

Firmness QTL mapping using an 'Ambrunés' x 'Sweetheart' sweet cherry population

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Abstract

Sweet cherry cultivation has high cultural and economic interest in the Jerte Valley (Extremadura, Spain). 'Ambrunés' is one of the main cultivated varieties in this area and it is marketed under the Protected Origin Designation "Cereza del Jerte". 'Ambrunés' is a sweet cherry landrace, remarkably adapted to the local growing conditions, that shows exceptional organoleptic characteristics, especially fruit firmness, a trait appreciated by marketers and consumers. As the market increasingly demands high quality cherries with good postharvest quality, 'Ambrunés' is a relevant genetic resource for sweet cherry breeding. In this work, a breeding population of the Sweet Cherry Breeding Program belonging to CICYTEX in Extremadura, that comes from the crossing of the sweet cherry cultivars 'Ambrunés' x 'Sweetheart', was used to study the genetic control of fruit quality traits, particularly fruit firmness. Fruit traits (size, weight and firmness) were phenotyped in two different harvest seasons. A high heritability of fruit firmness was detected and segregation was distorted towards softer fruits. The family was genotyped using the RosBREED whole genome cherry 6K Illumina Infinium® SNP array v1, and a saturated linkage map was developed. Firmness QTL analysis identified a major QTL on LG1 and confirmed a previously described sweet cherry firmness QTL on LG6. Haplotype analysis permitted the identification of favorable alleles that can assist selection of firm offspring from 'Ambrunés'. Ultimately, the genetic map developed will allow the genetic analysis of further traits in this family.