P1-1

Mapping QTLs for nut and kernel traits in almond.

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Abstract

Almond breeding is increasingly considering kernel quality as an objective. Information on the parameters to be considered in evaluating almond quality as well as nut and kernel physical parameters has been recently compiled. However, the genetic control of such traits has been scarcely studied, although this information would improve the efficiency of the breeding programs. A map with 56 SSR markers was constructed for an almond population showing a wide range of variability for the chemical components and the nut and kernel physical parameters. A total of 26 putative quantitative trait loci (QTL) controlling these chemical and physical traits have been detected in this analysis, corresponding to 7 genomic regions of the 8 almond linkage groups. Some QTLs were clustered in the same region or shared the same molecular markers, as indicated by the correlations between the traits. The logarithm of the odds values for any given trait ranged from 2.12 to 5.17, explaining from 11 to 44% of the phenotypic variance of the trait. These results offer the opportunity to consider new genetic information in almond breeding programs. Increases in the positive traits of kernel quality and nut/kernel physical traits may be looked for simultaneously whenever they are genetically independent, even if they are negatively correlated. The first genetic framework for the chemical components of almond kernel, with twelve QTLs, in agreement with a large number of genes controlling their metabolism is reported.