O37 Independent mutations in a single locus, the transcriptional factor *MYB10*, control natural variation in fruit color among *Fragaria* species

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External and internal fruit color are important traits in strawberry (*Fragaria* spp.) breeding programs, where different preferences are sought depending on whether the fruits are produced for fresh consumption or processing. Therefore, there is a great interest in the development of predictive markers that effectively speed the development of new cultivars with increased consumer acceptance and/or which address processed fruit industry´s preferences. In order to identify *loci* controlling fruit color variation, two mapping populations were generated: one crossing diploid *F. vesca* parentals and another interspecific population between two octoploid species: the cultivated and the Chilean strawberry, *F.* × *ananassa* and *F. chiloensis*. Both populations allowed the detection of a QTL spanning a region of the *F. vesca* linkage group 1 (LG I) that includes the *MYB10* gene, a known key regulator of anthocyanin biosynthesis. Mapping by sequencing in the *F. vesca* population revealed an LTR retrotransposon inserted in the third exon of *FvMYB10*, which produces a premature stop codon, and co-segregates with white fruits in the entire population. Genotyping by Sanger sequencing of additional white-fruited *F. vesca* accessions resulted in the identification of another three independent mutations in *MYB10*, two of them not previously described[1]. In octoploid strawberry, a mayor QTL on LG I-3 controls about 55% variation in internal flesh color and is associated with an insertion in the promoter region of *FcMYB10*. Similar insertions have been detected in other *F. chiloensis* accessions bearing white fruits. In all cases, transient over-expression of *FvMYB10* restored anthocyanin biosynthesis and red color in fruit flesh and skin, indicating that lack of function of *MYB10* was the underlying cause of white fruits in all analyzed cases.

[1]Hawkins, C., et al. (2016). Genome-scale DNA variant analysis and functional validation of a SNP underlying yellow fruit color in wild strawberry. Sci. Rep. 6, 29017.

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