Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 9.24

EPIGENETICS ASPECTS OF POLYPLOIDIZATION: STUDIES OF EXPRESSION PATTERN OF DNA METHYLATION GENES IN *MEDICAGO SATIVA* L.

LEONETTI P.*, DE GIOVANNI C.**, VIGGIANO L.***, ROSELLINI D.****, VERONESI F.****

*) Institute of Plant Protection – CNR, Research Division Bari (Italy)
**) Department of Agroforestry, Enviromental Biology and Chemistry, University of Bari (Italy)
***) Department of Biology, University of Bari (Italy)
****) Department of Applied Biology, University of Perugia (Italy)

Alfalfa, epigenetics, polyploidization, DNA methyltransferase genes

The widespread occurrence of epigenetic alterations as a consequence of polyploidization in plants indicates that DNA methylation systems may be perturbed by polyploidy changes. DNA methylation genes are involved in many vital developmental and physiological processes of plants.

In this work, we seek novel information on epigenetic consequences of autopolyploidization in alfalfa (*Medicago sativa*). In particular, genes responsible for the DNA methylation status are studied in 2x, 3x and 4x genotypes progenies obtained by crossing two 2x plants that produce both n and 2n eggs and pollen, respectively. To identify DNA methyltransferase genes and their expression patterns we examined some of the elements of three major DNA methyltransferase families MET1, CMT and DRM. Methylation at CG nucleotides is maintained in plants by the the enzymes of the MET1 family typical of higher eukariotes. The second family, called Domain Rearranged Methyltransferase (DRM) has characteristic rearrangement of conserved motifs in the catalytic domain and probably catalyzes methylation of native DNA. The chromomethylases (CMT) are unique of higher plants. These enzymes maintain methylation of CHG trinucleotides.

In silico searches have lead to the identification of *M. sativa* methyltransferase genes homologous to known plant methyltransferase genes. Oligonucleotides have been designed from these sequences in order to analize the expression pattern of these genes. Gene expression changes induced by polyploidization are being investigated using qRT-PCR and expression data will be validated and jointly analyzed to identify ploidy-affected genes.