

EFFECT OF GRAFTING ON DNA METHYLATION IN TOMATO GRAFTED PLANTS

DI MARSICO M.*, MARCONI G.*, CASSIBBA V.***, PORCEDDU A.***, ALBERTINI E.*

*) Dipartimento di Scienze Agrarie Alimentari e Ambientali, Università degli Studi di Perugia

**) Southern Seed s.r.l., Vittoria (RG)

***) Dipartimento di Agraria, Università degli Studi di Sassari

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Grafting is an agricultural technique that involves the union of the root system of a plant with the aerial part of another, resulting in the connection of the vascular system of two different genotypes and the production of a symbiotic relationship. After the phasing out of the bromomethane, several sustainable practices have been used: grafting is one of these. Thanks to grafting, it is possible to avoid the usage of pesticides, providing an alternative in the fight against parasites. In herbaceous plants, like tomato, advantages are the resistance against soil-borne pathogens, increased vigor, and tolerance to abiotic stress. Grafting could also influence the yield of crops, determining the production of higher quality fruits. Grafting has also essential effects on fruit quality. It seems that rootstocks negatively affect the sweetness of the tomato fruits. Our work aimed to identify DNA methylation changes occurring in a commercial variety of tomato when grafted on different interspecific and intraspecific rootstocks and how these epigenetic modifications could affect its phenotype. To perform these analyses, we employed MCSeEd at different methylation contexts (CG, CHG, CHH, 6mA). We perform phenotypic analysis on two different seasons and the methylation and RNAseq analysis only on the second season by comparing the commercial variety grafted onto different rootstocks with the ungrafted and self-grafted one. Each comparison showed that differences in methylation levels between grafted plants and control groups were primarily due to the effect of grafting itself since the two groups of samples clustered separately. Evaluation of methylation levels of differentially methylated regions highlighted a common relative methylation in most of the contexts evaluated. Then, we

compared the results of the BRIX analysis with the DNA methylation analysis, focusing on interspecific rootstocks, since they showed the stronger significant differences with controls. We identified differentially methylated genes involved in carbohydrate metabolism, gene silencing and cellular response to starvation, highlight that grafting has an important effect on the DNA methylation in tomato and could lead to the regulation of genes linked to the carbohydrate metabolism and the concentration of sugar in the fruits. Moreover, thanks to the transcriptomic analysis, we were able to compare the results from the DNA methylation analysis with the differentially expressed genes identified. In particular, we identified genes (both differentially expressed and differentially methylated) that might highlight that grafting clearly has an effect on the pathway of the plant hormones, but also that it could regulate the accumulation of sucrose.