

Abstract

Plant phenotype is shaped by genetic and epigenetic information, because epigenetic marks participate in regulation of gene expression. Many genes are silenced during plant's life, because they play a role for example only in a certain stage of plant development or in a stress response. Transposable elements and other repetitive sequences are also silenced, because they could threaten the genome stability. One of the epigenetic marks is DNA methylation, transfer of a methyl group from donor to C5 position of the cytosine in DNA. DNA methylation is mediated by methyltransferases and usually has repressive effect on the gene expression thanks to methylation recognition proteins. In addition to DNA methylation, the chromatin state has also an effect on gene expression and can occur in either a loosened state (euchromatin) or a condensed state (heterochromatin). Genes located in heterochromatin are not active (silenced), as heterochromatin is substantially compact and isn't accessible to proteins involved in gene expression. Condensation of chromatin is often directly connected with DNA methylation. Condensation of chromatin is also associated with repressive histone modifications and repressive histone variants, these histone modifications and histone variants are also often associated DNA methylation. The aim of this work is to summarize and connect the known interactions between DNA methylation, histone modifications, histone variants and chromatin state, which all together participate in regulation of gene expression.

Key words: cytosine/DNA methylation, cytosine/DNA demethylation, MBD proteins, SUVH proteins, H3K9me2, H3K9me3, heterochromatin, euchromatin, H3, H2A.W, H2A.Z