Histone modification

Histones are subject to various **post-translational modifications**, such as **acetylation**, **methylation**, **phosphorylation** and other changes.

Phosphorylation of histone H1 is related to **condensation of chromosomes,** dephosphorylation with decondensation. Similarly, acetylation and deacetylation of histones (of the nucleosome core) are related to changes in chromosome condensation and regulation of gene activity. Histones are acetylated in transcriptionally active chromatin and hypoacetylated in inactive chromatin. Acetylation cancels the positive charge of histones and allows release of the bond with DNA and transcription. Deacetylation of histones leads to an increase in positive charge and a tight electrostatic bond with DNA in inactive chromatin. These modifications are provided by the Enzymes **histone acetyltransferases** and **histone deacetylases**. Many transcription factors have **histone acetyltransferase** activity, which acts as a coactivator of transcription, or **histone deacetylase**, then acts as a corepressor gene expression.



Acetylation (1st row) and deacetylation (2nd row) of histones – PDX1 is an essential transcription factor for the proper development and function of pancreatic beta cells. Maternal malnutrition is associated with intrauterine growth retardation (IUGR) and low birth weight, and may result in reduced PDX1 expression through reduced histone acetylation at the PDX1 proximal promoter. Reduced expression of PDX1 can lead to improper beta-cell formation and increases the risk of type 2 diabetes in offspring

Histone deacetylation is closely related to DNA methylation and remodeling of chromatin into an inactive form. The enzyme complex containing histone deacetylases binds to methylated DNA via binding proteins MeCP1 and MeCP2, this leads to changes in chromatin structure. This process is complex, other proteins are involved in it (e.g. HP1 protein is typical for heterochromatin). If this process is disturbed, there is a change in the transcriptional activity of genes.

The modification of histones forms an **epigenetic regulatory mechanism**, applied in normal as well as pathological cellular processes. Post-translational modifications of histones that determine specific chromatin changes associated with the regulation of gene activity are called **histone code**.

DNA methylation and histone modifications, chromatin structure and other changes that affect gene expression without changing the primary DNA structure are called epigenetic mechanisms.

Links

Related Articles

- Histone
- Genomic Imprinting
- Genomic imprinting and human pathologies
- DNA Methylation
- Histone Code
- Epigenetics
- Transcription