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Gene Technology

Perspective

DNA Methylation: Genetic Diversity in *Brassica Rapa* and *Brassica oleracea*

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DESCRIPTION

DNA methylation is an epigenetic alteration that regulates a variety of functions, including transposable element expression, stress responses, and gene expression. Numerous studies have shown that modifying DNA methylation offers an alternate strategy for crop development, making it a crucial target for such manipulation. *De novo* methylation, maintenance of methylation, and active DNA demethylation are the three processes that make up DNA methylation; each of these three steps is catalysed by a different enzyme [1]. *De novo* methylation in plants refers to the RNA-directed DNA methylation (RdDM) route, which is used by RNA polymerases particular to plants. A specific transcription apparatus, including RNA Polymerase IV (Pol IV) and Pol V, is necessary for the RdDM pathway. RNA-dependent RNA polymerase 2 (RDR2) turns the single-stranded RNAs that Pol IV synthesises from RdDM target loci into double-stranded RNAs (dsRNAs). These dsRNAs are broken down by Dicer-like protein 2 (DCL2), DCL3, and DCL4 to produce small-interfering RNAs (siRNAs). In order to recruit Domains Rearranged Methylase 2 (DRM2), which catalyses *de novo* DNA methylation, the siRNAs are then loaded onto Argonaute 4 (AGO4) or AGO6 and couple with scaffold RNAs produced by Pol V. Different DNA methyltransferases catalyse the mechanisms for DNA methylation maintenance depending on the context of the cytosine sequence (CG, CHG, or CHH, H=T, C, A) [2].

Methyltransferase 1 (MET1) maintains the methylation of CG cytosine, to put it simply. Chromomethylase 3 (CMT3) and CMT2 maintain the cytosine methylation of CHG. CMT2 and DRM2 support the maintenance of CHH cytosine methylation. Passive DNA Demethylation (PDD) and Active DNA Demethylation are the two types of DNA demethylation (ADD). PDD is dependent on DNA replication, whereas ADD is controlled by the DNA glycosylases family Demeter (DME), Demeter-Like 2 (DML2), and Demeter-Like 3 (DML3), as well as Repressor of Silencing 1. (ROS1). The ADD pathway in plants involves numerous protein complexes and transcription factors, and it is a complicated process in plants. Numerous significant horticultural species can be found in the genus Brassica, which is a member of the plant family Brassicaceae. Among them, two significant representative vegetable crops are *Brassica Rapa* and *Brassica oleracea*. Recent findings have shown that after they separated from Arabidopsis thaliana, *Brassica* species have undergone further Whole-Genome Triplication (WGT) events, which were followed by significant gene loss and the divergence of three sub genomes. Extensive gene loss resulted in various sub genome-dominant phenomena in *B. Rapa* and *B. oleracea*, such as gene loss bias and expression dominance between homologous genes from different sub genomes. Among the three sub genomes, the dominant sub genome is referred to as the least fractionated sub genome, while the other two recessive sub genomes are referred to as the medium fractionated sub genome and the most fractionated sub genome [3]. Recently, the impact of DNA methylation on polyploidy genome evolution has been documented in *B. Rapa* and *B. Oleracea*.

Additionally, it was shown that several plant species exhibit widespread variance in DNA methylation. Small RNA, gene expression, and whole-genome DNA methylation were all systematically examined in *B. Rapa*. The findings demonstrated that single-copy genes have much higher levels of methylation in their genic regions than multi-copy genes. Generally speaking, in *B. Rapa*, the copy number or sub genomes affected the degree of gene expression, which was inversely linked with the mean gene methylation content. Additionally, there are significant TE variations in *B. Rapa* and *B. Oleracea*, and TEs are tightly linked to DNA methylation. These data demonstrate the importance of researching the divergent evolution of DNA Methylation-Related (DMR) genes, which are responsible for the variations in TEs and their methylation between *B. Rapa* and *B. oleracea*. But *B. Rapa* and *B. Oleracea* still lack thorough DMR gene discovery and characterization. High-throughput sequencing technology has made it possible to obtain a significant amount of nucleic acid data for both *B. Rapa* and *B. oleracea* in recent years, which has made it much easier to research DMR genes in *B. Rapa* and *B. Oleracea*. This is due to the rapid development of genomics [4].

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By comparing the genomes of A. thaliana, B. Rapa, and B. Oleracea, we were able to identify the DMR genes in this work. We next examined the retention and evolutionary differences in the DMR genes between *B. Rapa* and *B. Oleracea* following WGT. Between *B. Rapa* and *B. oleracea*, we evaluated the evolutionary selection pressures and expression variations of the DMR genes. In addition, we calculated nucleotide diversity and Tajima's D in 199 *B. Rapa* and 119 *B. Oleracea* accessions to determine the population diversity of DMR genes. Future work on the distinct development of DNA methylation between the genomes of *B. Rapa* and *B. Oleracea* will benefit greatly from the resources provided [5].

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