



QTL MAPPING IN MULTIPLE SWEET CHERRY POPULATIONS REVEAL LG4 AS MAJOR DETERMINANT OF FRUIT DEVELOPMENT, MATURITY AND QUALITY TRAITS.



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ABSTRACT:

The release of new sweet cherry (*Prunus avium* L.) cultivars adapted to consumer and producer demands, and that confront challenges like global warming; make it necessary to advance in the biological mechanisms of most relevant phenology and fruit quality traits to develop tools that allow optimizing the breeding process. Therefore, in this work, 411 individuals derived from six different sweet cherry populations (four F1 and two F2 populations) were used to investigate the genetics underlying maturity date, fruit development period, and fruit quality traits including fruit firmness and solid soluble content (SSC). These populations descend from cross- and/or self-pollinations of landraces ('Cristobalina' and 'Ambrunés') and bred cultivars ('Brooks', 'Lambert' and 'Vic') which show large phenotypic variation for the analyzed traits. The populations were genotyped using RosBREED Cherry 6K SNP array and phenotyped during two years. QTL analyses were carried out for the six populations, using FlexQTL software, to maximize QTL/allele detection in these plant materials. Fruit development and SSC QTL analyses are first reported in sweet cherry in this work. Major QTLs for the four traits were identified overlapping on a narrow region of linkage group 4. Additionally a high positive correlation was observed among them, with large fruit development period correlated to late maturity, high firmness and high SSC. Haplotypes of breeding interest, short/large fruit development period associated with early/late maturity date, and low/high firmness and SSC were identified. The results will be discussed in terms of the relationship between these traits, their relation with bloom time QTLs results previously reported for the same plant material, and their application for breeding purposes.



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