Genetic analysis of phenolic compounds in sweet cherry

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Introduction

Sweet cherries are an excellent source of numerous phytochemical compounds with health-promoting properties, which also play relevant roles in sensory fruit traits such as color, flavor, taste or astringency. Polyphenols present in sweet cherry derive from shikimate acid, being anthocyanins and hydroxycinnamic acids the most abundant. Despite the importance of polyphenols, most studies in sweet cherry have been focused on the variation of these compounds at genotype level, and little information about their genetic control has been reported in *Prunus* species.

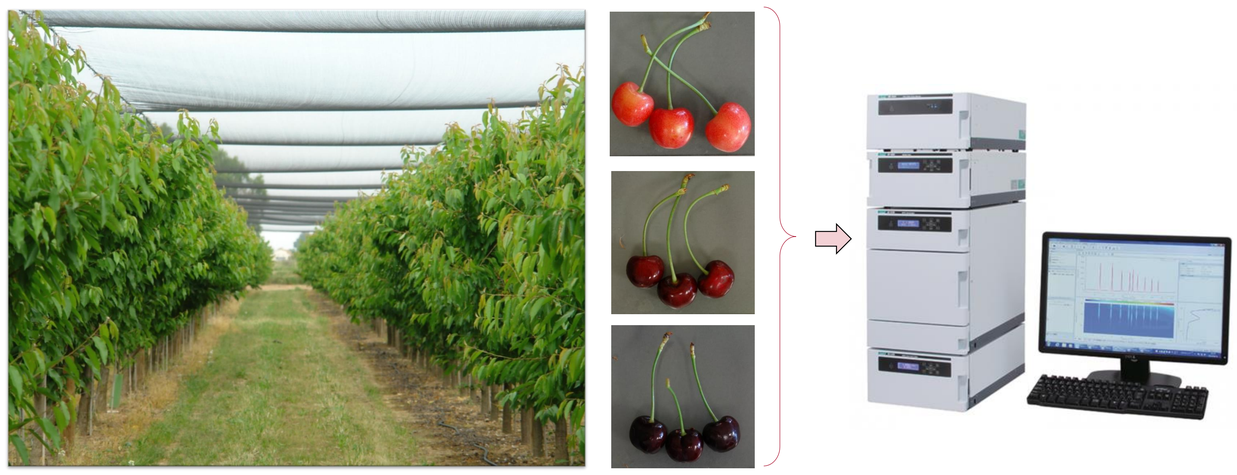

Figure 1. V×C population, fruits from selected trees, and chromatography equipment used for phenotyping polyphenols.

Materials and methods

An F_1 sweet cherry population (N=161) from 'Vic' × 'Cristobalina' (V× C) was used. Phenolic compounds for each individual were extracted and quantified as described by Serradilla et al. (2011) by chromatographic analysis (Figure 1). Genome-wide SNP genotyping in the population was carried out using RosBREED Cherry 6+9K Illumina Infinium SNP array. SNP filtering, clustering and parental linkage map construction were developed as previously described in Calle et al. (2018). For QTL analyses, MapQTL v.6.0 was used through Interval mapping and MQM mapping strategies.

Results and Discussion

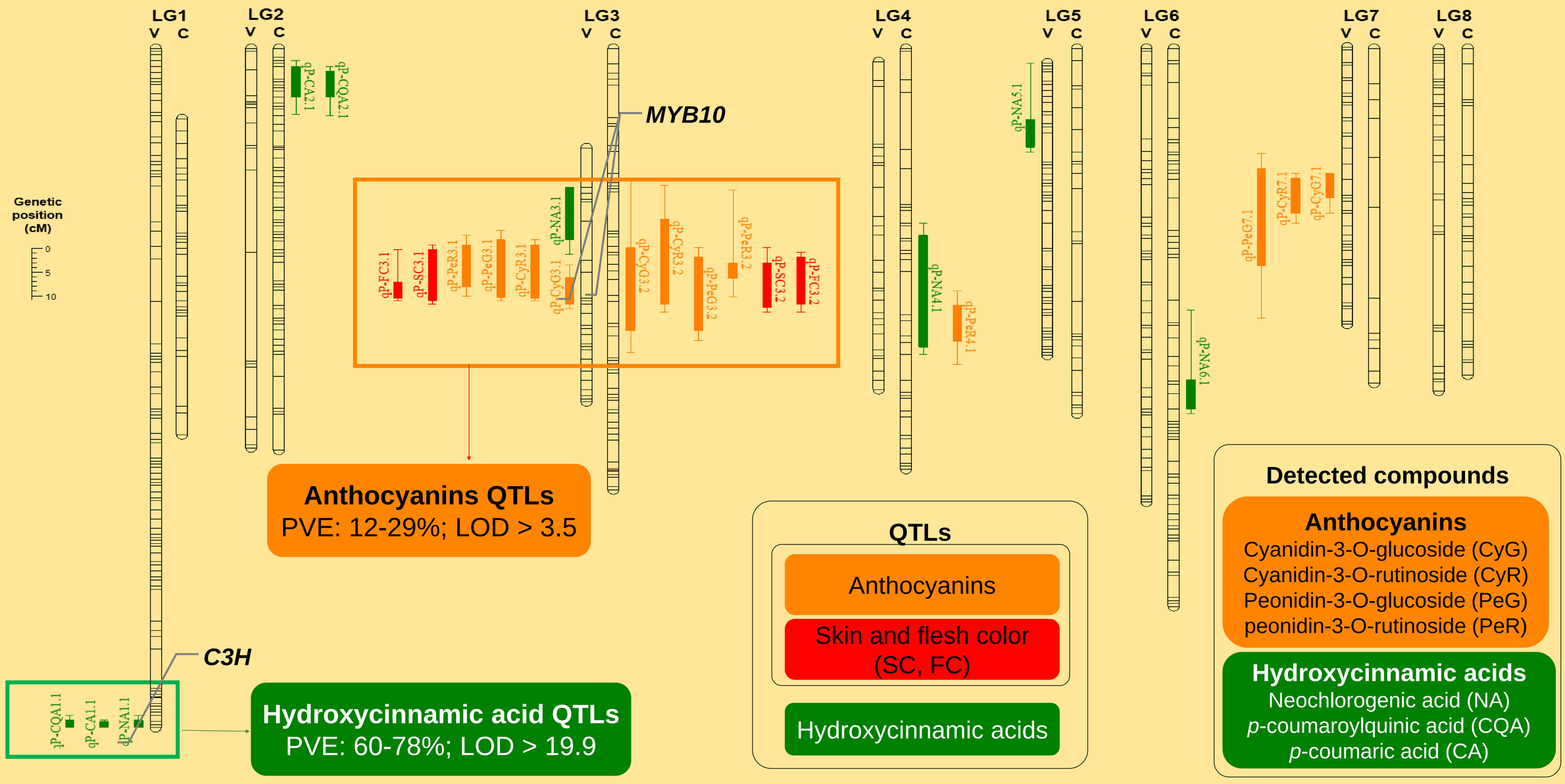

Figure 2. 'Vic' (V) and 'Cristobalina' (C) linkage maps developed with 9+6K SNP array, and detected QTLs for anthocyanins, skin and flesh color, and hydroxycinnamic acids.

Hydroxycinnamic acids

Major QTLs (Figure 2) for hydroxycinnamic acids were found on a narrow region at the bottom of LG1 (Figure 2), revealing the genetic regulation of these compounds is determined by a major gene. Candidate gene *ρ-coumarate 3-hydroxylase* (*C3H*) was found to co-localize with these QTLs (Figure 2). *C3H*, is therefore a strong candidate for hydroxycinnamic acid content regulation in sweet cherry and probably in other *Prunus* species. Additional minor QTLs associated to hydroxycinnamic acids were identified on LGs 2, 3, 4, 5 and 6 (Calle et al., in press).

Anthocyanins

Most significant anthocyanins content QTLs were found on LG3 (Figure 2). These QTLs overlapped with skin and flesh color QTLs, in the same genomic region where candidate gene *MYB10* is located. The results confirms *MYB10* transcription factor as main determinant of sweet cherry color by anthocyanin biosynthesis regulation. Additional anthocyanins QTLs on LGs 4 and 7, revealed new *loci* associated with anthocyanin content in the species (Calle et al., in press)

References
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Serradilla et al. (2011) Physicochemical and bioactive properties evolution during ripening of 'Ambrunés' sweet cherry cultivar. *LWT-Food Sci. Tech.* 44:199- 205.

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