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Gene expression patterns and RdDM-mediated epigenetic regulations of duplicated genes in *Brassica napus* subgenomes A and C

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Plant genome polyploidization and subsequent evolution is a crucial process for trait innovation and new species formation. Building of gene expression patterns of polyploidy duplicated genes is a first step in the process. Previous researches have indicated that these duplicated genes may inherit progenitors' expression patterns or form new patterns. In some polyploids, duplicated gene expression is biased toward one genome (genome dominance) while others are not. In all cases, mechanisms to form these expression patterns are poorly understood. In this study, we used a set of materials including the extracted AA subgenome (AeAe, n=10) plants and its corresponding tetraploid *Brassica napus* (AnAnCnCn, n=18) plus the tetraploid progenitors *B. rapa* (ArAr, n=10) and *B. oleracea* (CoCo, n=9) genomes to investigate duplicated gene expression patterns and further regulatory mechanisms of the patterns. Through analyses of whole genome re-sequencing and RNA-sequencing data, we found 80% of duplicated genes (in total about 23,000 gene pairs in leaves) inherited progenitors' gene expression patterns and 20% showed altered expression patterns. For the regulatory mechanisms of the altered patterns, we hypothesized that 24-nt siRNAs might be a kind of regulators because A and C have a big difference in transposable elements (TE) producing 24-nt siRNAs which mediate RNA-directed DNA methylation (RdDM) and thus affect nearby gene expression. To test this hypothesis, we performed small RNA sequencing and DNA methylation sequencing. By comparing to Ae, we found that 20% of the genes with expression alteration can be explained by RdDM. For the inheritable gene expression patterns, we found that TEs which were asymmetrically inserted and then methylated by a small RNA-directed pathway, both already formed in each progenitor genome, have performed fixation on the inheritable patterns. The trends also exist in 15MYA-triplicated subgenomic expression dominance. Our results revealed expression patterns of *B. napus* polyploidy duplicated genes and provided new insights into the regulatory mechanism of the expression patterns in polyploid evolution.

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