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Dynamique de la méthylation de l'ADN en temps réel lors de la reproduction chez les plantes

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Summary

Cytosine methylation (mC) is an epigenetic mark playing key roles for transcriptional control and genome integrity in plants and mammals. During mammalian reproduction, DNA methylation is reprogrammed to notably facilitate the acquisition of zygotic totipotency. In plants, it is still a debate whether DNA methylation reprogramming takes place as methylome of reproductive cells is only partial. To track DNA methylation dynamics during plant reproduction, we generated genetically encoded fluorescent sensors called DYNAMET that selectively report mCG and mCHH methylation. Although global CG methylation pattern remains stable throughout male and female sporogenesis, a marked reduction of CG methylation was observed in the egg cell that was rapidly restored in the young embryo. In contrast, we detected rapid and massive loss and regain cycles of CHH methylation during male and female germline formation. Genetic analyses indicate that the DNA methyltransferase DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2), ortholog of mammalian Dnmt3, is the key enzyme depositing CHH methylation in the egg cell, in a cell-specific, siRNA-independent manner.

Our DNA methylation reporters provide unprecedented insights into global DNA methylation dynamics at the single cell level that could potentially be used in living mammalian cells.

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