

## HOW DOES THE PARENTAL EPIGENOME INFLUENCE THE FRUIT QUALITY OF PROGENIES?

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Modern approaches for *Solanum lycopersicum* L. breeding aim at implementing yield, firmness, long shelf-life, and resistance to diseases. However, the tomato market is fighting a lack of variety rich in flavors and organoleptic features. Taking into consideration that tomato fruits are subjected to several epigenetic changes that can influence the expression of genes involved in the organoleptic pathways, new breeding techniques, coupled with a deep knowledge of those epigenetic mechanisms of gene regulation, may represent powerful selection tools in tomato breeding. As methyltransferases are highly expressed during the early stages of fruit development, most DNA methylation changes occur during the mature green stage. Despite that, we investigated the methylation status of fruits at the commercial mature red stage. This was mainly because we were interested in the influence of epigenetics on the organoleptic characteristics of commercial fruits, precisely, the mature red stage.

In this study, we employed three commercial varieties belonging to the United Genetics Italia S.p.A – Kagome Group company. In these varieties, we analyzed the DNA methylation status in F1 hybrids and their relative pure parental lines to investigate how epigenetic traits were inherited, and how they influenced the quality of the final product.

We used the MCSeEd (Methylation Content Sensitive Enzyme ddRAD) technique, and this allowed us to identify differences in the relative methylation status of the F1 and each parental line. Thus, several differentially methylated regions (DMRs) and differentially methylated genes (DMGs) were identified. The role of these differentially methylated genes on fruit

flavor and quality was investigated and will be critically discussed.