

Chromatin Remodeling: Fundamental Process

Toyonobu Oshita*

Department of Molecular Biology, Sichuan University, Chengdu, Sichuan, China

DESCRIPTION

Chromatin remodeling refers to the dynamic changes in the structure of chromatin, which is the complex of DNA and proteins that makes up the genetic material of eukaryotic cells. Chromatin remodeling is a fundamental process that regulates many biological processes, including gene expression, DNA replication, and DNA repair. It involves the modification of the nucleosomes, which are the basic repeating units of chromatin, to allow or restrict access to DNA. These chromatin remodeling mechanisms can act independently or in concert to regulate gene expression, chromatin condensation and DNA accessibility.

The structure of chromatin is dynamic and can be modified by a variety of proteins, including histones and chromatin remodeling complexes. These modifications can alter the accessibility of DNA to transcription factors and other regulatory proteins, which can have a profound effect on gene expression. Histones are the primary proteins that make up the nucleosomes, which are the building blocks of chromatin. They can be modified by various chemical groups, including acetyl, methyl, and phosphate groups, which can alter their structure and function. For example, acetylation of histones can lead to the relaxation of chromatin structure and increased accessibility of DNA to transcription factors, while methylation of histones can lead to the formation of compact chromatin structures and reduced accessibility of DNA.

Histone modifiers include enzymes that add or remove chemical groups from histones, including acetyltransferases, deacetylases, methyltransferases, and demethylases. These enzymes can alter the structure and function of histones, which can have a profound effect on gene expression. For example, histone acetyltransferases can add acetyl groups to histones, which can lead to the relaxation of chromatin structure and increased accessibility of DNA to transcription factors, while histone deacetylases can remove acetyl groups from histones, which can lead to the formation of compact chromatin structures and reduced accessibility of DNA.

1. ATP-dependent chromatin remodeling: This type of remodeling involves the use of energy from ATP hydrolysis to alter the position of nucleosomes, which are the basic units of chromatin. ATP-dependent chromatin remodeling complexes, such as SWI/SNF and ISWI, use ATP to slide nucleosomes along the DNA, change their positioning or remove them altogether.

2. Histone modification: This refers to the addition or removal of chemical groups, such as acetyl, methyl, or phosphate groups, to the histone proteins that make up the nucleosomes. These modifications can alter the charge of the histones, thereby changing their interaction with DNA, other histones, or regulatory proteins.

3. DNA methylation: This involves the addition of a methyl group to a cytosine base in DNA, which can affect gene expression by blocking the binding of transcription factors or other proteins.

4. Histone variant incorporation: This involves the substitution of one type of histone for another within the nucleosome structure. This can change the properties of the nucleosome and alter the way that the DNA is packaged.

CONCLUSION

Chromatin remodeling complexes are protein complexes that can alter the structure of nucleosomes and chromatin. These complexes are classified into two main groups: ATP-dependent chromatin remodelers and histone modifiers. ATP-dependent chromatin remodelers use ATP hydrolysis to alter the position of nucleosomes along the DNA, while histone modifiers can add or remove chemical groups from histones to alter their structure and function. There are several families of ATP-dependent chromatin remodelers, including SWI/SNF, ISWI, CHD, and INO80. These complexes can interact with specific DNA sequences and alter the position of nucleosomes to regulate gene expression.

Correspondence to: Toyonobu Oshita, Department of Molecular Biology, Sichuan University, Chengdu, Sichuan, China, E-mail: oshita.tb@om.asahikasei.co.cn

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