

## Mapping of QTL for Sugars in Ananas Melon

**Soon O. Park and Kevin M. Crosby**

*Texas Agricultural Research and Extension Center, Texas A&M University, Weslaco, TX 78596 and Vegetable & Fruit Improvement Center, Texas A&M University, College Station, TX 77843*

**Kil S. Yoo**

*Vegetable & Fruit Improvement Center, Texas A&M University, College Station, TX 77843*

**Zhoo-Hyeon Kim**

*Department of Horticulture, Gyeongsang National University, Chinju, 660-701, South Korea*

**Introduction:** Sugar components such as sucrose, fructose, glucose, and total soluble solids are major factors influencing mature melon (*Cucumis melo* L.) fruit sweetness. Molecular markers linked to genes regulating synthesis of sugar components may improve the breeder's ability to recover high sugar genotypes and aid in the development of high sugar cultivars. Therefore, our objective was to identify RAPD markers associated with QTL for sucrose, glucose, fructose, total sugars (TS), and total soluble solids (TSS) in an existing molecular marker-based linkage map constructed by means of an F<sub>2</sub> population derived from the melon cross of 'Deltex' (high sugars) x TGR1551 (low sugars).

**Materials and Methods:** One hundred-eight F<sub>2</sub> plants from the cross of 'Deltex' x TGR1551 were planted in a greenhouse at the Texas Agricultural Research and Extension Center-Weslaco in 2003. The 'Deltex' parent is an ananas type with good fruit quality, while the TGR1551 parent is a wild type with poor fruit quality. Data for sucrose, glucose, fructose, and TS were obtained from the 108 F<sub>2</sub> plants using HPLC. Total soluble solids data were also obtained from the F<sub>2</sub> plants using a temperature corrected refractometer with digital readout. A RAPD marker-based linkage map was recently developed by Park and Crosby (3) using the 108 F<sub>2</sub> plants of the same cross. MAPMAKER version 3.0 (2) was used for the linkage analysis of 208 RAPD markers. The name of each RAPD

marker is derived from an "O" prefix for Operon primers, the letters identifying the Operon kit, Operon primer number, and the approximate length (bp) of the marker (3). Simple linear regression (SLR), for each pairwise combination of quantitative traits and marker loci, was used to analyze the data for detection of QTL affecting sucrose, glucose, fructose, TS, and TSS content. Significant differences in trait associations were based on F-tests ( $P < 0.05$ ) (1). Loci with the lowest  $P$  value per QTL were chosen and then were added in a stepwise multiple regression (SMR) to select the best set of markers ( $P < 0.05$ ) for prediction of the total trait phenotypic variation explained by the identified QTL (4). Pearson correlations of mature fruit sweetness traits including three sugars were also determined in our population. All statistical analyses were conducted using the Statistical Analysis System (SAS Inst., Cary, N.C.).

**Results and Discussion:** Continuous frequency distributions for sucrose, glucose, fructose, TS, and TSS were observed in the F<sub>2</sub> population (Figure 1), indicating that the fruit sweetness traits were quantitatively inherited.

Twenty-four RAPD markers, located on several different linkage groups of the molecular marker-based melon map (Figure 2), were found to be significantly associated with QTL affecting sucrose, glucose, fructose, TS or TSS in the F<sub>2</sub> population of

the 'Deltex' x TGR1551 cross in the greenhouse based on SLR (Table 2).

Two RAPD markers were significantly associated with QTL for sucrose content in our population on the basis of SLR (Table 2). The two markers on linkage groups 1 and 3 associated with QTL (Figure 2) were significant in a SMR analysis where the full model explained 10% of the total phenotypic variation for sucrose. Five markers were significantly associated with QTL regulating glucose content in this population by means of SLR. Particularly, three unlinked markers (OK10.1500, OJ09.800, and OG17.1050), amplified from 'Deltex', accounted for 10% to 12% of the variation for the trait. The five markers were significant in the SMR analysis with a total variation of 32% for the glucose trait. We identified significant associations of nine RAPD markers, located on different linkage groups, with QTL controlling fructose concentration in the population by SLR. Eight markers were significant in the SMR analysis with a total fructose variation of 41%. Four unlinked markers were associated with QTL affecting TS and TSS in the mapping population based on SLR, respectively. In the SMR analysis the two groups of the four markers were significant with total  $R^2$  values of 18% and 23% for the TS and TSS traits, respectively.

These RAPD markers associated with the sugar synthesis QTL in the molecular linkage map detected here could be useful in melon breeding for improving the mature fruit sweetness.

#### Literature Cited:

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Table 1. Correlations of sucrose, glucose, fructose, total sugars, and total soluble solids in an F2 population derived from the melon cross of 'Deltex' x TGR1551.

Sweetness trait	Sucrose	Glucose	Fructose	Total sugars
Total soluble solids	0.63**	0.17	0.07	0.71**
Total sugars	0.79**	0.35**	0.26**	
Fructose	-0.30**	0.70**		
Glucose	-0.24*			

\*, \*\*Significant at  $P \leq 0.05$  or 0.01, respectively.

Table 2. Simple linear regression (SLR) and stepwise multiple regression (SMR) analyses of marker and data for detection of QTL for three sugars, total sugars (TS), and total soluble solids (TSS) in an F2 population derived from the cross of 'Deltex' (high sugars) x TGR1551 (low sugars).

Sugar trait	RAPD marker	Linkage group	SLR		SMR	
			<i>P</i>	<i>R</i> <sup>2</sup>	<i>P</i>	<i>R</i> <sup>2</sup>
Sucrose	OJ07.900	3	0.009	6	0.009	6
	OG16.650	1	0.039	4	0.031	4
					Cumulative <i>R</i> <sup>2</sup>	10
Glucose	OK10.1500	4	0.000	12	0.000	12
	OJ09.800	2	0.000	10	0.003	7
	OF05.500	unassigned	0.009	6	0.006	6
	OG17.1050	1	0.001	10	0.019	4
	OK04.600	unassigned	0.022	5	0.033	3
					Cumulative <i>R</i> <sup>2</sup>	32
Fructose	OE08.600	1	0.001	10	0.001	10
	OR02.800	unassigned	0.005	7	0.007	6
	OK20.1050	9	0.013	6	0.010	5
	OE14.700	7	0.023	5	0.013	5
	OK17.600	1	0.007	7	0.018	4
	OK10.1500	4	0.036	4	0.020	4
	OI12.300	3	0.012	6	0.023	4
	OJ09.800	2	0.019	5	0.039	3
	OJ13.400	unassigned	0.031	4		
					Cumulative <i>R</i> <sup>2</sup>	41
TS	OE14.700	7	0.012	6	0.012	6
	OC14.1400	3	0.030	4	0.021	5
	OM14.500	12	0.032	4	0.029	4
	OJ09.350	2	0.045	4	0.042	3
					Cumulative <i>R</i> <sup>2</sup>	18
TSS	OK10.550	6	0.002	8	0.002	8
	OC18.900	2	0.008	6	0.009	6
	OB12.550	8	0.013	6	0.017	5
	OC14.1400	3	0.021	5	0.038	4
					Cumulative <i>R</i> <sup>2</sup>	23

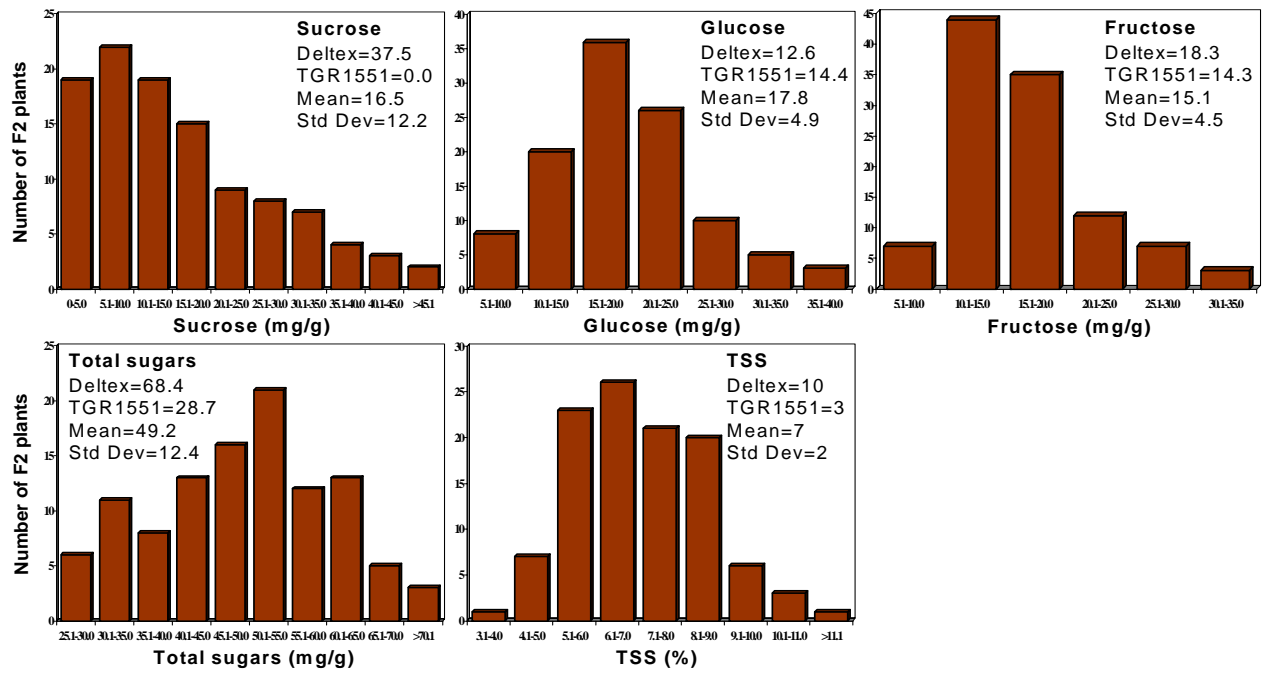


Figure 1. Frequency distributions for sucrose, glucose, fructose, total sugars, and total soluble solids (TSS) of F2 plants derived from the melon cross of 'Deltex' x TGR1551.

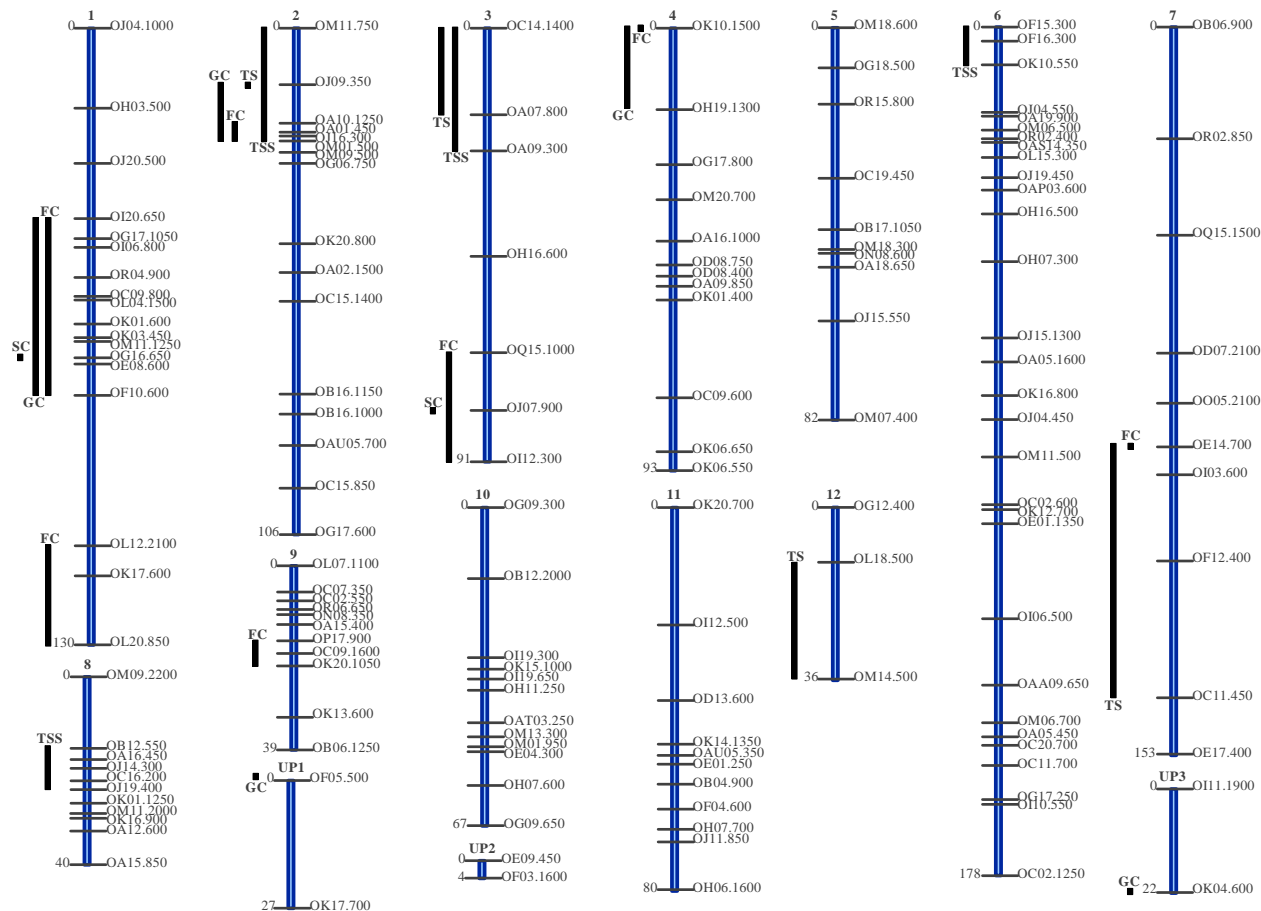


Figure 2. Linkage map for the 'Deltex' x TGR1551 mapping population with locations of QTL for mature melon fruit sweetness traits. Bars to the left of each linkage group indicate the intervals having significant trait associations ( $P < 0.05$ ). For traits evaluated in the current study: SC = sucrose content; GC = glucose content; FC = fructose content; TS = total sugars; and TSS = total soluble solids.