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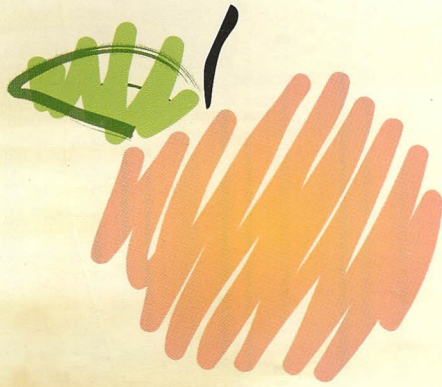
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New insights on blood-flesh determinants in peach

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The red colour in peach is a key fruit quality trait that contributes a lot to the attractiveness of peaches and nectarines. Most of commercial peach cultivars exhibit fruit with fully red skin. Besides this, as in many other Rosaceous fruit species, there are some genotypes having fruits with an intensively pigmented mesocarp, here referred to as blood-flesh peach. In addition to their high fresh fruit market value, red pigments, which are mainly anthocyanins, represent an excellent source of antioxidants, with potential health benefits for consumers. Therefore, both for peach breeders and molecular biologists, the peach cultivars with anthocyanin-rich fruit constitute an attractive starting point for the development of novel varieties by integrating plant genomics and classical breeding. Among other challenges, the most important are the development of molecular markers to accelerate breeding by marker-assisted selection and inheritance study of novel alleles for increasing our understanding of allelic variation in peach, presently for fully red pigmentation of the flesh. In this presentation, the phenotypic and biochemical characterization, genetic mapping and gene candidate approach developed at the INRA-Avignon (France) from F2 families coming from i) an old blood-flesh peach cultivar bearing the *bf* locus, and ii) the Chinese accession 'Wu Yue Xian', that presents an other blood-flesh phenotype, under a different genetic control and non-allele to the *bf* or *Cs* loci, will be discussed. "FruitBreedomics" European project has been designed by an international consortium including scientists, stakeholders and breeding companies. One of its aims is to increase the efficiency of breeding programs in apple and peach by developing Marker Assisted Breeding (MAB) using novel genomic tools. In the frame of this project, six peach mapping populations (two intraspecific F2, two interspecific F1 derived from *P. davidiana*, one self pollinated derived from Bolinha and one advanced pseudo-backcross) segregating for mendelian traits and/or Quantitative Trait Loci (QTLs) for pest resistance and fruit quality were genotyped using an Infinium II Illumina bead-chip containing 8144 SNPs derived from the sequencing of the peach genome. Mapping results were contrasted depending on the population considered. All maps align with the corrected peach genome sequence v1.0 (IPGI), but the best polymorphisms and coverage were obtained with the F2 and pseudo-backcross populations. Twenty to twenty-nine percent of the SNPs were polymorphic. However, they were unevenly distributed in 500 loci on average, although covering most of the peach genome; in contrast, only 5% of the SNPs were polymorphic for the F1 and selfing of Bolinha., resulting in low coverage and very heterogeneous distributions. As primary consequence, these demonstrate the poor transferability of such a tool between species, even tightly related, and additionally highlight the relatively low efficiency of SNPs in term of useful polymorphism in the peach germplasm. Consequently, regions containing QTLs and major genes could be insufficiently covered and need additional SNP development for MAB. The relevancy of using general medium-range SNP bead-chips for breeding purposes is discussed in this study.

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