

PEACH VOLATILE COMPOUNDS QTL ANALYSIS AND CANDIDATE GENE CO-LOCALISATION

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Peach flavour is the sum of the interaction of sugars, acids and a set of around 23 volatile compounds. Some of these volatiles impart desirable qualities while others are perceived as off-flavours. The identification of the aroma compounds and their interactions that most influence flavour perception are seen as important target in peach breeding programs. In peach fruits, the aroma formation is a dynamic process during which the concentration of VOCs changes both in quantity and quality, and depends basically on genotype, ripening stage, pre- and post-harvest conditions. Moreover, peach breeding programs have traditionally focused on agronomic traits such as fruit size and firmness, productivity, resistance to biotic and abiotic stress and easy tree training, and traits affecting aroma and flavour have often been overlooked. The aims of this study were to identify QTLs for VOCs in peach, to further understand the genetic basis of these components and to pave the way towards breeding-assisted selection programs by identifying molecular markers linked to some of these QTLs. We report for the first time the identification of peach genome regions controlling the variability of volatile compounds through QTL detection in a cross between two peach cultivars. The progeny assessed in this study is an F₁ of 129 seedlings obtained from a cross between the peach cultivars 'Bolero' (B), melting flesh, and 'OroA' (O), non-melting flesh. QTLs were identified for 19 out of 23 VOCs analysed, including three major QTLs for nonanal, linalool and p-menth-1-en-9-al. Using the map position available for a large number of fruit quality candidate genes on the *Prunus* reference map, two putative candidate genes were co-localised with the QTL: A lipoxygenase (LOX) putatively involved in nonanal biosynthesis and a geranylgeranyl diphosphate synthase (GGPPS), putatively involved in the biosynthesis of linalool and p-menth-1-en-9-al. Despite the difficulty in working on the dissection of this complex trait, the results are encouraging. The identification of genes putatively involved in peach aroma variability opens new paths of research to further validate these results in other progenies.