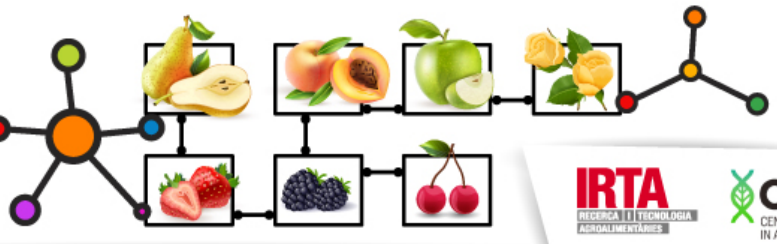

GENETIC ANALYSIS OF PHENOLIC COMPOUNDS IN SWEET CHERRY

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ABSTRACT:

Sweet cherries (*Prunus avium* L.) are an excellent source of phytochemical compounds with health-promoting properties, of which polyphenols are the most abundant. These compounds also play a substantial role in some sensory fruit traits such as color, taste, flavor or astringency. Despite this relevance, many studies have focused on the evaluation of these compounds at cultivar level, and less information has been reported about their genetic control. In this work, we used a color segregating F1 sweet cherry population ('Vic' × 'Cristobalina', N=161) to investigate phenolic content genetics, and their relationship with fruit color. This population was phenotyped for anthocyanins and hydroxycinnamic acids by high-performance liquid chromatography (HPLC) and genotyped with RosBREED 15K SNP array. Linkage maps constructed for the parental cultivars 'Vic' (910 SNPs; 636.7 cM) and 'Cristobalina' (789 SNPs; 666.0 cM) using JoinMap 4.1 were used for (QTL) analyses with MapQTL 6.0. Major overlapping QTLs on linkage group 3 for anthocyanins (cyanidin-3-*O*-glucoside, cyanidin-3-*O* -rutinoside, peonidin-3-*O*-glucoside and peonidin-3-*O* -rutinoside) and for skin and fresh color, were identified. These results confirm *PavMYB10* (linkage group 3) as candidate gene of anthocyanin biosynthesis regulation and fruit color in sweet cherry. Hydroxycinnamic acids genetic analysis was carried out by first time in *Prunus* species in this study. Overlapping major QTLs of hydroxycinnamic acids detected (neochlorogenic, *p*-coumaroylquinic and chlorogenic acids) were found on a narrow region at bottom of linkage group 1 (PVE 77.9%). Candidate gene of hydroxycinnamic acid regulation, reported in a syntenic region of linkage group 1 of *Malus* species (*shikimate/quinate O-hydroxycinnamoyl transferase, HCT/HQT*), may be also be candidate gene for sweet cherry and *Prunus* species.