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Identification and validation of a QTL for fruit firmness on linkage group 4 in three sweet cherry populations

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Introduction

Fruit firmness is an important market driven trait in sweet cherry (*Prunus avium* L.) as consumers prefer firm sweet cherries (3). The firmness exhibited by modern sweet cherry varieties is a derived trait as wild cherry has small soft fruit. These increases in fruit size and firmness are the two major traits associated with domestication. However, little is known about the genetic control of fruit firmness in sweet cherry. Therefore, the objectives of this study were to identify and characterize loci that control fruit firmness in sweet cherry from three different germplasm populations, one of which contain representatives from wild cherry.

Materials and Methods

- ❖ Three sweet cherry populations were evaluated in this study: Pop1- an INRA bi-parental F₁ population from the cross of 'Fercer' × 'X' (X=unknown parent), Pop2 - an INRA diversity population, and Pop3 - RosBREED's pedigreed populations.
- ❖ Fruit firmness was evaluated using Durofel® and BioWorks' FirmTech 2 texture analyzer for INRA and RosBREED populations, respectively.
- ❖ All the individuals were genotyped with RosBREED Illumina Infinium® cherry SNP array (2).
- ❖ MultiQTL (MultiQTL Ltd, Haifa, Israel) and FlexQTL™ (1) softwares were used for QTL mapping in the F₁ and RosBREED populations, respectively. A general linear model was employed to test the marker-trait association in the diversity population.

Results

Fig. 1. Frequency distributions of fruit firmness for the three sweet cherry populations: (a) Pop1 (n=67); (b) Pop2 (n=193); (c) Pop3 (n=528).

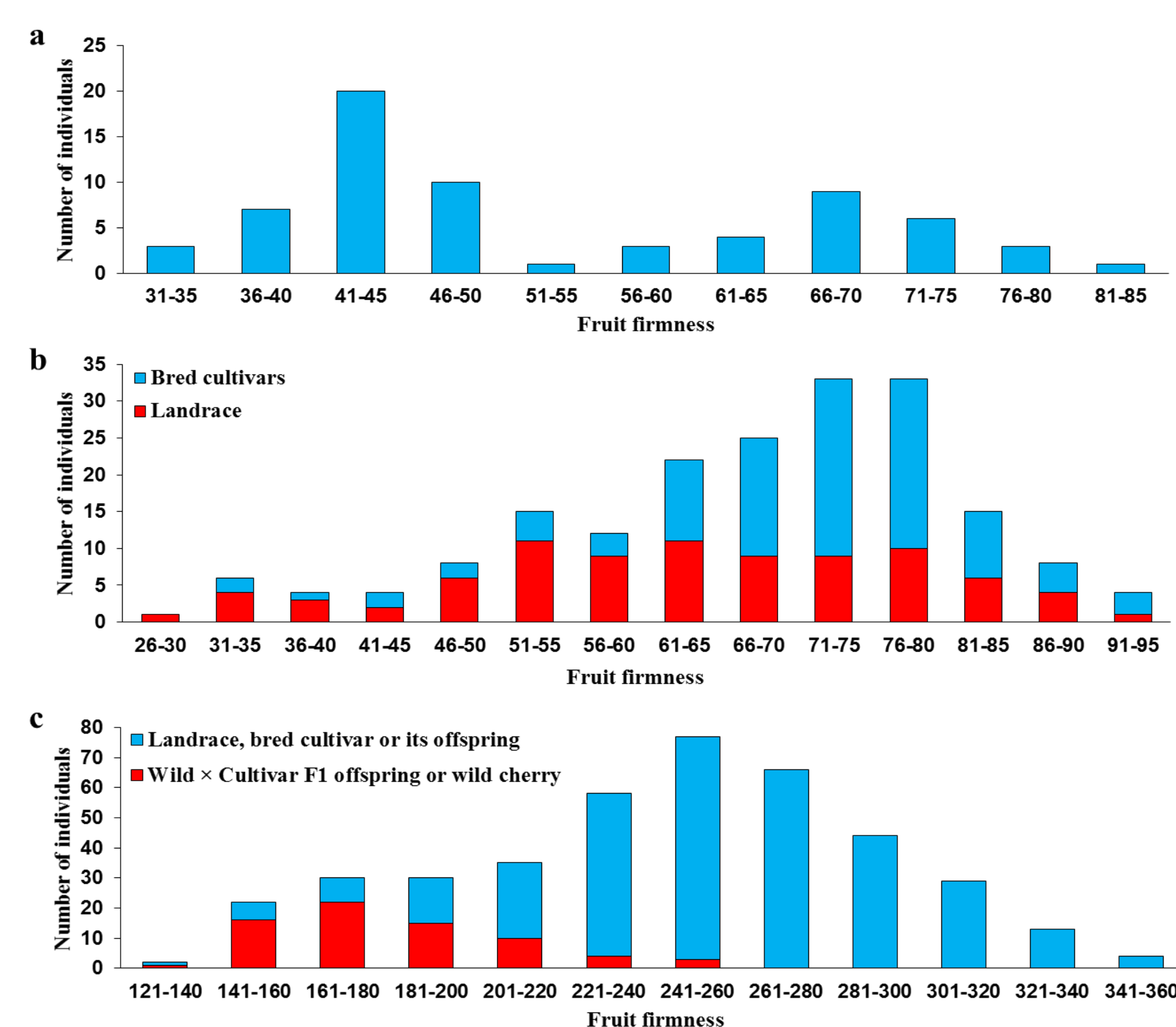


Fig. 2. The major QTL identified in the 'Fercer' × 'X' F₁ population mapped to the 'X' linkage group 4. Explained percentage of variance is given for each QTL. This previously unidentified QTL that was named *qP-FF4.1*.

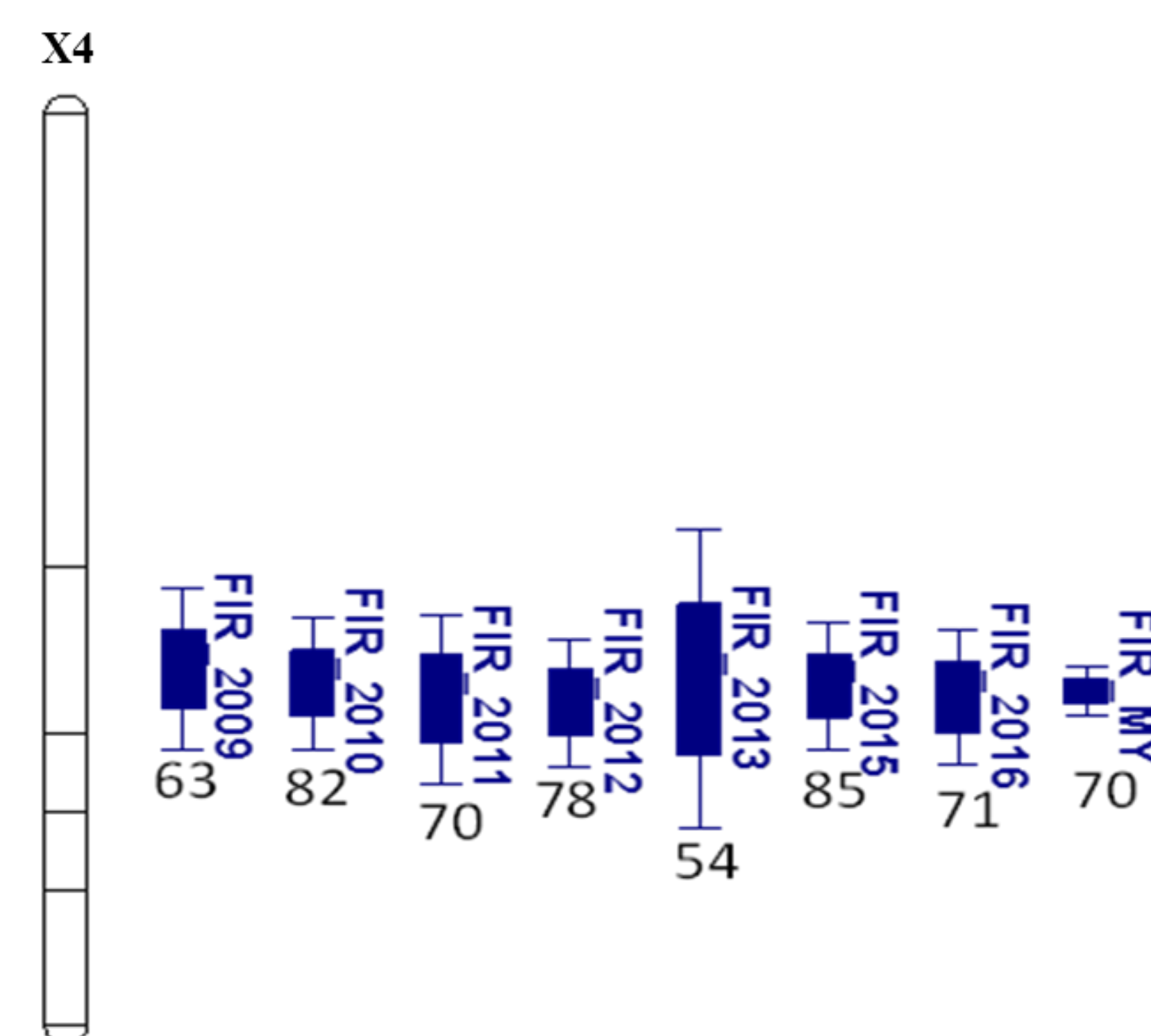


Fig. 3. Association of chromosome 4 SNP markers with fruit firmness in the INRA diversity population. (a) P values for all the SNP markers on chromosome 4. (b) Phenotypic means based on the genotype of two SNP markers that fall within the *qP-FF4.1* interval, the SNP marker ss4905522928, and (c) the SNP marker ss490552906. Phenotypic means that were significantly different (P < 0.05) are identified by different letters.

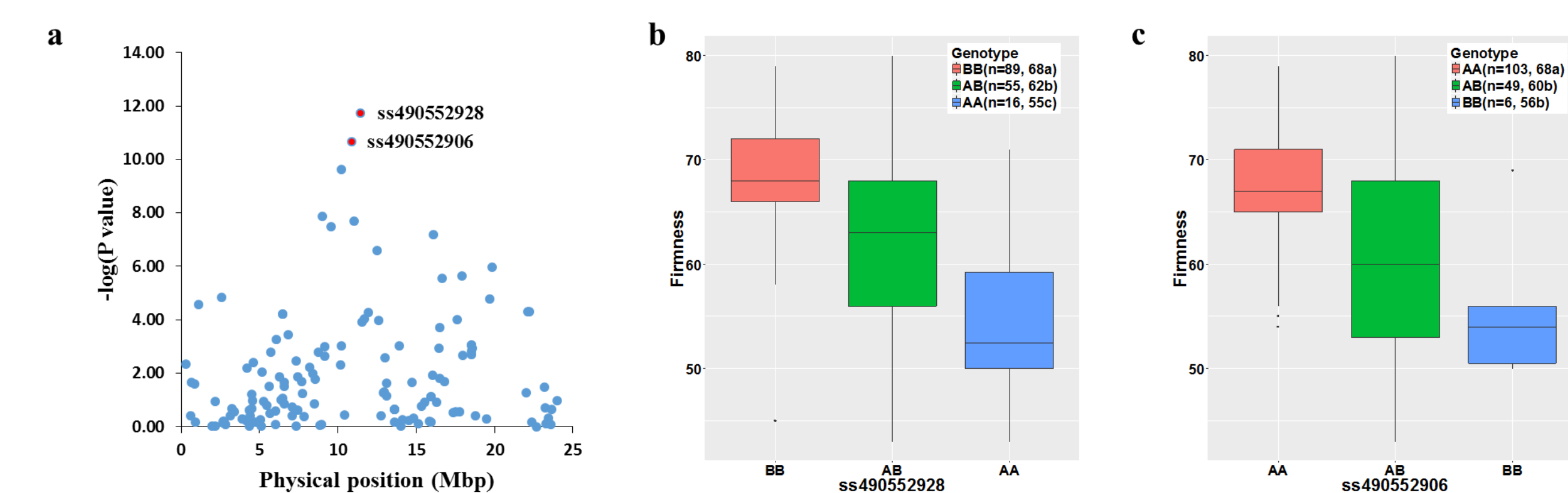


Fig. 4. *qP-FF4.1* was identified in the RosBREED pedigreed population. The QTL positions along the genome estimated by FlexQTL™ are illustrated by trace plots (top) and posterior probabilities (bottom).

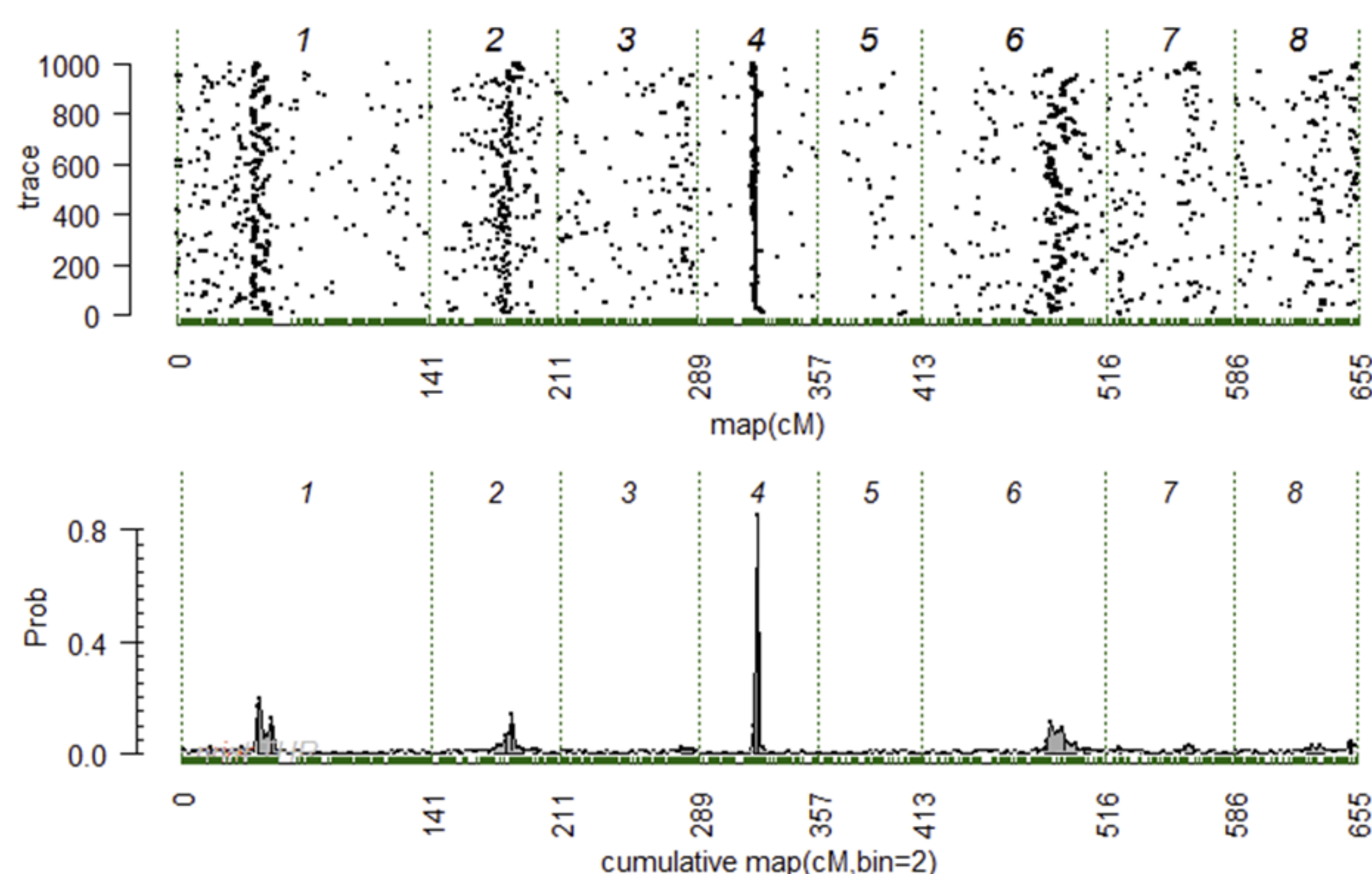
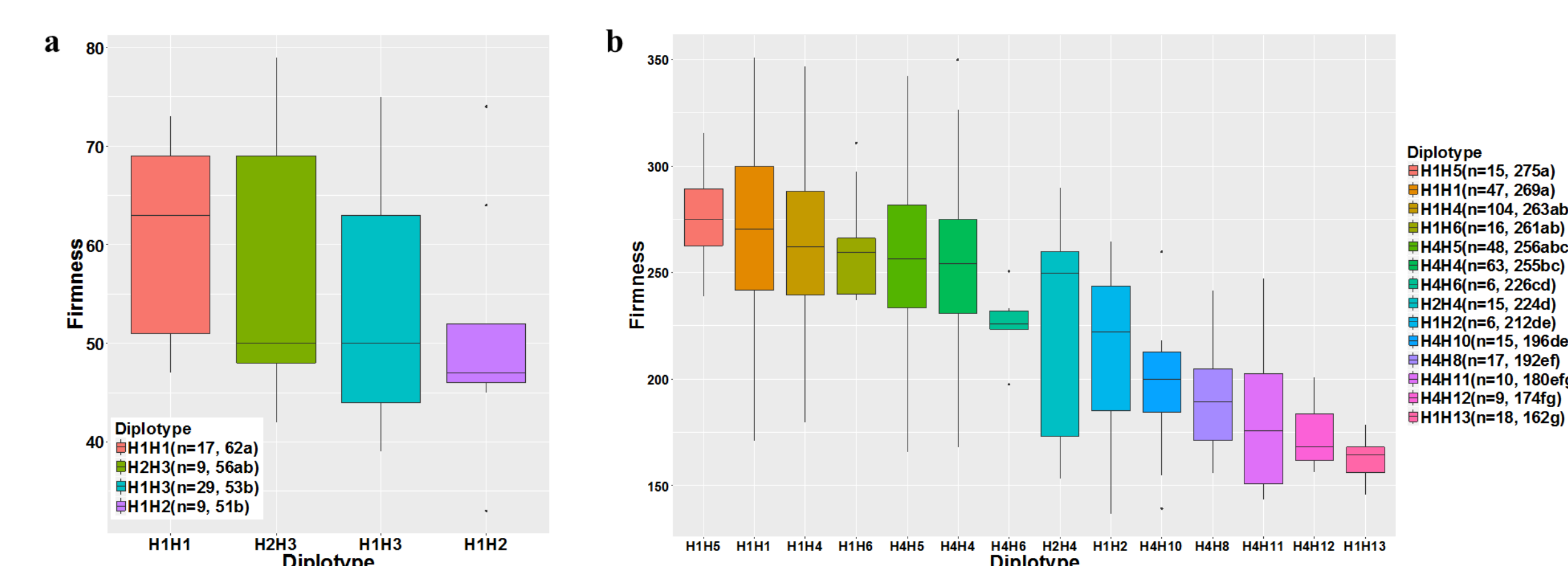


Fig. 5. Haplotypes for the fruit firmness QTL, *qP-FF4.1*. Haplotypes only identified in wild sweet cherry are marked as blue. The haplotypes were deduced to be associated with soft or firm fruit based on diplotype analysis in sweet cherry (Fig. 6).

Marker	SNP	ss490552883	ss490559054	ss490552906	ss490552912	ss490552928
	Physical position (bp)	10,241,247	10,414,884	10,880,163	11,044,975	11,472,398
	Genetic position (cM)	33.5	33.6	33.7	33.7	33.8
H1 (firm)		B	B	A	B	B
H2 (soft)		A	B	B	A	A
H3 (soft)		B	B	B	A	A
H4 (firm)		A	A	A	B	B
H5 (firm)		B	B	A	B	B
H6 (firm)		B	B	A	B	B
H7 (firm)		B	A	A	B	B
H8 (soft)		A	A	B	B	A
H9 (soft)		A	B	B	B	A
H10 (soft)		A	B	A	B	A
H11 (soft)		B	A	B	B	A
H12 (soft)		A	A	B	B	B
H13 (soft)		B	B	B	B	A

Fig. 6. Comparison of fruit firmness for progeny based on their diplotypes for *qP-FF4.1* from (a) 'Fercer' × 'X' F₁ population; and (b) RosBREED pedigreed population. Only diplotypes represented by six or more individuals were included. Phenotypic means that were significantly different (P < 0.05) are identified by different letters.



Conclusions and Future Work

A newly identified QTL for fruit firmness, named *qP-FF4.1*, was identified on LG4 in all three sweet cherry populations. The "soft fruit" alleles for *qP-FF4.1* contributed by the wild 'mazzard' cherries were dominant over the "firm fruit" alleles. These results advance our understanding of the genetic basis of fruit firmness and will help to enable the use of DNA informed breeding for this trait in sweet cherry breeding programs. Future work will include the identification of candidate genes within the QTL interval.

References

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3. Yue et al. 2017, Agriculture and Resource Economics Review 46:103-122