

New Strawberry QTLs for Pleasant Key Aroma Compounds in F1 Population

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Strawberry is a plant with vegetative reproduction whose fruits are highly appreciated due to its organoleptic properties and health benefits. Cultivated strawberry (*Fragaria x ananassa*) is an allo-octoploid species with a fairly small genome, mostly diploidized. Wild strawberry (*F. vesca*) is a diploid species with small and soft, but very aromatic, fruits. The aroma of cultivated strawberry has been widely studied: the profile of volatiles obtained by gas chromatography and mass spectrometry (GC-MS) is above 350 compounds, in particular esters, terpenes, furans, lactones, alcohols, aldehydes and sulphur compounds. Analysis of the volatile compounds and the threshold of aroma detection indicate that only 20 compounds significantly contribute to the aroma of strawberry with esters being the most representative, which give fruity aromas. Other important compounds are Z-3 and E2-hexenal which give an unpleasant smell (green aroma) detected in some cultivars. A recent analysis using GC-MS for the lines *F. vesca* Reina de valles and *F. vesca* Yellow Wonder and a collection of NILs (Near Isogenic Lines) in strawberry established the volatilome and the QTL map of wild strawberry for all the compounds (Urrutia et al 2017). To determine the genomic regions responsible for the variation in aromatic compounds of cultivated strawberry, we generated a segregating F1 population of the cross between two lines segregating for aroma in wild strawberry, "Dream x Starlette" (70 individuals). This population was genotyped with the IStraw35K® array giving a map of 28 linkage groups (14,335 SNPs, 3,167 loci) covering >92% of the genome compared with the consensus map. Volatile analyses (GC-MS) of the population mature fruit, measured over a period of three years and at different stages of harvest, detected more than 300 segregating compounds. Analyses of the 19 specific compounds responsible for strawberry aroma revealed 62 QTLs, 14 of them highly significant in all of the analyses. We specifically detected a single QTL which regulates accumulation of the esters methyl hexanoate and ethyl hexanoate, both responsible for a fruity aroma in strawberry, in a region limited by LG4B. New QTLs will be checked for candidate genes, which genes are in these regions and select some of these as candidate genes. All these new QTLs should be checked in different populations.

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