

# QTL mapping in multiple sweet cherry populations reveals LG4 as major determinant of fruit development, maturity and quality traits

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## Introduction

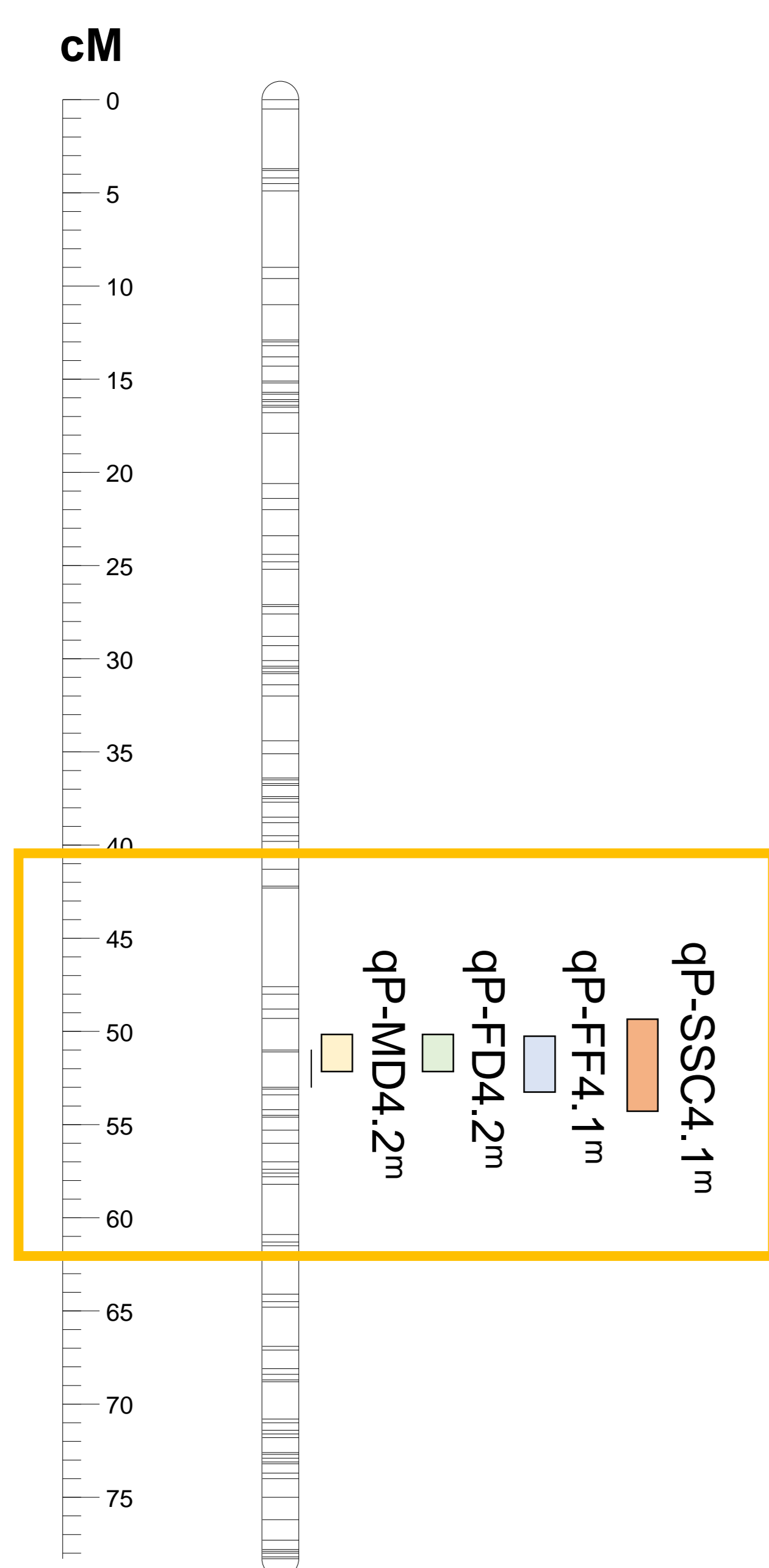
Sweet cherries are mainly consumed as fresh fruit and their market profitability is related to maturity date and fruit quality. It is therefore important to understand the mechanism regulating these traits in order to optimize the breeding process. The genetics of some of these traits have been studied in some *Prunus* species, including in some sweet cherry populations. In this work, we investigate the genetics of maturity date, firmness, fruit development time and solid soluble content (SSC) using a multifamily QTL mapping approach. Fruit development time and SSC QTL mapping are first described in this work.



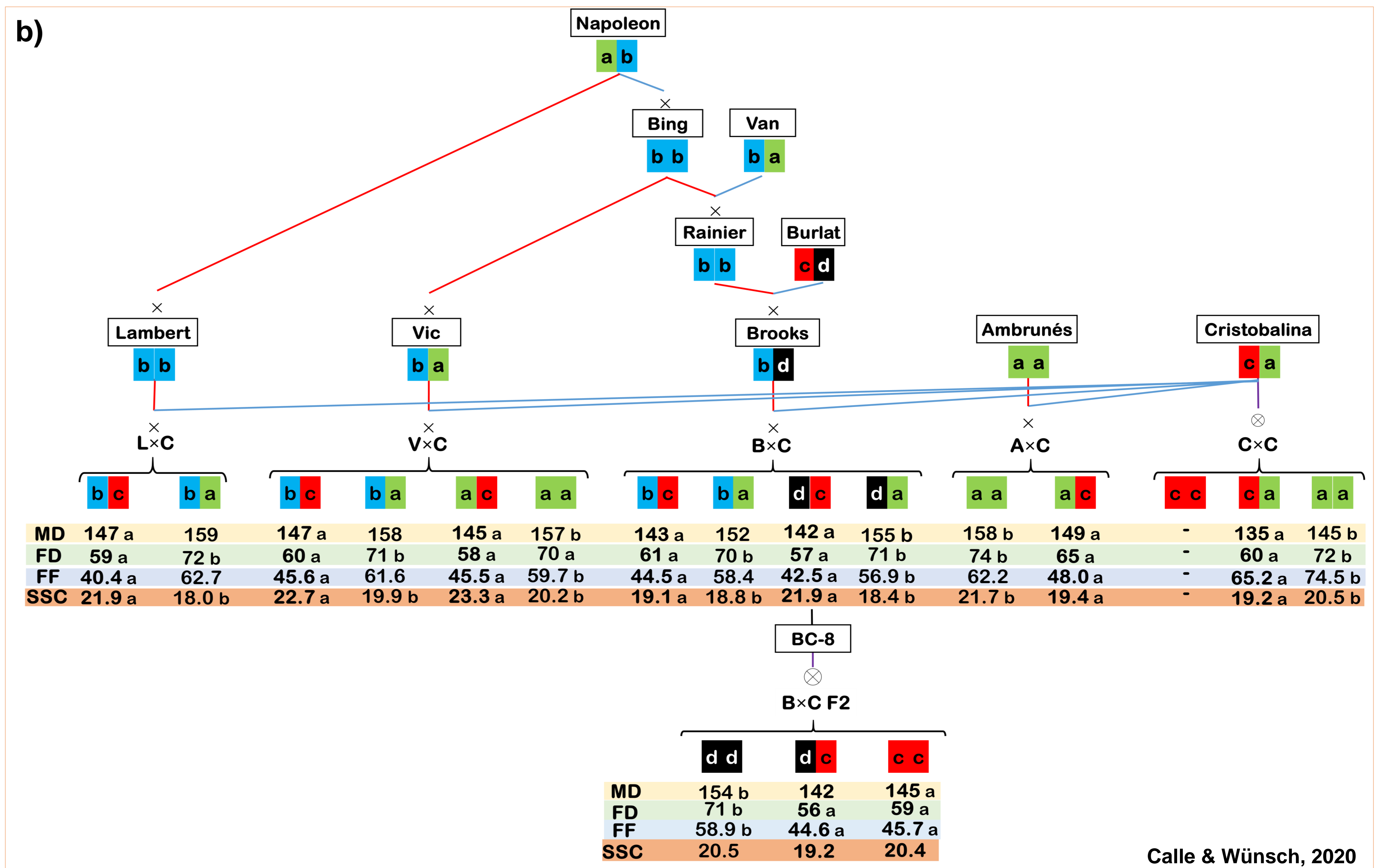
## Materials and methods

Maturity date (calendar days), fruit development time (days between blooming and maturity date), fruit firmness (% DuroColor), and SSC (°Brix) were evaluated in 411 sweet cherry individuals from six populations and in their respectively parental and ancestors during two years (Figure 1). QTL analyses in the six families were done using FlexQTL software by MCMC simulations with a minimum of 500,000 iterations until at least 100 effective chain samples. The 2lnBF (Bayes factors) was used to determinate the number and position of QTLs. Parental and ancestor haplotypes were constructed for major QTLs detected on LG4 (50-54 cM). Mean phenotypic values for each segregating class of each population were also estimated for the four traits at this locus.

### a) Linkage group 4



### b)



**Figure 1** a) Genetic positions of major LG4 QTLs. b) Haplotypes of LG4 major QTLs for maturity date (MD), fruit development time (FD), fruit firmness (FF) and solid soluble content (SSC). Mean phenotypic values of both years of each segregating class in each population are shown. Significant differences between classes are indicated by letters ( $p < 0.05$ ).

## Results and Discussion

Large phenotypic variability was observed for the evaluated traits in the plant material analyzed (Calle & Wünsch, 2020). The QTL analyses revealed a cluster of major QTLs for maturity date, fruit development time, fruit firmness, and SSC on a narrow region of linkage group 4 between 50 to 54 cM (Figure 1; Table 1; Calle & Wünsch, 2020). This region is syntenic to other Rosaceae species, in which QTLs for same traits were reported in similar position. The overlapping of QTLs on the same region allowed us to construct sweet cherry haplotypes of breeding interest. Two haplotypes (c and d) were only found on the early ripening cultivars 'Burlat' and 'Cristobalina', and their descendants. Comparison of mean phenotypic values within classes of each family revealed that those individuals that carried the 'c' haplotype showed significant early ripening, short fruit development time, lower firmness and sweetness than those individuals without this haplotype (Calle & Wünsch, 2020). These knowledge will allow early selection for early or late ripening date, high or low fruit firmness and soluble solid content in sweet cherry related to this plant material.

**Table 1.** Detected QTLs both years.

Trait	QTL name	LG	Genetic position (cM)	Average 2lnBF	Additive effect	PVE (%)
Fruit Develop. Time	<i>qP-FD3.1<sup>m</sup></i>	3	17-62	6.2	2.9	4.8
	<i>qP-FD4.1<sup>m</sup></i>	4	8-32	5.9	5.4	12.0
	<i>qP-FD4.2<sup>m</sup></i>	4	51-53	11.8	11.2	64.9
Maturity Date	<i>qP-MD1.1<sup>m</sup></i>	1	50-77	7.6	3.75	7.0
	<i>qP-MD2.1<sup>m</sup></i>	2	68-76	11.7	4.4	11.0
	<i>qP-MD3.1<sup>m</sup></i>	3	13-52	8.1	4.6	13.1
	<i>qP-MD4.1<sup>m</sup></i>	4	5-33	7.7	5.0	7.6
	<i>qP-MD4.2<sup>m</sup></i>	4	51-53	11.8	11.3	49.6
Fruit Firmness	<i>qP-FF4.1<sup>m</sup></i>	4	50-54	9.5	14.7	56.0
	<i>qP-FF6.1<sup>m</sup></i>	6	74-109	2.3	3.3	1.9
Solid Soluble Content	<i>qP-SSC3.1<sup>m</sup></i>	3	18-69	4.2	1.2	8.9
	<i>qP-SSC4.1<sup>m</sup></i>	4	50-59	6.8	2.3	28.2