

# Chromatin Remodeling: In Context Of Gene Expression

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## **ABSTRACT:**

*Chromatin remodeling refers to all types of covalent modifications that changes the chromatin structure in order to give access to the replication and transcriptional machinery. It is an important regulatory mechanisms for cell where cell decides which set of genes to be expressed at any given point of time. The present review describes three important types of covalent histone modifications.*

**KEYWORDS:** *Chromatin remodeling, Histone, acetylation, phosphorylation, methylation.*

## **1. INTRODUCTION:**

Structure of chromatin is an important determinant of many vital processes of life such as DNA replication and transcription (Zentner and Henikoff 2011). During DNA replication or transcription the DNA which is packed tightly in the form of chromatin, must be loosen in order to give access to the DNA or RNA polymerases and other proteins involved in the processes (Li et al 2007). Chromatin remodeling refers to all those covalent modifications in the chromatin structure that occur during replication / transcription.

In nucleosome, core histones i.e., H<sub>2</sub>A, H<sub>2</sub>B, H<sub>3</sub> and H<sub>4</sub> as well as linker histone, H<sub>1</sub> are subjected to a number of covalent modifications. Acetylation, methylation and phosphorylation are among the most significant modifications. Others include ubiquitylation, sumoylation and biotinylation.

### *Histone acetylation:*

Histone acetylation refers to the addition of acetyl group to the lysine residue of histone protein. Histone acetylation plays important role in transcriptional switch. Positively charged histones are tightly bound to negatively charged DNA strand. Lysine acetylation makes histone protein relatively lesser positive and a force of repulsion originates between DNA and histone thereby making DNA strands available for polymerases and other accessory proteins. Histone acetylation is considered to be a transcriptional activator (Kouzarides 2007).

### *Histone Methylation*

Methylation refers to the addition of methyl group to the lysine and arginine amino acid residues of histone protein. Histone methylation is considered to be both transcriptional activator or repressor, depending upon the position of methylated lysine or arginine residues (Li et al 2007).

### *Histone phosphorylation*

Histone phosphorylation refers to the addition of phosphate group to the serine, threonine and tyrosine amino acid residues. Similar to acetylation, phosphorylation is associated with the transcriptional activation (Li et al 2007).

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