

Abstract

Cytosine bases of the nuclear genome in higher plants are often extensively methylated. Cytosine methylation has been implicated in the silencing of both transposable elements (TEs) and endogenous genes, and loss of methylation may have severe functional consequences. The recent methylation profiling of the entire *Arabidopsis* genome has provided novel insights into the extent and pattern of cytosine methylation and its relationships with gene activity. In addition, the fresh studies also revealed the more dynamic nature of this epigenetic modification across plant development than previously believed. Cytosine methylation of gene promoter regions usually inhibits transcription, but methylation in coding regions (gene-body methylation) does not generally affect gene expression. Active demethylation (though probably act synergistically with passive loss of methylation) of promoters by the 5-methyl cytosine DNA glycosylase or DEMETER (DME) is required for the uni-parental expression of imprinting genes in endosperm, which is essential for seed viability. The opinion that cytosine methylation is indispensable for normal plant development has been reinforced by using single or combinations of diverse loss-of-function mutants for DNA methyltransferases, DNA glycosylases, components involved in siRNA biogenesis and chromatin remodeling factors. Patterns of cytosine methylation in plants are usually faithfully maintained across organismal generations by the concerted action of epigenetic inheritance and progressive correction of strayed patterns. However, some variant methylation patterns may escape from being corrected and hence produce novel epialleles in the affected somatic cells. This, coupled with the unique property of plants to produce germline cells late during development, may enable the newly acquired epialleles to be inherited to future generations, which if visible to selection may contribute to adaptation and evolution.