

DNA METHYLATION PATTERN ANALYSIS ON *IN VITRO* PROPAGATED GLOBE ARTICHOKE PLANTS

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globe artichoke, somaclonal variation, DNA methylation, in vitro culture

Globe artichoke (*Cynara cardunculus* L. var. *scolymus*, $2n = 2x = 34$) represents one of the main horticultural species of the Mediterranean basin, and '*Spinoso sardo*' is the most widespread and economically relevant varietal type in Sardinia. In the last decades, *in vitro* culture of meristematic apices, widely used in globe artichoke propagation for obtaining both virus-free material and high multiplication rates, has increased the frequency of the appearance of an aberrant phenotype after open field transplantation of *in vitro* germinated globe artichoke plantlets. These *off-type* phenotypes showed highly pinnate-parted leaves and late inflorescence budding, and emerged from some branches of the *true-to-type* '*Spinoso sardo*' plants. The phenotypic variability observed amongst regenerated plants, commonly known collectively as 'somaclonal variation', has a negative agronomical impact as it is severely reducing the genetic uniformity required for the maintenance of '*Spinoso sardo*' genotype. This phenomenon might be associated to both gene mutations and changes in epigenetic marks.

Here we report the first exploratory study on DNA methylation patterns in *off-type/true-to-type* globe artichoke plants, using a restriction-enzyme-based method, followed by the Illumina sequencing of the generated DNA fragments. This approach allowed the identification of 744 differentially methylated loci (DML) in CG, 280 in CHH and 597 in CHG methylation contexts. Functional annotation of DML consented the identification of candidate genes coding for proteins involved in flower development and its regulation, maintenance of epigenetic modifications and vegetative development. Differences in the methylation status of some genes of interest were confirmed by transcriptional analysis, providing clues as a possible involvement of epigenetic regulation in the emergence and spread of the '*Spinoso sardo*' non-conventional phenotype.