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DNA METHYLATION ANALYSIS IN RAPESEED (*BRASSICA NAPUS* VAR. *OLEIFERA* DEL.) UNDER SALT STRESS BASED ON M-SAP MARKERS

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Salinity is an important limiting environmental factor for rapeseed production worldwide and can hamper initial developmental stages in Mediterranean climates where the crop is sown in late summer. DNA methylation is known to play a crucial role in regulating plant development and tissue differentiation. In this study, we compared the extent and pattern of cytosine methylation in one tolerant and one sensitive rapeseed (*Brassica napus*) cultivar, germinated in distilled water and grown either in distilled water or in a 150 mM NaCl solution, using the technique of methylation-sensitive amplified polymorphism (M-SAP). Analysis of amplification products generated by eleven primer combinations showed that the rapeseed genome is hypermethylated with several polymorphic fragments. In particular, under salt stress conditions, the tolerant cultivar showed more DNA methylations than the stress sensitive one.

Forty-six methylation-related fragments were recovered from tolerant and sensitive cultivars, cloned, sequenced and subjected to BLAST analysis. Eight sequences shared high homology with *Arabidopsis thaliana* genes somehow related to stress tolerance: trehalose phosphatase/synthase, LEUNIG, SH3 domain-containing proteins, radical SAM domain, fringe-related protein, glutamine fructose 6 phosphate, CYP86A8 and DNA methyltransferase.

Validation of results through the analysis of tissue-specific gene expression using real-time PCR is reported and discussed.