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Gene effects for fruit yield and its component traits in cucumber (*Cucumis sativus*) using generation means

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ABSTRACT

Generation mean analysis in cucumber (*Cucumis sativus* L.) was carried out during 2006–07 to study gene effects for fruit yield and its components in interacting and non-interacting crosses using 3-parameter model and 6-parameter model, respectively. For this purpose, six promising parents selected out of 17 genotypes were crossed in a half-diallel fashion to generate 15 F_1s. Top five high-yielding F_1s were advanced to F_2s, B_1s and B_2s. The estimates of gene effects obtained through analysis of six generations revealed preponderance of both additive and dominance effects for fruit weight, fruit length and fruit diameter. Epistatic interactions were observed for earliness, number of fruits/plant and yield/plant. However, scaling test was non-significant for fruit weight and length in all the five crosses showing absence of epistasis in the control of these characters. Some crosses showed duplicate type of interaction while others showed complementary epistasis. For instance, for fruit yield/ plant, CRC 8 × Pusa Uday and CHC 2 × DC 1 showed complementary epistasis, which would increase the heterosis in positive direction. The magnitude and direction of the gene effects varied from cross to cross. Thus, characters such as fruit weight and fruit length which are governed by entirely additive components could be improved through individual selection while for days to first female flower opening, days to first fruit harvest, number of fruits/plant and fruit yield/plant showing predominant dominance gene effects and interaction effects, biparental mating and recurrent selection would exploit both additive and non-additive type of gene effects efficiently.

Key words: Additive, Cucumber, Dominance, Epistasis, Gene effects, Generation mean analysis

Cucumber (*Cucumis sativus* L., 2n = 2 × = 14) belonging to family Cucurbitaceae is an important summer vegetable in India. Cucumber has great economic importance as food plant. Apart from being used as salad, it is also used for pickling and *rayata* preparation. Being native to India it possesses vast genetic variability for vegetative and fruit characters. Despite this fact, not much organized efforts have gone into the improvement of this crop primarily due to lack of sufficient and reliable information on gene effects for economically important traits. Determination of suitable breeding method and selection strategy for improvement of a trait would depend on knowledge of gene effects operating in the breeding population.

Generation mean analysis, a concept developed by Hayman (1958) and Jinks and Jones (1958), is an efficient tool to understand the nature of gene effects involved in the expression of a character. The generation mean analysis utilizes six different generations of a cross, viz parents P_1, P_2, their F_1, F_2, backcross B_1 and B_2 for estimation of gene effects and components of genetic variation in interacting and non-interacting crosses. Though generation mean analysis has been extensively used to understand the gene effects in different crops, but very few reports are available on the use of this technique for understanding the gene effects in cucumber. Earliness is an important trait in cucumber along with the higher yield. In view of this, the present study was undertaken to estimate different kinds of gene effects in inheritance of fruit yield and its component traits.

MATERIALS AND METHODS

The present investigation was carried out during 2006–07 at research farm of Division of Vegetable Science of Indian Agricultural Research Institute, New Delhi. Out of the 17 genotypes of cucumber available for field evaluation, six most promising and diverse genotypes, viz Pusa Uday, DC 1, CH 20, CRC 8, CHC 2 and G 338 (Table 1) were crossed in 6 × 6 half diallel fashion (excluding reciprocals) to obtain 15 F_1 hybrid combinations.

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Table 1 *Per se* performance of parents selected for the study

Genotype	Days to first female flower opening	Days to first fruit harvest	Fruit weight (g)	No of fruits/ plant	Fruit length (cm)	Total yield/ plant (g)
CRC 8	52.10	60.20	120.83	8.20	14.60	943.78
CHC 2	54.43	62.33	116.30	7.80	12.70	860.53
G 338	55.27	63.57	129.57	7.60	13.23	872.97
CH 20	56.17	63.57	142.80	7.07	14.33	1 128.80
Pusa Uday	57.33	64.57	152.13	6.62	14.60	1 513.80
DC 1	56.57	62.43	159.80	5.64	16.43	1 265.30
Range	52.10–57.33	60.20–64.57	116.30–159.80	5.64–8.20	12.70–16.43	860.53–1 513.80

Table 2 Significant scaling tests in select crosses for six quantitative traits in cucumber

Cross	Days to first female flower opening	Days to first fruit harvest	Fruit weight (g)	No of fruits/ plant	Fruit length (cm)	Fruit yield/ plant (g)
CRC 8 × Pusa Uday	*C, D*	*C, D*	NS	*B, D*	NS	*B, C, D*
CRC 8 × DC 1	*C*	*D*	NS	NS	NS	*C*
CHC 2 × Pusa Uday	*B, C, D*	*A*	NS	*B*	NS	*B, C, D*
CHC 2 × DC 1	NS	NS	NS	*B*	NS	*B, C, D*
G 338 × Pusa Uday	NS	NS	NS	NS	NS	NS

NS, Non-significant

The five F_1's which performed well with respect to fruit yield, viz CRC 8 × Pusa Uday, CRC 8 × DC 1, CHC 2 × Pusa Uday, CHC 2 × DC 1 and G 338 × Pusa Uday were advanced to F_2 (F_1's selfed), B_1 ($F_1 \times P_1$) and B_2 ($F_1 \times P_2$) generations. The six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of these five crosses were evaluated under randomized block design with three replications. The seeds of six generations were sown in rows of 1.5 m with 50 cm spacing between the plants. All the recommended package of practices was followed to raise a healthy crop. Data were recorded on five plants each, of parents (P_1 and P_2) and F_1, 15 plants each of B_1 and B_2 and 40 plants each of F_2 from each replication on six quantitative characters, viz. days to first female flower opening, days to first fruit harvest, fruit weight (g), number of fruits/plant, fruit length (cm) and fruit yield/plant (g). The data were subject to scaling tests (Hayman 1958) to identify the interacting and non-interacting crosses. The data from interacting crosses were analyzed through 6-parameters model (Hayman 1954, Hayman 1958, Jinks and Jones 1958). The estimates of mean and gene effects for interacting crosses, i.e mean (*m*), additive (*d*), dominance (*h*), additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*) were obtained for yield and its components. The data from non-interacting crosses were analysed using three parameters (*m*, *d* and *h*) model of Jinks and Jones (1958). The generation means of P_1, P_2, F_1, F_2, B_1 and B_2 were used for scaling tests and estimation of gene effects.

RESULTS AND DISCUSSION

Identification of interacting and non-interacting crosses

The interacting and non-interacting crosses out of select five crosses have been identified by testing the adequacy of scale through scaling tests (Hayman 1958) for all the six characters recorded. In this technique, four tests (*A*, *B*, *C* and *D*) for scale effects have been used. When the scale is adequate, the values of *A*, *B*, *C* and *D* would be non-significant. When the scales are significant, *A* and *B* indicated additive × dominance (*j*), *C* dominance × dominance (*l*) and *D* additive × additive (*i*) type of gene interactions. The results of the scaling tests are presented in Table 2.

Table 2 reveales that none of the five select crosses were having a significant scale for fruit weight and fruit length indicating the absence of epistasis for these traits in the select crosses. However, for remaining traits, at least three crosses had at least one significant scale. Three crosses for fruit yield/ plant had significant *B*, *C* and *D* scales indicating the presence of all three types of non-allelic interactions. In the cross, G 338 × Pusa Uday all four scaling tests were non-significant indicating the adequacy of additive-dominance model.

Gene effects in non-interacting crosses

The gene effects for six quantitative characters in non-interacting crosses have been presented in Table 3. The cross G 338 × Pusa Uday exhibited negative dominance (*h*) component for both days to first female flower opening and days to first fruit harvest signifying that these components tend to induce earliness while CHC 2 × DC 1 showed significant negative additive (*d*) effect (–1.49).

Significant positive *h* components were recorded in G 338 × Pusa Uday for number of fruits/plant, fruit length and fruit yield/ plant. Although for fruit yield/ plant, *d* (320.42) component was also significant, very much larger *h*

Table 3 Estimates of gene effects in non-interacting crosses (3-parameter model)

Cross	m	d	h
Days to first female flower opening			
CHC 2 × DC 1	51.0± 0.82**	–1.45± 0.69*	-4.59± 4.3
G 338 × Pusa Uday	50.20± 1.43**	–1.03± 1.10	11.97± 4.21**
Days to first fruit harvest			
CHC 2 × DC 1	60.33± 0.53**	–1.12± 1.42	–11.01± 3.71**
G 338 × Pusa Uday	64.23± 2.59**	–0.50± 1.40	–17.20± 4.63**
Number of fruits/ plant			
CRC 8 × DC 1	7.36± 0.61**	1.28± 0.40**	6.64± 4.01
G 338 × Pusa Uday	6.73± 0.34*	0.59± 0.51	9.56± 3.46**
Fruit weight			
CRC 8 × Pusa Uday	159.17± 4.59**	15.65± 3.43**	27.95± 24.73
CRC 8 × DC 1	165.83± 4.19**	19.485± 5.21**	27.71± 22.71
CHC 2 × Pusa Uday	164.23± 4.87**	17.915± 8.07*	45.31± 24.98
CHC 2 × DC 1	148.83± 4.39**	21.75± 8.43*	25.21± 23.76
G 338 × Pusa Uday	152.67± 5.37**	11.28± 7.94	22.21± 28.60
Fruit length			
CRC 8 × Pusa Uday	16.27± 0.63**	0.00± 0.22	5.67± 4.09
CRC 8 × DC 1	16.50± 0.56**	0.92± 0.72	11.32± 5.44*
CHC 2 × Pusa Uday	16.33± 0.56**	0.95± 0.42*	6.25± 3.86
CHC 2 × DC 1	17.20± 0.61**	1.87± 0.45**	10.89± 6.01
G 338 × Pusa Uday	15.27± 0.60**	0.69± 0.70	9.34± 4.71*
Total yield/ plant			
G 338 × Pusa Uday	1420.56± 30.40**	320.42± 68.61**	2001.3± 190.5**

*P=0.05, **P=0.01%

component (2001.3) appear to over power *d* component.

In case of fruit weight, all the crosses except G 338 × Pusa Uday (recorded non significant *d* and *h*), exhibited significant *d* component and non-significant *h* implying that the entire genetic variation in these crosses is due to additive component. For fruit length, CHC 2 × Pusa Uday and CHC 2 × DC 1 showed significant *d* component, while CRC 8 × DC 1 and G 338 × Pusa Uday exhibited significant positive *h* component.

Importance of additive gene action in some cases and non-additive gene action in some others for fruit characters were earlier reported by Shahi *et al.* (2005) and Choudhary and Singh (2010) in cucumber. The importance of both *d* and *h* components for fruit yield and higher magnitude of *h* were in conformity with the findings of Cao *et al.* (1997) and Sun *et al.* (2006) in cucumber.

Gene effects in interacting crosses

The gene effects in crosses with significant scaling tests indicated the presence of one or more significant interaction components (Table 4). For days to first female flower opening, *l* (dominance × dominance) was significant in all three interacting crosses. In CHC 2 × Pusa Uday, the *l* component is very large and hence seems to overpower *d* (additive effect). In CRC 8 × DC 1, except *i* and *j* (additive × additive and additive × dominance) all other gene effects were negatively significant. The direction of both *h* and *l* being negative represents complementary epistasis indicating the dominance at the loci in negative direction, i e towards early flowering and hence tend to increase heterosis in negative direction. The value of *h* (–2.57) and *l* (–3.81) put together is more than that of *d* (–3.57) tend to overpower additive effect and implies the predominance of dominance gene action for this trait in this cross. In the cross CRC 8 × Pusa Uday, *h* and *l* being positively significant (complementary epistasis) and are very large compared to negatively significant *d* (–3.73) exhibiting positive heterosis which is not desirable for the character like days to first female flower opening.

For days to first fruit harvest, in the cross CRC 8 × Pusa Uday and CRC 8 × DC 1, all kinds of gene effects, except *j*, were significant and epistasis was of duplicate type in the former while it was complementary in the latter. Moreover, in the latter cross, *d*, *h* and *l* being negatively significant tended to produce individuals with early maturity.

Thus, in the above two earliness related characters, both additive and dominance components were significant along with the interaction components indicating the operation of both gene actions with predominance of dominance in the inheritance of these characters. The results on earliness with respect to days to first female flower opening and days to first fruit harvest were in conformity with the findings of Shahi *et al.* (2005) and Choudhary and Singh (2010) in cucumber.

The results on number of fruits/plant showed significant and larger *h* components in CRC 8 × Pusa Uday (7.45) and CHC 2 × Pusa Uday (5.81) compared to that *d* with duplicate epistasis in the former. All the three interacting crosses had significant *d* and *j* components with predominance of *d* in CHC 2 × DC 1.

In case of fruit yield/plant, all types of gene effects were positive and significant in CRC 8 × Pusa Uday and CHC 2 × DC 1 with complementary epistasis, which would increase the heterosis. Hence additive, dominance, and epistatic

Table 4 Estimates of gene effects in interacting crosses (6-parameter model)

Cross	*m*	*d*	*h*	*i*	*j*	*l*
Days to first female flower opening						
CRC 8 × Pusa Uday	49.30±0.58**	–3.73±1.72*	6.08±2.28*	12.80±4.14**	1.05±1.79	17.09±7.56**
CRC 8 × DC 1	49.90±0.89**	–3.57±1.04*	–2.57±1.01*	4.6±4.0	–1.33±0.15	–3.81±0.185*
CHC 2 × Pusa Uday	52.20±0.55**	–3.46±0.64**	1.52±2.79	7.46±2.55*	–1.95±0.81*	–11.82±4.04**
Days to first fruit harvest						
CRC 8 × Pusa Uday	58.73±0.29**	–3.57±1.36*	3.89±1.08**	9.80±2.95**	–1.38±1.46	–16.8±5.82**
CRC 8 × DC 1	58.53±0.28**	–2.90±1.23*	–4.45±1.86*	3.83±1.71*	–1.28±1.36	–5.10±1.36**
CHC 2 × Pusa Uday	63.63±2.9**	–2.90±0.82**	–11.71±11.76	–6.2±11.71	–1.78±0.92*	0.63±12.2
No of fruits/plant						
CRC 8 × Pusa Uday	7.1±0.53**	2.09±0.91**	7.45±2.88*	4.6±2.81	2.31±0.94*	–3.37±1.41*
CHC 2 × Pusa Uday	7.10±0.43**	1.7±0.39**	5.81±1.98**	3.27±1.91	1.11±0.47*	–0.97±2.58
CHC 2 × DC 1	7.43±0.44**	1.87±0.31**	3.74±1.94	0.80±1.87	0.79±0.37*	1.44±2.40
Total yield/plant						
CRC 8 × Pusa Uday	1566.9±31.8**	89.8±39.9*	873.2±210.7**	61.0±24.3**	374.8±82.5**	149.7±59.1**
CRC 8 × DC 1	1353.7±24.0**	199.8±69.4*	726.2±176.3**	120.2±168.8	360.6±71.7**	24.8±31.9
CHC 2 × Pusa Uday	1640.3±34.5**	189.8±65.3**	1243.7±197.1**	400.5±190.2*	526.4±68.5**	-926.8±313.1**
CHC 2 × DC 1	1360.3±34.5**	234.0±49.3**	950.7±175.2**	321.6±169.8*	436.3±52.7**	574.2±256.0*

*P=0.05, **P=0.01

components were important in the inheritance of this trait in these crosses. Moreover, the *h* component was larger in all the four interacting crosses compared to *d* though both the components were statistically significant and positive and main effects were greater than the epistatic effects. The components of gene effects therefore suggested greater importance of non-additive gene effects for this attribute. However, opposite direction and larger value of *h* and *l* components in CHC 2 × Pusa Uday indicated duplicate epistasis and hence would decrease the heterosis in positive direction. Importance of additive and non-additive gene effect for total yield/plant was in consonance with Cao *et al.* (1997), Shahi *et al.* (2005) and Choudhary and Singh (2010) in cucumber.

The crosses in which the gene effects were entirely additive can be relied upon to practice individual plant selection for the improvement of those traits. However, in crosses with predominant dominance gene effect, biparental mating and recurrent selection would be suitable breeding methods.

The overall results of the study showed the significance of dominance, additive and epistatic components in most of the crosses for different quantitative characters. However, for fruit weight and fruit length epistatic components were non-significant in all the five crosses. The preponderance of non-additive and additive component of variance suggested the importance of heterosis breeding and recurrent selection for effective exploitation of dominance and additive variance of variation. The estimation of different types of gene effects provided a test for gene action and was useful for analyzing genetic architecture of different characters. The estimates obtained from each cross may be unique in varying degrees and may not be applicable to parental population as also observed in the present study. Hence, each cross should be considered individually while going for selection and determining the breeding procedure while dominance genetic variance formed the major part of the genetic variance for yield and yield components. Biparental mating and recurrent selection followed by selection in early segregating generations would help in exploitation of dominance, additive and epistatic gene effects. Further, this approach is likely to break some undesirable linkages resulting in the establishment of rare and useful recombinants.

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