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Mapping quantitative trait loci for nut quality in almond

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Almond breeding is increasingly taking into account kernel quality as a breeding objective. Information on the parameters to be considered in evaluating almond quality, such as protein and oil content, as well as oleic acid and tocopherol concentration, has been recently compiled. The genetic control of these traits has not yet been studied in almond, although this information would improve the efficiency of the almond breeding programs. A map with 56 simple sequence repeat or microsatellite (SSR) markers was constructed for an almond population showing a wide range of variability for the chemical components of the almond kernel. A total of 12 putative quantitative trait loci (QTL) controlling these chemical traits have been detected in this analysis, corresponding to seven genomic regions of the eight almond linkage groups (LG). Some OTLs were clustered in the same region or shared the same molecular markers, according to the correlations already found between the chemic al traits. The logarithm of the odds (LOD) values for any given trait ranged from 2.12 to 4.87, explaining from 11.0 to 33.1% of the phenotypic variance of the trait. The results produced in the study offer the opportunity to include the new genetic information in the almond breeding programs. Increases in the positive traits of kernel quality may be looked for simultaneously whenever they are genetically independent, even if they are negatively correlated. We have provided the first genetic framework for the chemical components of the almond kernel, with twelve QTLs in agreement with the large number of genes controlling their metabolism.