Title:
The Catalytic Core of DEMETER Guides Active DNA Demethylation in Arabidopsis

Abstract:
The Arabidopsis DEMETER (DME) DNA glycosylase demethylates the maternal genome in the central cell prior to fertilization, and is essential for seed viability. DME preferentially targets small transposons that flank coding genes, influencing their expression and initiating plant gene imprinting. DME also targets intergenic and heterochromatic regions, and how it is recruited to these differing chromatin landscapes is unknown. The C-terminal DME catalytic core consists of three conserved regions required for catalysis in vitro. We show that the catalytic core of DME guides active demethylation at endogenous targets, rescuing the developmental and genomic hypermethylation phenotypes of DME mutants. However, without the N-terminus, heterochromatin demethylation is significantly impeded, and abundant CG-methylated genic sequences are ectopically demethylated. We used comparative analysis to reveal that the conserved DME N-terminal domains are only present in the flowering plants, whereas the domain architecture of DME-like proteins in non-vascular plants mainly resembles the catalytic core, suggesting that it might represent the ancestral form of the 5mC DNA glycosylase found in all plant lineages. We propose a bipartite model for DME protein action and suggest that the DME N-terminus was acquired late during land plant evolution to improve specificity and facilitate demethylation at heterochromatin targets.

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