Triple test cross analysis for epistatic components in a cross between Thai melon (*Cucumis melo* var. *conomon*) and cantaloupe (*C. melo* var. *cantalupensis*)

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Abstract

The study aimed to investigate whether epistasis was significant in the genetic components controlling fruit characters of a cross between Thai melon and cantaloupe. The 15 families obtained from crossing 5 F_2 plants (derived from a cross between Thai melon and cantaloupe lines) to their parents and F_1 progenies, were planted together with their parental lines, F_1 and F_2 (total 23 entries) in the randomized complete block design (RCBD) with 2 replications. Statistical analysis showed that families were significantly different ($P<0.01$) for all studied traits except fruit width and fruit cavity width. Significant differences ($P<0.01$) were found between Thai melon and cantaloupe lines for all fruit traits. The results from the genetic analysis revealed that additive × dominance and dominance × dominance epistatic components were significant ($P<0.05$) for fruit length, fruit cavity length, fruit shape index and fruit flesh thickness.

Keywords: *Cucumis melo*, triple test cross, epistasis

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Introduction

Melon (*Cucumis melo* L.; 2n=2x =24) is one of the economically important vegetable species grown in Thailand. It is a large polymorphic, encompassing a large number of botanical and horticultural varieties (Musmade and Desai, 1998), which is subdivided into seven botanical varieties i.e. var. *reticulatus*, *cantalupensis*, *inodorus*, *flexuosus*, *conomon*, *chito* and *dudaim* (Paje and van der Vossen, 1993). It is due to freely cross-pollinating between different cultivars and there are therefore many intermediate types (George, 1999). Cantolupensis group is generally much more economically important than conomon group. It has globular to slightly ovoid fruit, smooth or reticulating, ribbed, grayish-green rind with orange flesh and high sugar content. Whereas, conomon group produces elongate or round fruit with smooth skin, white flesh and low sugar content (Robinson and Deckor-Walters, 1997). Since great morphological variation exists in fruit characteristics of melon (*Cucumis melo*) such as size, shape, color and texture, taste and composition (Kirkbride, 1993; Bates and Robinson, 1995), and it could be cross-pollinated among groups within the species (Mathew *et al*., 1986) such as between var. *flexuosus* (non-sweet group) and var. *reticulates* (sweet group) (Burger *et al*., 2003), thus crossing between Thai melon and cantaloupe was considerable to produce more genetic variations for selection in Thai melon.

The information of the genetic components that control the characters to be selected determines largely the efficiency of the breeding procedures. Though various biometrical methods have been used for estimating the mode of gene action controlling plant characters, most of them were assumed the absent of non-allelic interactions. The triple test cross method described by Kearsey and Jinks (1968), which is basically an extension of the Comstock and Robinson (1948) design III, precisely estimates the importance of non-allelic interaction in the inheritance of plant characters. Triple test cross analysis provides unambiguous test for the presence of epistasis regardless of gene frequencies, degree of inbreeding and linkage relationship (El-Lawendey *et al*., 2010). The information obtained through triple test cross would help in understanding the genetic basis and making breeding strategy for the development of high performance plant cultivars. Thus the objectives of this project were to study the existence of the epistasis and to determine the additive (D) and dominance (H) variances of some horticultural characters from the cross between Thai melon (*Cucumis melo* var. *conomon*) and Cantaloupe (*C. melo* var. *cantalupensis*).

Materials and Methods

The study was conducted at the experimental field of Department of Plant Production Technology, the Faculty of Agriculture and Natural Resources, Rajamangala University of Technology Tawan-ok, Chonburi province, during 2012-2013 for crossing and yield trial. Three testers; Thai melon line (W-S_4) (L_1), cantaloupe line (A-S_3) (L_2) and their F_1 hybrid (L_3) were each crossed to their five F_2 derived lines to produce 15 crosses. These 15 crosses along with their 8 parents (i.e. 3 testers and 5 F_2 derived lines) were planted in a randomized complete block design (RCBD) with two replications from August to October 2013. Each experimental unit was a 2-row plot, 3 m long with 50 cm plant spacing, and 60 cm row spacing, 1 plant/hill, totally 12 plants/plots. Plants were grown under trellising system using bamboo stakes, standard furrow irrigation, cultural practices, and pest control practices. Of each plot, data were separately recorded on plant length, fruit width, fruit length, fruit cavity width, fruit cavity length, fruit shape index (fruit length/fruit width), fruit flesh thickness, flesh sweetness, fruit weight and yield. Data were analyzed statistically by analysis of variance according to the RCBD. Comparison between groups (such as parents and crosses) was analyzed using a single degree of freedom comparison (contrast). Genetic analysis was conducted according to the method of Ketata *et al*. (1976) which is based on procedure of Kearsey and Jinks (1968), as detailed by Singh and Chaudhary (2012). The genetic model is following;

$$L_{ijk} = M + G_{ij} + R_k + E_{ijk}$$

Where,

L_{ijk} = Phenotypic value of cross between tester i and line j in k replication.

M = Overall mean of all single and three way crosses.

G_{ij} = Genotypic value of cross between tester i and line j.

R_k = Effect of k^{th} replication.

E_{ijk} = Error.

The test of significance of the difference, $L_{1i} + L_{2i} - 2L_{3i}$, provides information about presence or absence of epistasis. The overall epistasis is partitioned into (i) type of epistasis (additive × additive) and (j+l) type due to additive × dominance and dominance × dominance gene interactions. The estimation of additive (D) and dominance (H) genetic components was detected from the sums of $L_{1i} + L_{2i}$ and the differences of $L_{1i} - L_{2i}$, respectively, The correlation coefficient (r) between these sums and differences were evaluated to detect the direction of dominance, according to Jinks and Perkins (1970).

Results and Discussion

The analysis of variance (Tables 1 and 2) showed that mean squares due to genotypes and parents were highly significant for all studied characters except plant length. Crosses were highly significant for the fruit length, the fruit cavity length, the fruit shape index, the flesh thickness, the fruit weight and sweetness. Lines were highly significant for the fruit length, the fruit cavity length, the fruit shape index, the fruit weight, sweetness and yield. Testers were significant for all characters except the plant length, indicating Thai melon line, cantaloupe line and their F_1 hybrid were different in those characters, and it was affirmed by the difference between P_1 VS P_2. Lines VS testers and crosses VS parents were also highly significant for most characters.

The estimation of genetic components of variance was based on the analysis of sums and differences. The genetic analysis revealed that additive × dominance and dominance × dominance (j+l) epistatic components played a significant role in controlling the fruit length, the fruit cavity length (Table 3), the fruit shape index and the flesh thickness (Table 4), thus epistasis should not be ignored when plant breeders are planning breeding programs to improve these characters. The effects of additive and dominant components were not significantly detected since the experiment was conducted only in two replications that gave low efficiency for testing the effects. However, in consideration of the estimates of these two genetic components, most characters had more dominant gene effect than additive gene effect, especially for fruit cavity length, which had high degree of dominance (3.1884) and significant negative correlation coefficient (Tables 5 and 6), indicating that the increasing type of genes are dominant (Singh and Chaudhary, 2012).

Table 1 Mean squares of the analysis of variance of triple test cross for plant length, fruit width, fruit length, fruit cavity width and fruit cavity length.

source	df	plant length (cm)	fruit width (cm)	fruit length (cm)	fruit cavity width (cm)	fruit cavity length (cm)
rep.	1	8×10^{-6}	0.5241	4.3958	0.1458	5.6490
genotypes	22	0.1357	4.7910 **	43.5683 **	1.9383 **	37.8996 **
crosses (C)	14	0.1355	1.6927	38.7306 **	0.5324	32.6965 **
parents (P)	7	0.1165	8.2746 **	59.0700 **	2.6947 **	53.6405 **
lines (L)	4	0.1114	2.9635	74.7940 **	0.9817	68.1778 **
testers (T)	2	0.0025	14.2860 **	54.1408 **	2.1783 *	51.3783 **
L vs T	1	0.3650	17.4960 **	6.0325	10.5798 **	0.1152
C vs P	1	0.2716	23.7818 **	2.7851	16.3250 **	0.5562
P1 vs P2	1	0.0042	27.5100 **	97.3182 **	4.2025 *	75.5164 **
error	22	0.0722	1.3644	4.6159	0.6784	4.1866

* and ** Significant at $P<0.05$ and 0.01, respectively.

The results of fruit length and fruit cavity length were agreed with Pornsuriya *et al*. (2012), which reported in Thai melon that these characters were controlled by the dominance gene component and all epistasis gene actions i.e. additive x additive, additive x dominance and dominance x dominance, where dominance x dominance component was the most effective. However, Fernandez-Silva *et al*. (2009) reported that heterosis of the melon fruit shape was prominently controlled by two dominant genes, round fruit was recessive to elongate, and epistasis had slight effect on controlling fruit shape. Pornsuriya and Pornsuriya (2009) reported that the fruit shape (round, oblong and elongate) of Thai melon was governed by a single additive gene, and it was agreed with their study from generation mean analysis, which revealed that fruit shape index was under additive gene effect.

From this study indicating that epistatic components performed an important role in controlling fruit length, fruit cavity length, fruit shape index and flesh thickness; besides, most characters had more the dominant gene effect than the additive gene effect. Thus, the breeding program for these characters should be focused on selecting elite lines with high combining ability for F_1 hybrid production.

Table 2 Mean squares of the analysis of variance of triple test cross for fruit shape index, flesh thickness, fruit weight, sweetness and yield.

source	df	fruit shape index	flesh thickness (cm)	fruit weight (g)	sweetness (°brix)	yield (ton/rai)[1/]
rep.	1	0.0351	0.0793	0.0263	0.0184	0.0119
genotypes	22	0.4019 **	0.6466 **	0.6972 **	2.7757 **	3.2358 **
crosses (C)	14	0.3243 **	0.6882 **	0.2180 **	0.8496 **	1.4897
parents (P)	7	0.5884 **	0.6327 **	1.4670 **	4.7281 **	4.9450 **
lines (L)	4	0.1520 **	0.1621	1.9386 **	2.8375 **	5.7928 **
testers (T)	2	1.2562 **	1.8261 **	0.5163 **	1.7433 **	4.8496 **
L vs T	1	0.9985 **	0.1279	1.4821 **	18.2602 **	1.7442
C vs P	1	0.1814 *	0.1624	2.0163 **	16.0747 **	15.7163 **
P1 vs P2	1	2.4492 **	3.0625 **	1.0302 **	3.1329 **	9.4556 **
error	22	0.0339	0.0700	0.0518	0.2322	0.7703

* and ** Significant at *P<0.05* and *0.01*, respectively.

[1/] 1 rai = 1,600 m^2.

Table 3 Mean squares of the analysis of variance for testing the presence of epitasis in a triple test cross for plant length, fruit width, fruit length, fruit cavity width and fruit cavity length.

source	df	plant length (cm)	fruit width (cm)	fruit length (cm)	fruit cavity width (cm)	fruit cavity length (cm)
i epistasis	1	3.38	12.84	1721.87	0.58	1590.62
j+l epistasis	4	0.61	8.78	51.15 *	3.51	32.35 *
total epistasis	5	1.16	9.59	385.29	2.93	344.01
i epistasis × blk	1	3.38	12.84	1721.87	0.58	1590.62
j+l epistasis × blk	4	0.55	11.01	7.96	4.90	4.47
total epis. × blk	5	1.11	11.38	350.74	4.04	321.70

* Significant at *P<0.05*.

i = additive × additive, j = additive × dominance, l = dominance × dominance.

Table 4 Mean squares of the analysis of variance for testing the presence of epitasis in a triple test cross for fruit shape index, fruit flesh thickness, fruit weight, fruit sweetness and yield.

source	df	fruit shape index	flesh thickness (cm)	fruit weight (g)	sweetness (°brix)	yield (ton/rai)[1/]
i epistasis	1	16.51	4.44	1.78	6.53	0.42
j+l epistasis	4	0.28 *	5.26 *	0.21	3.44	1.60
total epistasis	5	3.53	5.10	0.52	4.05	1.36
i epistasis × blk	1	16.51	4.44	1.78	6.53	0.42
j+l epistasis × blk	4	0.06	0.40	0.33	1.14	4.18
total epis. × blk	5	3.35	1.21	0.62	2.22	3.42

* Significant at *P<0.05*.

i = additive x additive, j = additive × dominance, l = dominance × dominance.

[1/] 1 rai = 1,600 m^2.

Table 5 Estimates of additive (D), dominance (H), degree of dominance $(H/D)^{1/2}$, and correlation coefficient (r) between sums and differences of triple test cross for plant length, fruit width, fruit length, fruit cavity width and fruit cavity length.

parameter	plant length (cm)	fruit width (cm)	fruit length (cm)	fruit cavity width (cm)	fruit cavity length (cm)
additive (D)	0.1528	-9.1435	14.6599	0.9143	5.9916
dominance (H)	0.2811	3.6519	61.8101	-1.0056	60.9087
degree of dominance	1.3563	-0.6320	2.0536	-1.0487	3.1884
correlation coefficient	0.4838	0.2060	-0.4885	0.3540	-0.8910 *

* Significant at *P<0.05*.

Table 6 Estimates of additive (D), dominance (H), degree of dominance $(H/D)^{1/2}$, and correlation coefficient (r) between sums and differences of triple test cross for fruit shape index, fruit flesh thickness, fruit weight, fruit sweetness and yield.

parameter	fruit shape index	flesh thickness (cm)	fruit weight (g)	sweetness (°brix)	yield (ton/rai)[1/]
additive (D)	0.1146	-0.3563	0.4499	2.6105	2.3783
dominance (H)	0.0707	0.7909	1.2013	3.9915	3.2429
degree of dominance	0.7855	-1.4899	1.6340	1.2365	1.1677
correlation coefficient	-0.8722	-0.4634	-0.0471	-0.2600	0.8861

[1/] 1 rai = 1,600 m^2.

Conclusions

Significances of genotypes, crosses, parents, lines and testers were detected for most characters. Additive x dominance and dominance x dominance (j+l) epistatic components were significant for controlling fruit length, fruit cavity length, fruit shape index and flesh thickness. Dominance genetic component was more important than additive genetic component for most characters.

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