

EPIGENETIC REGULATION OF ENDOREDUPPLICATION PROCESS: A KEY ROLE FOR A CORRECT PEACH FRUIT SIZE AND RIPENING TIMING

FARINATI S., GALLA G., RASORI A., VAROTTO S., BONGHI C.

Department of Agronomy Food Natural Resources Animal and Environment - DAFNAE,
University of PADUA, Viale dell'Università 16, 35020 Legnaro (Italy)

peach, fruit growth, endoreduplication, histone marks, Cromatin immunoprecipitation

Among the several phenotypic traits which characterize the fruit quality, the fruit dimension is one of the major aspects evaluated in the present worldwide socio-economical context, since it could be directly related to food and human nutrition supply. From a molecular point of view the fruit growth and the related fruit size are influenced by different biological processes, including endoreduplication events in pericarp tissue. In plants, endoreduplication can occur in different cell types, putatively related with peculiar functions. In fruit crops, endoreduplication have been largely studied during fruit growth from an ultrastructural and cytologic point of view, while the molecular and genetic basis of this process are still poorly understood. The genetic control of endoreduplication during fruit growth is functional to a better understanding of regulatory mechanisms governing fruit size and ripening timing.

In this research we focused our attention on endoreduplication events occurring in different peach cvs (*Prunus persica* L. Batsch) characterized by different size and harvest time, that are Springcrest (early ripening) and Fantasia (late ripening). In addition, we took advantage of a peach mutation identified in a free-pollinated population of Fantasia named slow ripening (SR). SR phenotype is associated to an altered transcriptional regulation of genes involved in mesocarp identity, and shows a reduction of final fruit size together to the loss of fundamental ripening traits. In the three cultivars, genes activating endoreduplication (orthologous to Arabidopsis WEE1 and KRP3) are more expressed in Fantasia in comparison to Springcrest and SR. These transcription profiles are consistent with flow cytometry data that pointed out an altered endoreduplication level in Springcrest and SR. In parallel, the involvement of specific epigenetic marks (H3K4me3, H3K27me3 and H3K9ac) were analyzed at the target gene loci with the goal to link fruit endoreduplication events to epigenetic control.