

POLYPLOIDIZATION: EFFECT ON THE TRANSCRIPTOME AND METHYLOME IN *MEDICAGO SATIVA*

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The modifications that occur as a consequence of polyploidization in plants can influence economically important traits. These modifications may be caused by changes in gene expression and/or in DNA sequence. While the genetic and epigenetic effects of polyploidization have been studied in both model and cultivated disomic polyploids, polysomic polyploidy has not received much attention. The objective of our work is to gain insight into the effects of chromosome doubling on gene expression and DNA methylation in alfalfa, an important forage species with tetrasomic inheritance. We used two diploid ($2x=16$) plants of the subspecies *Medicago falcata* and *M. coerulea* that produce $2n$ eggs and $2n$ pollen, respectively. From their cross, diploid and tetraploid ($4x=32$) progenies from bilateral sexual polyploidization (BSP) were obtained. We have used three $2x$ and three $4x$ progeny plants to investigate polyploidization-induced changes by analyzing: 1) gene expression for a large part of the genome, by using microarrays of cDNA-derived sequences of *Medicago truncatula* and *Medicago sativa* (Affymetrix), and 2) genomic DNA methylation, by using the Methylated Site Amplified Polymorphism (MSAP) technique. Microarray analysis has evidenced about 200 genes differentially expressed between $2x$ and $4x$ progenies. Fifty of them appear to change expression as a consequence of polyploidization. A full Gene Ontology analysis of these genes was performed. MSAP analysis has been initiated using selective primers capable of a high-polymorphism detection, based on previous assays on alfalfa. Our preliminary results revealed some methylation changes in the BSP progenies with respect to their $2x$ parents. Dry matter yield and fertility of the parents and progenies were compared and discussed in the light of the molecular data obtained.