

## Abstract

Cytosine methylation of DNA is a pivotal epigenetic mark, which contributes to the regulation of the gene expression, silencing of transposable elements, and co-defines chromatin state. There are three cytosine contexts: CG, CHG and CHH (where H stands for C, A, or T). *Arabidopsis thaliana* (and plants in general) has an arsenal of molecular mechanisms capable of cytosine methylation in all of its contexts. That said, there are two tasks at hand: maintaining of pre-existing methylation and if need be, creating new methylated spots. The actual process of maintaining of the methylation depends on the cytosine context. Methylation of symmetrical contexts of CG and CHG can utilize the information about the methylation pattern from the second DNA strand. The asymmetrical context of CHH, and also CHG need to look for this information elsewhere: in the methylation of the lysine 9 of H3 histone. This creates a self-reinforcing loop and a crosstalk between two epigenetic mechanisms. Maintenance of methylation of CHH is also navigated by small RNA complementary to the locus in question. This mechanism of enzyme navigating by RNA is also used in establishing a new methylated site for all of the contexts. CG methylation is most prevalent in both heterochromatin and euchromatin. It also has a special function of increasing transcription processivity of long, constitutively expressed genes.

**Keywords:** *Arabidopsis*, epigenetics, chromatin, methyltransferase, histone methylation