

Biochemical and genetic implications of the slow ripening phenotype in peach fruit

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Abstract

The peach [*Prunus persica* L. (Batsch)] slow ripening (SR) trait is a mutation preventing the normal fruit ripening process. It is determined by a single Mendelian gene (*Sr/sr*) located on linkage group 4, where only homozygous individuals for a recessive allele (*sr*) show the SR phenotype and are generally discarded from breeding programs. Ripening-related traits such as fruit weight, firmness loss, ethylene production, ACO activity, sugars and organic acids composition, malondialdehyde, antioxidant capacity and total phenolic content were evaluated in a segregating population for the SR trait during two consecutive harvest seasons and at different maturity stages. Although there is no commercial value for the slow ripening (*srsr*) individuals, our results demonstrate that a heterozygous combination involving *sr* and another allele at this locus (*Sr2*) showed interesting traits including a longer harvest window and improved postharvest behaviour if harvested at the appropriate maturity ($I_{AD} \geq 2$). All these traits seem to be linked to a delayed ripening behaviour mediated, in turn, by a lower ethylene production capacity and an altered sugar (mainly sucrose) and organic acid accumulation/utilisation on-tree. The selection of this allelic combination could be an easy and efficient strategy to obtain new peach cultivars with potentially improved shelf life.