

MicroRNA expression changes following synthesis of three full-sib *Populus* triploid populations with different heterozygosities

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Abstract

Key message Through high-throughput sequencing, we compared the relative expression levels of miRNA in three full-sib *Populus* triploid populations with that in their parents and one diploid hybrid population. We found similar numbers of miRNAs differentially expressed between the parents and the four progeny hybrid populations. In addition, unbalanced parental expression level dominance of miRNAs were found in the three allotriploid and interspecific hybrid populations, which may reprogram gene expression networks and contribute to the growth of *Populus* hybrids. These results indicated that hybridization has a great impact on the miRNA expression variation in the newly synthesized *Populus* triploid and diploid hybrid populations. However, we also found no significant differences in miRNA expression among one diploid and three triploid hybrid populations, hinting that miRNA abundances do not

increase with the genome content. No dosage effect of miRNA expression could lead to dosage-dependent negative effects on target genes and their downstream pathway in polyploids. We speculate that polyploids may gain advantages from the slight decrease in miRNA regulation, suggesting an important molecular mechanism of polyploid advantage.

Abstract Hybridization with three types of induced 2n gametes transmitted different parental heterozygosities has been proven as an efficient method for *Populus* triploid production. Several researches have shown that miRNA could be non-additively expressed in allopolyploids. However, it is still unclear whether the non-additively expressed miRNAs result from the effect of hybridization or polyploidization, and whether a dose response to the additional genomic content exists for the expression of miRNA. Toward this end, through high-throughput sequencing, we compared the expression levels of miRNA in three full-sib *Populus* triploid populations with that in their parents and one interspecific hybrid population. We found similar numbers of miRNAs differentially expressed between the parents and the four progeny hybrid populations. Unbalanced parental expression level dominance of miRNAs were found in the three triploid and diploid hybrid populations, which may reprogram gene expression networks and affect the growth of *Populus* hybrids. These results indicated that hybridization has a great impact on the miRNA expression variation in the newly synthesized *Populus* triploid and diploid hybrid populations. However, we also found no significant differences in miRNA expression among the three triploid populations and the diploid hybrid population. No dosage effect of miRNA expression could lead to dosage-dependent negative effects on target genes and their downstream pathway in polyploids. We speculate that polyploids may gain advantages from the decrease in miRNA negative regulation,

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