Mapping of QTL for Fruit Size and Shape Traits 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

Zhoo-Hyeon Kim
Department of Horticulture, Gyeongsang National University, Chinju, 660-701, South Korea

Introduction: Mature fruit size and shape are important traits of most melon (*Cucumis melo* L.) types. The former is also an important component of yield in melon. Information on molecular markers linked to genes for these fruit traits may contribute to our understanding of the genetics of fruit size and shape and offer prospects for the use of molecular markers in modification or maintenance of fruit characteristics in melon breeding programs. Therefore, our objective was to identify RAPD markers linked to QTL for fruit weight, length, and diameter in an existing molecular marker-based linkage map constructed by means of an F2 population derived from the melon cross of 'Deltex' (larger fruit size) x TGR1551 (smaller fruit size).

Materials and Methods: One hundred-eight F2 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 larger fruit size, while the TGR1551 parent is a wild type with smaller fruit size. Phenotypic data for fruit weight, length, and diameter were recorded from the 108 F2 plants along with their parents. A RAPD marker-based linkage map was recently developed by Park and Crosby (3) using the 108 F2 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 fruit weight, length, and diameter. 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 fruit size and shape traits 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 fruit weight, length, and diameter were observed in the F2 population (Figure 1), indicating that the fruit size and shape traits were quantitatively inherited. Mature fruit weight was found to be significantly and positively correlated with fruit length and diameter in the population (Table 1). We also noted a significant positive correlation between fruit length and diameter.

Twenty-two 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 controlling fruit weight, length, or diameter in the F2 population of the 'Deltex' x TGR1551 cross in the greenhouse on the basis of SLR (Table 2).

A total of nine RAPD markers were identified to be significantly associated with QTL for fruit weight in our population based on SLR

(Table 2, Figure 2). Seven unlinked markers associated with QTL were significant in a SMR analysis where the full model explained 42% of the total phenotypic variation for fruit weight.

Five markers were detected to be significantly associated with QTL regulating fruit length in this population by means of SLR (Table 2, Figure 2). Particularly, marker OR02.850 on linkage group 7 amplified from 'Deltex' accounted for 20% of the phenotypic variation for the trait. The five markers were significant in the SMR analysis with a total phenotypic variation of 40% for the fruit length trait.

We found significant associations of eight RAPD markers, located on several different linkage groups of the molecular linkage map, with QTL affecting fruit diameter in the population on the basis of SLR (Table 2, Figure 2). Seven markers were significant in the SMR analysis with a total phenotypic variation of 37% for the fruit diameter trait.

Of the RAPD markers associated with nine QTL for fruit weight in the molecular marker-based linkage group detected here, four on linkage groups 3, 6, 7 and 9 and three on linkage groups 3, 7 and UP3 (Figure 2) were also observed to be significantly associated with QTL for fruit length and diameter, respectively (Table 2), suggesting that in this cross these fruit size and shape traits are controlled partially by the same QTL.

These RAPD markers associated with QTL controlling the mature fruit size and shape traits in the molecular linkage map identified here are expected to be useful in melon breeding programs for modifying fruit size.

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:

1. Edwards, M.D., C.W. Stuber, and J.F. Wendell. 1987. Molecular marker-facilitated investigations of quantitative trait loci in maize. I. Numbers, genomic distribution, and types of gene action. Genetics 116:113-125.
2. Lander, E.S., P. Green, J. Abrahamson, A. Barlow, M.J. Daly, S.E. Lincoln, and L. Newburg. 1987. MAPMAKER: An interactive computer package for constructing primary genetic linkage maps with experimental and natural populations. Genomics 1:174-181.
3. Park, S.O. and K.M. Crosby. 2007. Construction of a RAPD marker-based linkage map in ananas melon. Cucurbit Genetics Cooperative 30:submitted.
4. Paterson, A.H., S. Damon, J.D. Hewitt, D. Zamir, H.D. Rabinowitch, S.E. Lincoln, E.S. Lander, and S.D. Tanksley. 1991. Mendelian factors underlying quantitative traits in tomato: Comparison across species, generations, and environments. Genetics 127:181-197.

Table 1. Pearson correlations of fruit weight, length, and diameter in an F2 population derived from the melon cross of 'Deltex' x TGR1551.

Fruit weight and length	Fruit weight and diameter	Fruit length and diameter
0.79**	0.73**	0.24**

**Significant at $P \leq 0.01$.

Table 2. Simple linear regression (SLR) and stepwise multiple regression (SMR) analyses of marker and data for detection of QTL for fruit weight, length, and diameter in an F2 population derived from the cross of 'Deltex' (larger fruit weight) x TGR1551 (smaller fruit weight).

Fruit trait	RAPD marker	Linkage group	SLR		SMR	
			P	R^2	*P*	R^2
Weight	OB06.900	7	0.000	10	0.000	10
	OI03.600	7	0.001	9	0.001	9
	OP17.900	9	0.003	8	0.004	7
	OJ04.450	6	0.005	7	0.007	6
	OQ15.1000	3	0.008	6	0.026	4
	OG05.1050	unassigned	0.026	5	0.034	3
	OG09.300	10	0.038	4	0.045	3
	OK04.600	unassigned	0.028	4		
	OA10.1250	2	0.047	4		
					Cumulative R^2	42
Length	OR02.850	7	0.000	20	0.000	20
	OP17.900	9	0.001	9	0.001	9
	OJ04.450	6	0.017	5	0.015	5
	OQ15.1000	3	0.030	4	0.032	3
	OJ13.400	unassigned	0.040	4	0.043	3
					Cumulative R^2	40
Diameter	OI03.600	7	0.002	8	0.002	8
	OI11.1900	unassigned	0.004	8	0.004	8
	OM06.500	6	0.016	5	0.011	5
	OJ07.900	3	0.011	6	0.013	5
	OC15.1400	2	0.013	6	0.015	5
	OK20.700	11	0.028	4	0.033	3
	OL18.500	12	0.034	4	0.047	3
	OB16.500	unassigned	0.049	4		
					Cumulative R^2	37

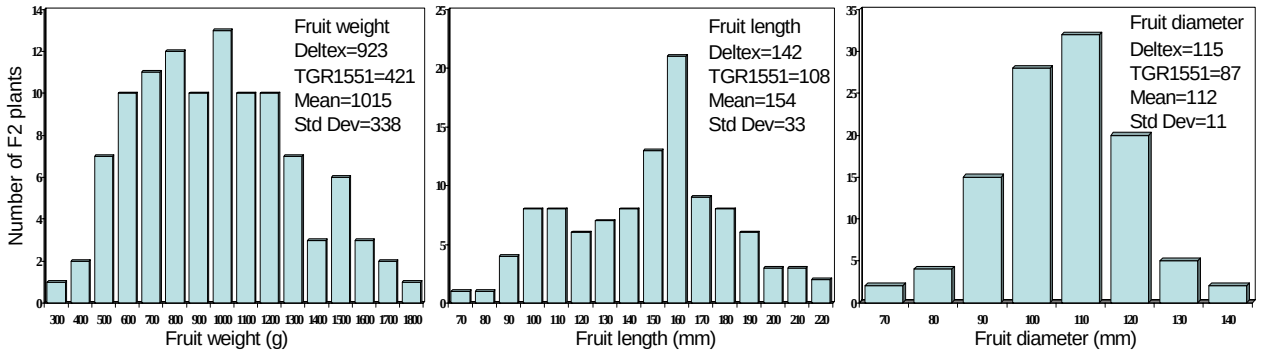

Figure 1. Frequency distributions for fruit weight, length, and diameter of F2 plants derived from the melon cross of 'Deltex' (larger fruit weight) x TGR1551 (smaller fruit weight).

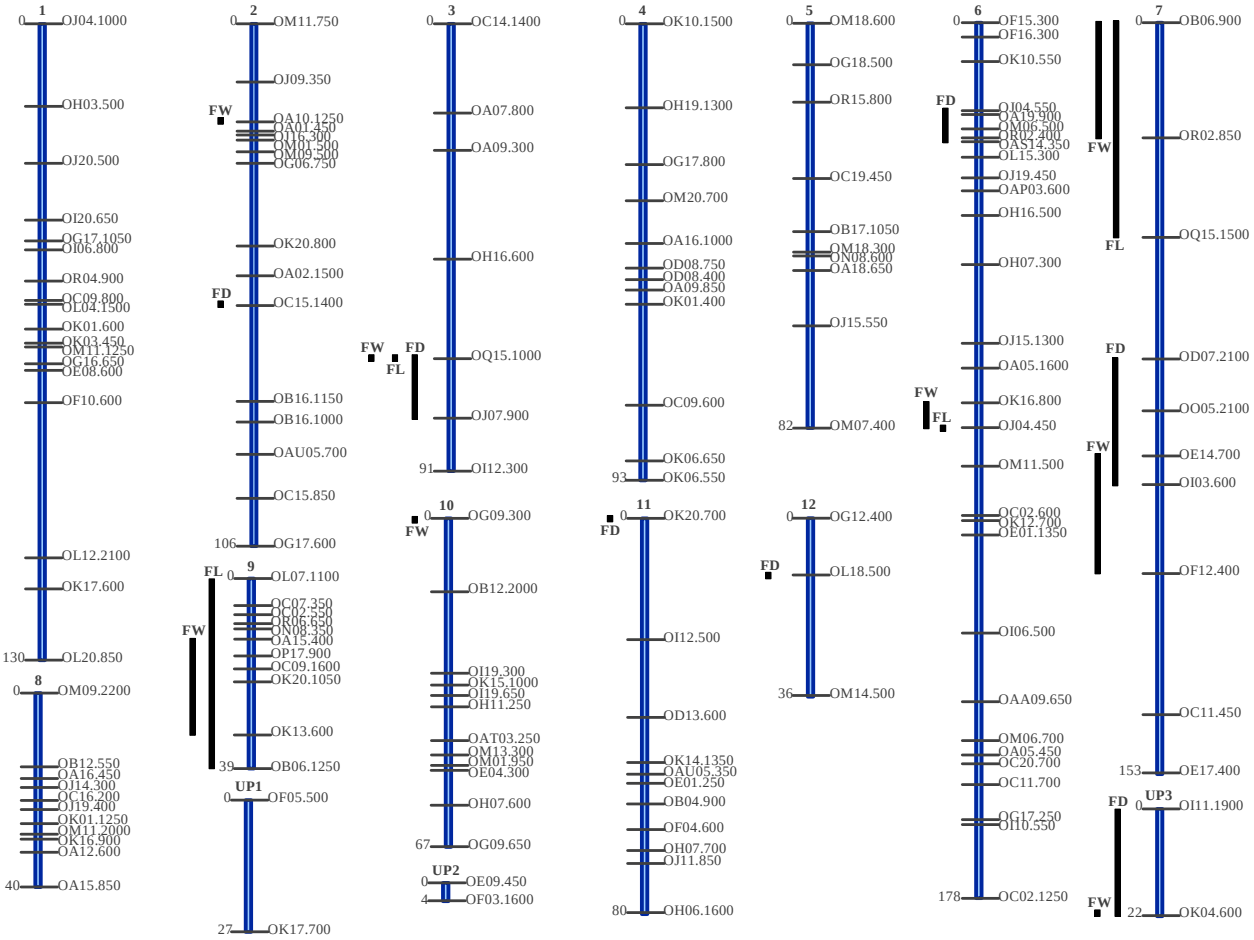

Figure 2. Linkage map for the 'Deltex' x TGR1551 mapping population with locations of QTL for melon fruit size and shape traits. Bars to the left of each linkage group indicate the intervals having significant trait associations ($P < 0.05$). For traits evaluated in the present study: FW=fruit weight; FL=fruit length; and FD=fruit diameter.