
Study on genetic effects in fruit shape of oriental pickling melon

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Genetic effects in fruit shape of oriental pickling melon were studied using generation means analysis in six populations including round fruit line (P_1), cylindrical fruit line (P_2), F_1 and F_2 generations, and backcrosses of the F_1 to each parent (BC_1 and BC_2). Only additive gene effect was significantly found in controlling fruit length and fruit shape index (fruit length/fruit width), whereas all three types of epistatic effect were significant for fruit width (additive x additive, additive x dominance and dominance x dominance). The estimates of the number of genes governing fruit length, fruit width and fruit shape index were 0.84, 0.29 and 1.33, respectively. Visual classifications and chi-square tests were performed in the segregating generations. The F_1 generation had all oblong fruit plants, whereas the F_2 progenies segregated to round : oblong : cylindrical in the ratio of 1 : 2 : 1 ($X^2 = 0.733$, $P = 0.693$). The BC_1 plants segregated to round : oblong in the ratio of 1 : 1 ($X^2 = 0.133$, $P = 0.715$), where the BC_2 plants were oblong : cylindrical in the ratio of 1 : 1 ($X^2 = 0.133$, $P = 0.715$). The results stated that fruit shape (round; oblong and cylindrical) of oriental pickling melon was governed by a single gene which had additive effect in gene actions.

Key words: Oriental pickling melon, genetic effects, fruit shape

Introduction

Oriental pickling melon (*Cucumis melo* L. var. *conomon* Makino) is well known in Thai names as Taeng-thai and Taeng-lai (Paje and van der Vossen, 1993). Its immature fruits can be consumed as a fresh vegetable like cucumber, whereas ripe fruits are also consumed as a Thai traditional dessert. Since it is a naturally cross-pollinated crop, its variations could be found on almost characters. Fruit shape is the one of those, which is highly diverse too. According to Esquinal-Alcazar and Gulick (1983), fruit shape of *Cucumis melo* is classified to seven types. More and Seshadri (1998) suggested that shape index may be a specific method for denoting fruit shape that was used by Bains and Kang (1963) in determining fruit shape of F_2 to round-flat: oblong:

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cylindrical in the ratio of 1:2 : 1 from the cross of round-flat x cylindrical muskmelon. Pornsuriya and Pileuk (2005) reported in the study of immature fruit shape of oriental pickling melon that cylindrical fruit shape was incompletely dominant to round fruit and governed by a single gene. However, it was suspected that the similar result should be obtained or not in the ripe fruits, and what kind of gene effects are responsible for controlling ripe fruit shape. The objective of this study was to determine the genetic effects in ripe fruit shape of oriental pickling melon.

Materials and methods

The cross between a round fruit line (P_1) and a cylindrical fruit line (P_2) was made to obtain F_1 generation. The F_1 was self-pollinated and also backcrossed to both parents to obtain F_2 , BC_1 and BC_2 generations. The P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 were laid out with the used completely randomized design (CRD) with unequal replications during June to August 2007 at Faculty of Agriculture and Natural Resources, Rajamangala University of Technology Tawan-ok. Number of plots varied with generations, two plots in P_1 , P_2 and F_1 , three plots in BC_1 and BC_2 and twelve plots in F_2 . Each plot contained ten plants in a single row with the space of 0.5 m within row. Data were collected from a ripe fruit of each plant. Generation means analyses were carried out on the original scale to determine the gene effects of fruit shape. Six-parameter model for estimation of various genetic components proposed by Hayman (1958) including m = mean, $[d]$ = additive effect, $[h]$ = dominant effect, $[i]$ = additive x additive type of gene interaction, $[j]$ = additive x dominance type of gene interaction and $[l]$ = dominance x dominance type of gene interaction. The significance of gene effects was tested by calculating the variances, standard errors, and "t" values separately for each effect as discussed by Singh and Chaudhary (1979).

Gene number was estimated by the formula from Lande (1981), which assumes equal gene effects. Estimated broad-sense heritability was obtained using the formula from Kearsley and Pooni (1996). The equations are as follows.

$$\text{Minimum number of genes (n)} = (\bar{P}_1 - \bar{P}_2)^2 / [8(V_{F_2} - V_{F_1})]$$

$$\text{Broad-sense heritability (h}_b^2\text{)} = (V_{F_2} - V_E) / V_{F_2},$$

$$\text{where } V_E = (V_{P_1} + V_{P_2} + V_{F_1}) / 3$$

Fruits of F_2 , BC_1 and BC_2 were visually classified and the segregation ratios were tested by Chi-square method to observe the fit goodness and to get the expected classification ratios.

Results

Means and standard errors of fruit length, fruit width and fruit shape index of the six populations were presented in Table 1. Cylindrical fruit line had significantly more fruit length and fruit shape index than round fruit line. Fruit length of F_1 and F_2 was not different from that of mid-parent, but the F_1 and F_2 values for fruit width and fruit shape index were significantly different from mid-parent values (based on single degree of freedom contrasts). The BC_1 mean of fruit length was not different from the P_1 mean, whereas those of fruit width and fruit shape index differed from those of P_1 . Each of BC_2 value was significantly different from each of P_2 . All of the generations had fewer values than the cylindrical fruit lines (P_2), excluding fruit width character.

Genetic components estimated from generation mean analyses for fruit length, fruit width and fruit shape index using six-parametric model are presented in Table 2. The both fruit length and fruit shape index, only additive effects were significant ($P < 0.01$), which indicated the importance of the additive mode of gene actions. All three epistatic components were significant for fruit width.

The estimated minimum number of genes controlling fruit length, fruit width and fruit shape index and broad-sense heritability estimates are presented in Table 3. The minimum number of genes for controlling fruit length, fruit width and fruit shape index were estimates was 0.84, 0.29 and 1.33, respectively. Broad-sense heritability estimates based on variance of different generations were 0.65, 0.55 and 0.88, respectively.

Types of fruit shape were visually classified to round, oblong and cylindrical, thus segregation ratios and Chi-square tests for fruit shape of F_2 , BC_1 and BC_2 were performed and their results are shown in Table 4. F_1 plants are all oblong fruit. F_2 progenies were observed as 32, 62 and 26 of round, oblong and cylindrical fruits, respectively and they fitted a 1:2:1 ratio ($X^2 = 0.733$, $P = 0.693$). BC_1 plants segregated in a 1:1 ratio with 14 round : 16 oblong ($X^2 = 0.133$, $P = 0.715$), whereas BC_2 plants comprised 16 oblong : 14 cylindrical, also supporting the expect ratio of 1 : 1 ($X^2 = 0.133$, $P = 0.715$).

Table 1. Means and standard errors for fruit length, fruit width and fruit shape index of the six generations of the oriental pickling melon cross (round fruit (P₁) x cylindrical fruit (P₂)).

Generations ^Z	Characters ^Y		
	Fruit length ^X (cm)	Fruit width (cm)	Fruit shape index
P ₁	10.95 (0.49) d	11.64 (0.30) ab	0.94 (0.02) e
P ₂	20.69 (0.71) a	9.40 (0.27) d	2.20 (0.04) a
F ₁	16.48 (0.50) bc	12.10 (0.23) a	1.36 (0.02) c
F ₂	15.38 (0.40) c	11.42 (0.16) abc	1.36 (0.04) c
BC ₁	12.33 (0.42) d	10.69 (0.28) c	1.17 (0.04) d
BC ₂	17.89 (0.76) b	10.75 (0.29) bc	1.69 (0.08) b

^Z Mid-parent means of fruit length, fruit width and fruit shape index were 15.82, 10.52 and 1.57 cm, respectively, ^Y Means in a column followed by the same letter are not statistically different at 5% according to Duncan's new multiple range test, ^X The values in parentheses represent the standard errors of the generation means.

Table 2. Estimations of the genetic components from generation mean analyses obtained for fruit length, fruit width and fruit shape index using six-parametric model.

Components ^Z	Characters ^Y		
	Fruit length	Fruit width	Fruit shape index
m	15.38 (0.40)**	11.42 (0.16)**	1.36 (0.04)**
[d]	-5.57 (0.87)**	-0.06 (0.40)	-0.52 (0.09)**
[h]	-0.41 (2.45)	-1.22 (1.08)	0.05 (0.24)
[i]	-1.07 (2.36)	-2.79 (1.04)**	0.26 (0.24)
[j]	-0.70 (0.97)	-1.18 (0.45)*	0.11 (0.10)
[l]	5.22 (4.05)	5.16 (1.84)**	-0.12 (0.40)

^Z m = mean, [d] = additive component, [h] = dominance component, [i] = additive x additive epistatic component, [j] = additive x dominance epistatic component, [l] = dominance x dominance epistatic component, ^Y The values in parentheses represent the standard errors of the components, * and ** Significant at $P < 0.05$ and 0.01 , respectively.

Table 3. Estimated minimum number of genes and broad-sense heritability (h_b^2) for fruit length, fruit width and fruit shape index of the oriental pickling melon cross [round fruit (P₁) x cylindrical fruit (P₂)].

Characters	Minimum number of genes ^Z	Broad-sense heritability (h_b^2) ^Y
Fruit length	0.84	0.65
Fruit width	0.29	0.55
Fruit shape index	1.33	0.88

^Z Based on the formula from Lande (1981).

^Y Based on the formula from Kearsley and Pooni (1996).

Table 4. Segregation ratios and Chi-square tests for fruit shape of populations derived from the oriental pickling melon cross [round fruit (P₁) x cylindrical fruit (P₂)].

Pop.	No. of plant	Observed number			Expected ratio ^z	Chi-square tests	
		Round	Oblong	Cylindrical		X ²	P
F ₂	120	32	62	26	1:2:1	0.733	0.693
BC ₁	30	14	16	-	1:1	0.133	0.715
BC ₂	30	-	16	14	1:1	0.133	0.715

^z Based on a single gene model.

Discussion

Estimates of the minimum number of genes or effective factors controlling fruit width would be biased downward by failure to meet the analysis assumptions of no epistasis and no dominance (Wright, 1968), because all epistatic effects were present in this character. The magnitude of an additive effect was significantly found in fruit length and fruit shape index, in addition, there were no dominance and epistasis effects. Therefore, the estimates of the minimum number of genes for fruit length and fruit shape index were likely to be more accurate than that in fruit width. The likely high heritability estimates for fruit length and fruit shape index signified that high proportion of variation was under gene control.

The segregation ratios of fruit shape in F₂, BC₁ and BC₂ classified by visual observation supported evidence of a single gene inheritance. It was also supported by the estimates of the minimum number of genes controlling the studied characters. In the quantitative aspect, generation mean analyses showed the significance of the additive component for fruit length and fruit shape index supporting the additive gene effect. Significant estimates of additive gene effects for fruit length and fruit shape index were negative, indicating that additive effects contribute to more round than to cylindrical. Fruit length might have much more influence on fruit shape than fruit width. It was confirmed that the high correlation between fruit length and fruit shape index ($r=0.83$ in F₂ population, data not shown). The results indicated that a single gene with additive effect might governed ripe fruit shape in the cross between round and cylindrical fruit lines. However, they did not provide the conformity in immature fruits that they might be controlled by an incompletes dominant gene as reported by Pornsuriya and Pileuk (2005).

Conclusion

The additive gene effect was significant in controlling fruit length and fruit shape index (fruit length/fruit width). Visual classification of fruit shape in F₂ progenies fitted a 1:2:1 ratio of round:oblong:cylindrical, suggesting that fruit shape was under a single gene control.

Reference

- Bains, M.S. and Kang, U.S. (1963). Inheritance of some flower and fruit characters in muskmelon. *Indian J. Genetics Plant Breeding* 23: 101-106.
- Esquinas-Alcazar, J. T. and P. J. Gulick. 1983. Genetic Resources of Cucurbitaceae: A Global Report. International Board for Plant Genetic Resources, Rome. 101 p.
- Hayman, B.I. (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity* 12: 371-390.
- Kearsey, M.J. and Pooni, H.S. (1996). *The Genetical Analysis of Quantitative Trait*. Chapman and Hall, Inc., London. 400 p.
- Lande, R. (1981). The minimum number of gene contribution to quantitative variation between and within populations. *Genetics* 99: 541-553.
- More, T.A. and Seshadri, V.S. (1998). Genetic studies, pp. 129-153. *In* N.M. Nayar and T.A. More (eds.) *Cucurbits*. Science Publishers, Inc. Enfield, NH., U.S.A.
- Paje, M.M. and van der Vossen, H.A.M. (1993). *Cucumis melo* L., pp. 153-157. *In* Siemonsma J.S. and K. Piluek (eds.). *Plant Resources of South-East Asia No.8: Vegetables*. Prosea Foundation, Bogor, Indonesia.
- Pornsuriya, P. and Pileuk, K. (2005). Inheritance of fruit shape and fruit color in slicing melon (*Cucumis melo* L. var. *conomon* Makino). The 5th National Horticultural Congress. April 26-29, 2005.
- Singh, R.K., and Chaudhary, B.D. (1979). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi, India. 300 p.
- Wright, S. (1968): The genetics of qualitative variability. *In*: Wright S. (ed.): *Evolution and Genetics of Populations*. Vol I. Genetics and Biometrics Foundation. University of Chicago Press, Chicago.

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