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Identification of genomic regions and candidate genes involved in fruit ripening in two apricot (*Prunus armeniaca* L.) cultivars

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In apricot, there are major difficulties in keeping the ripening under control and predominantly at the post-harvest stage. Consequently, the knowledge of mechanisms involved in fruit ripening is particularly important. It is the reason why the identification of genomic regions involved in apricot ripening has been targeted.

An apricot F₁ population of 183 off springs has been constituted from a cross between two parents contrasting for their ripening features: 'Goldrich' (large, firm, orange fruit with a slow evolution during ripening, before and after picking), and 'Moniquí' (mean, soft, white fruit with a very rapid evolution and high ethylene production, particularly at the post-harvest stage). The parents and the off springs were characterized for fruit maturity date and ethylene production during two consecutive years. One SSR-based genetic linkage map anchored to the general map for *Prunus* was established for each of the parents and QTL analyses were performed for these traits. QTL stability was stated between years.

A very large variability was observed among the off-springs and QTLs were detected in several linkage groups. One common region for ethylene production and maturity date was detected in both maps. Candidate genes were identified in most of the QTL regions when compared to the annotated peach genome sequence. The sequences of the most likely genes were compared for polymorphism between parents as well as their expression and informative SNPs were identified.