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New advances on the flesh's red pigmentation in peach

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Abstract:

Anthocyanin-rich fruit, because of their antioxidant properties and strong attractiveness to consumers, generates great interest in varietal innovation programs that increasingly integrate genomics and plant breeding. This is the case in peach in which the anthocyanin concentration in the mesocarp of the fruit is controlled by three different loci: i) the dominant Cs locus, mapped to LG3 and probably associated with MYB10, determines a red pigmentation of the mesocarp around the stone; ii) the dominant locus DBF, for Dominant Blood-Flesh, that we recently mapped to LG5, determines a fully red mesocarp appearing at the later stages of the fruit development. Using the peach reference sequence, we identified as good candidates a cluster of three predicted members of the dihydroflavonol-4-reductase gene family in the 505-kbp region containing DBF; iii) similarly, we narrowed the region (<80-kpb) of the recessive locus bf, for blood-flesh, that had been previously mapped to LG4. It determines a more or less substantial accumulation of anthocyanin in both immature and mature fruits, associated with the red pigmentation of midrib (rpm) on the underside of leaves and a reduced tree height (rth). However for bf, uncertainty still exists over whether these simply inherited traits are controlled by three linked loci (bf, rpm, and rth) or one pleiotropic locus. From biochemical, molecular and genomics analyses of one segregating population of peach (850 progenies), we bring new elements to answer this question and propose candidate genes involved in anthocyanin expression and the growth of plants.

Keywords: *Prunus persica*, anthocyanin, blood-flesh, fine mapping, pleiotropy