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Inheritance of fruit traits and generation mean analysis for estimation of horticultural traits in bitter gourd

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ABSTRACT

Inheritance pattern of three fruit traits was studied using two diverse parents, namely, Sel-2 (~25 cm long, non-prominent tubercles and curved) crossed with small fruited type Pusa Purvi (DBG-34) (~4 cm long, prominent tubercles and straight). F_1 generation obtained was intermediate (av. ~10 cm) for fruit length and in F_2 generation variation ranged from 2.5 to 25 cm. This continuous variation in fruit length of progeny by frequency distribution of nine classes with interval of 2.5 cm indicated its quantitative inheritance and more than 4 genes involved in controlling this trait. Distribution curve for fruit length in F_2 generation skewed towards Pusa Purvi, which suggested that short fruit length is partially dominant over long fruit length. The broad sense heritability for this trait was reported to be 97.40% that is heritable variation and selection for fruit length will be useful for its improvement. The inheritance of tubercles and curviness of fruits in bitter gourd, governed by a single pair of nuclear gene and prominent tubercles was dominant over non tubercles. In cross Sel-2 × Pusa Purvi indicated that straight fruit is dominant over curved fruit and governed by a single pair of gene. Gene action for yield and its related traits in bitter gourd was studied using six basic generations (P_1, P_2, F_1, F_2, B_1 and B_2). The results revealed the presence of additive, dominance gene effects and epistatic interactions for all the characters studied in cross Sel-2 × Pusa Purvi indicating the importance of both additive and non-additive gene actions in the expression of the characters. Mean generation analysis for fruit length showed that dominance is the major contribution towards small fruits.

Key words: Bitter gourd, generation mean analysis, gene effects, non-allelic interactions.

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is one of the most important nutritional and medicinal cucurbitaceous vegetable crops grown for its tender fruits and leaves. It is well known for its antidiabetic properties due to presence of charantin, saponin, momordicin *etc*. The primary centre of diversity of bitter gourd is India, whereas China is considered as the secondary centre of diversity. In India, diverse range of genotypes available in this crop and hence, there is a vast opportunity for its genetic improvement (Behera *et al*., 1). It is grown in different parts of the tropics and preferences also vary from region to region with respect to fruit colour, length, diameter, shape, size and tubercles etc. Long fruited types are preferred in north India, while medium long fruited types are favoured in south India, whereas, short fruited types are in high demand in eastern states of India (Behera *et al*., 1). Fruit length has significant contribution in yield of any crop, so also in bitter gourd. But the preference based on fruit length is a consumer's choice. The study of the genetics of fruit traits (length, curviness, and tubercles) will pave the way for development of new varieties and hybrids with different length and fruit surface as per the consumer's preference. Kim *et al*. (6) reported that the small fruit was partially dominant over large fruit. Zhang *et al.* (15) reported that fruit length was found to be incompletely dominant and governed by a minimum of five genes.

Previous studies suggested that there would be no separate gene system for yield *per se* and the yield is an end product of the multiplicative interaction between the various components of yield. Estimation of the nature of gene effects involved in the inheritance of yield attributing traits is helpful in planning correct breeding programme for improvement of this crop. Determination of the most important suitable breeding method and selection strategy for improvement of a trait would depend on the knowledge of gene action operating in the breeding population, especially about the components of genetic variation, *viz*., additive, dominance and epistasis. Generation mean analysis is an efficient tool to understand the nature of gene effects involved in the expression of the characters. Though gene effects for yield and its related characters have been estimated in bitter gourd, information on epistatic gene effects is limited. It is pertinent to develop suitable variety possessing earliness, short to medium long and dark green fruits coupled with high yield. Thus, the present study was carried out to estimate gene effects in the inheritance of fruit length and generation mean analysis of yield and its related traits.

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MATERIALS AND METHODS

The experimental materials consist of six generations, *i.e.*, parents (P$_1$ and P$_2$), F$_1$, F$_2$, B$_1$ (F$_1$ × P$_1$) and B$_2$ (F$_1$ × P$_2$) of a cross, *viz.*, Sel-2 (*Momordica charantia* var. *charantia*) × Pusa Purvi (DBG-34) (*M. charantia* var. *muricata*). The parents (P$_1$ and P$_2$) were maintained by selfing for many seasons and to develop different generations. Six generations of the cross were evaluated at the Research Farm of Division of Vegetable Science, IARI, New Delhi, during spring-summer season of 2013 in a randomized block design with three replications. Seeds of the six generations for each family were sown in 50-cell plug-trays in the polyhouse. An artificial soil medium with leaf mold in the ratio of 1:1 was used for growing seedlings. The seedlings were transplanted at the two true leaf stage. The vines were spaced at 2.0 m between rows and 0.5 m within a row. All the recommended package of practices was adopted to raise healthy crop.

Data were recorded on five randomly selected plants in each parental line and its F$_1$ cross, 20 plants in F$_2$ and 15 plants in each B$_1$ and B$_2$ from each replication for estimation of gene effects. Observations were recorded on seven quantitative characters, *viz.*, number of days to open for first female flower, node bearing first female flowers, number of days to open first male flower, fruit length (cm), fruit number per plant, individual fruit weight (g) and yield per plant (kg). For studying the inheritance of fruit length, length of mature fruit was measured at marketing stage from proximal to distal end of individual fruit with peduncle removed. The observation was taken in each 15 plants of parents and 30 F$_1$s, 130 plants of F$_2$ and 30 plants of both B$_1$ and B$_2$. For inheritance studies of tubercles on fruit surface and curviness, total number of plants in each classes were counted and subjected to χ^2 analysis for goodness of fit to various classical Mendelian ratios (Panse and Sukhatme, 9).

The data were subjected to A, B, C and D scaling tests of Mather (8) for testing the adequacy of additive and dominance model. The gene effects (additive and dominance) and interactions [additive × additive (*i*), additive × dominance (*j*) and dominance × dominance (*l*)] for each character were estimated according to Hayman (4). For inheritance studies on fruit length, frequency distribution table of nine classes with interval of 2.5 cm were made and total number of plants contributing into different classes was counted. Estimates of the effective or minimum number of genes influencing such a trait are obtained by comparing the phenotypic means and variances of the character in parental, F$_1$, F$_2$ and backcross populations. The broad sense heritability was estimated by Kearsey and Pooni (5) formula. All statistical analysis were performed using software SPSS 16.0 version. Minimum number of genes was estimated according to Lande (7).

RESULTS AND DISCUSSION

The mean performance of first parent for majority of the traits was better than their F$_1$s and other segregating generations except for fruit number per plant and yield (Table 1) due to its dependence on number of fruits and their weight. It has been observed that on utilizing Sel-2 as female parent and Pusa Purvi as male parent, number of days to open for first female flower, node bearing first female flowers, number of days to open first male flower, fruit length and individual fruit weight in F$_1$ generation was intermediate to parental lines. B$_1$ (F$_1$× Sel-2) and B$_2$ (F$_1$× Pusa Purvi) resembled their respective recurrent parent with respect to all seven traits and F$_2$ individuals varied substantially for the yield related characteristics. The crosses obtained with diverse parents were subjected to A, B, C and D scaling test to sort out interacting and non-interacting crosses (Table 2). In the present study, the significance of scaling test revealed that out of four scaling tests, A scale was significant for all the characters except for node bearing first female flowers for which no scale was significant and also for the most important trait, *viz.,* yield. The factor B was significant

Table 1. Generation mean for different traits in Sel-2 × Pusa Purvi cross of bitter gourd.

Generation	No. of days to open for first female flower	Node bearing first female flowers	No. of days to open first male flower	Fruit length (cm)	Fruit No. per plant	Single fruit wt. (g)	Yield per plant (kg/plant)
P$_1$	69.73 ± 0.40	14.67 ± 0.27	63.87 ± 0.38	23.92 ± 0.20	30.33 ± 0.73	52.6 ± 1.59	1.59 ± 0.05
P$_2$	64.53 ± 0.41	10.73 ± 0.33	55.27 ± 0.36	4.07 ± 0.05	49.93 ± 0.89	7.68 ± 0.15	0.47 ± 0.02
F$_1$	62.40 ± 0.40	9.40 ± 0.31	57.53 ± 0.38	10.14 ± 0.10	42.33 ± 0.61	48.32 ± 0.87	2.50 ± 0.13
F$_2$	69.48 ± 0.23	11.00 ± 0.22	61.00 ± 0.28	11.71 ± .59	46.93 ± 0.41	39.40 ± 0.39	1.22 ± 0.07
B$_1$	69.66 ± 0.16	13.66 ± 0.16	64.73 ± 0.17	10.79 ± 0.07	27.80 ± 0.57	30.94 ± 0.39	1.45 ± 0.03
B$_2$	63.66 ± 0.22	7.46 ± 0.17	58.60 ± 0.21	8.39 ± 0.09	39.87 ± 0.66	18.30 ± 0.16	1.53 ± 0.04

P$_1$ = Sel-2, P$_2$ = Pusa Purvi

for fruit length and individual fruit weight. The factor C was highly significant for number of days to open for first male and female flower, fruit number per plant and also significant for individual fruit weight. The scale D was significant for fruit number per plant and single fruit weight. These results indicated the presence of non-allelic interactions in inheritance of these characters (Dalamu *et al*., 3). The opposite sign of dominance (*h*) and dominance × dominance (*l*) components were opposite sign to each other indicating duplicate epistasis for all the characters studied.

Estimates of components of generation means for different characters in bitter gourd are presented in Table 3. The results showed that for number of days to open first female flower, additive effect (*d*) was significant in desired direction. However, absolute magnitude of dominance (*h*) effect was higher than to additive effect. The epistasis for this was observed to be duplicate type and absolute magnitude of additive × additive (*i*) effect was higher than both of remaining, *i.e.*, additive × dominant (*j*) and dominant × dominant (*l*) interaction effects confirming the complex nature of inheritance of this character. Therefore, improvement in this trait can be achieved through simple selection method because of presence of non-allelic interaction effect. Similar results were reported by Tewari *et al*. (13). Additive (*d*) gene effect was found to be highly significant for node at 1st female flowers and among interaction effects also additive × dominance (*j*) was significant for this trait in desired direction. The predominant role of epistasis suggested that genetic improvement for it can be obtained through selection due to presence of significant amount of non-allelic interaction effects. These results are in agreement with the reports of Radha Rani *et al*. (10). Among main effects, only additive (*d*) effect was observed to be highly significant for number of days to opening of first male flower, whereas, absolute magnitude of dominance × dominance (*l*) effect was highest among interaction effects.

Numbers of fruits per plant and individual fruit weight directly contributes for yield per plant in bitter gourd. Duplicate epistasis with significant additive and additive × dominance (*j*) interaction component in opposite direction for fruit length suggests selection programme for this character. However, absolute magnitude of dominance (*h*) effect was higher than additive (*d*) one. High significant additive × dominance (*j*) interaction indicated that fruit length is governed by incomplete dominance and it was supported by Zhang *et al*. (15). In the present investigation, both additive (*d*) and dominance (*h*) gene effects were found to be significant with higher absolute magnitude of dominance (*h*) action for number of fruits per plant. Among epistatic gene action additive × additive (*i*) effect was highly significant and dominance × dominance (*l*) gene effect was reported to be highest in positive direction. Regarding individual fruit weight duplicate epistasis was reported with high significance of additive (*d*) component in desired direction and also absolute dominance (*h*) magnitude was significantly higher. Both additive × additive (*i*) and dominance × dominance (*l*) effects was highly significant for the same trait and among them only dominance × dominance (*l*) was in desired direction. Additive × dominance (*j*) effect was also significant for single fruit weight in negative direction. Dominance (*h*) gene effect played major role and it was higher in magnitude compared to additive (*d*) gene effect for yield per plant in the present study. Among the interaction effects, additive × dominance (*j*) were predominant, whereas, additive × additive (*i*) effect was higher in magnitude.

Frequency distribution, means and standard errors of P_1, P_2, F_1, F_2, B_1 and B_2 progenies of bitter gourd for fruit length (Table 4) indicated both the parents were highly diverse with respect to the fruit length; the parent Sel-2 had 23.92 cm long (av.) fruits and the parent Pusa Purvi had fruits of 4.07 cm long (av.) and hence, both are most suitable for genetic study of this character. Fruit length of plants in F_1 generation range was intermediate (average length 10.14 cm) to both of the parents showed partial dominance effect toward short fruit length. Plants of the F_2 generation segregated in various ranges of fruit length (2.5 to 25 cm), this continuous variation of progeny indicated that fruit length is a quantitative trait. The size of fruit

Table 2. Test of significance of A, B, C and D scales for different characters in bitter gourd.

Scale	No. of days to open for first female flower	Node bearing first female flower	No. of days to open first male flower	Fruit length	Fruit No. per plant	Single fruit weight	Yield per plant
A	7.19 ± 3.08*	3.25 ± 2.69	8.07 ± 3.07**	-12.47 ± 1.29**	-17.06 ± 8.48*	-39.04 ± 9.81**	-1.18 ± 0.59*
B	0.39 ± 3.75	-5.21 ± 2.90	4.40 ± 3.48	2.57 ± 1.27*	-12.52 ± 9.77	-19.4 ± 4.03**	0.10 ± 0.59
C	81.25 ± 8.08**	9.20 ± 7.33**	67.33 ± 9.29**	8.69 ± 18.21**	65.13 ± 14.19**	49 ± 15.28*	0.34 ± 1.46
D	5.64 ± 4.02	0.88 ± 3.73	-1.33 ± 4.66	4.23 ± 9.12	26.19 ± 8.60*	29.56 ± 7.08**	-0.54 ± 0.54

*, **Significant at 5 &1% levels

Table 3. Components of generation means and standard error for different traits in Sel-2 × Pusa Purvi cross of bitter gourd.

Character	m	d	h	i	j	l	Epistasis
No. of days to open for first female flower	69.48 ± 1.78**	6.00 ± 1.86**	-16 ± 8.26	-11.3 ± 7.48	3.4 ± 2.16	3.7 ± 10.98	duplicate
Node bearing first female flower	11 ± 1.69**	6.2 ± 1.59**	-5.1 ± 7.59	-1.8 ± 7.11	4.2 ± 1.79*	3.7 ± 9.71	duplicate
No. of days to open first male flower	61 ± 2.15**	6.1 ± 1.82**	0.6 ± 9.49	2.7 ± 8.91	1.8 ± 2.08	-15.1 ± 11.80	duplicate
Fruit length	11.71 ± 4.54*	2.4 ± 0.76*	-12.3 ± 18.25	-8.5 ± 18.20	-7.5 ± 0.86**	18.4 ± 18.47	duplicate
Fruit No. per plant	46.93 ± 3.16**	-12.1 ± 5.84*	-50.2 ± 17.50*	-52.4 ± 14.92**	-2.3 ± 6.25	82 ± 27.33*	duplicate
Single fruit weight	39.40 ± 3.05**	12.64 ± 3.6**	-40.94 ± 14.88*	-59.12 ± 14.01**	-9.82 ± 4.73*	117.56 ± 20.93**	duplicate
Yield per plant	1.22 ± 0.25**	-0.08 ± 0.17	2.55 ± 1.19*	1.08 ± 1.03	-0.64 ± 0.20$_{**}$	-0.01 ± 1.62	duplicate

*, **Significant at 5 & 1% levels

Table 4. Frequency distributions, means and standard error of fruit length in six generations of single cross (Sel-2 × Pusa Purvi) of bitter gourd.

Population	Class (cm)									n	Mean ± S.E.	No. of genes (N)	Heritability (%)
	2.5-5.0	5.0-7.5	7.5-10.0	10.0-12.5	12.5-15.0	15.0-17.5	17.5-20.0	20.0-22.5	22.5-25.0				
P_1 (Sel-2)							1	12	2	15	23.92 ± 0.20	4.79	97.40
P_2 (Pusa Purvi)	15									15	4.07 ± 0.05		
F_1 (Sel-2× Pusa Purvi)			14	16						30	10.16 ± 0.07		
F_2	5	31	52	21	15	5				130	9.47 ± 0.28		
B_1 (Sel-2× Pusa Purvi) × Sel-2			8	6	10	4	2			30	13.23 ± 0.59		
B_2 (Sel-2× Pusa Purvi) × Pusa Purvi		10	20							30	7.65 ± 0.22		

mainly segregated on five classes (Fig. 1) and highest frequency of fruit length was observed on fruit length of 7.5 to 10 cm range (52 plants) followed by 5.0 to 7.5 cm (31 plants), 10 to 12.5 cm (21 plants) and 12.5 to 15 cm (15 plants). Minimum number of fruits (5 plants) was found in range of 2.5 to 5 cm and 17.5 to 20 cm. The mean of fruit length (9.47 cm) in F_2 fell between mid parent and short parent, and the distribution skewed (Fig. 2) toward short fruit parent (Pusa Purvi) indicating that short fruit length is partially dominant over long fruit, which was supported by the earlier reports of Kim *et al*. (6). In addition, the narrow distribution of progeny may indicate that few genes are involved in the control of this trait. Minimum number of genes was obtained as more than 4, which was also reported in study of Zhang *et al.* (15). High broad sense heritability indicates the heritable portion of variation is adequate for selection progamme of improvement.

Inheritance pattern of tubercles on fruit surface and curviness of fruit was investigated in Sel-2 (no tubercles, curved) and Pusa Purvi (prominent tubercles, straight) of bitter gourd lines. All the fruits of F_1 generations had prominent tubercles, indicating that tubercles were inherited as dominant trait (Table 5). Out of total 130 plants in F_2 population, 102 had prominent tubercles and 28 plants had no prominent tubercles on fruits. The observed frequency of F_2 plants fitted well in the expected ratio of 3 prominent tubercled: 1 non-prominent as evident from the non significant χ^2 values of 0.83 (P = 0.50-0.30). The B_1 population segregated into 17 prominent tubercles and 13 non prominent fruited plants. The observed frequency of B_1 plants fitted well in the expected ratio of 1 prominent tubercled : 1 non prominent with non- significant χ^2 values of 0.53 (P = 0.50-0.30). Also, all the fruits of F_1 plants showed straight end of fruits (Table 6), indicating that this was inherited as dominant trait. Out of total 130 plants in F_2 population 105 were straight fruited and 25 were curved fruited plants. The observed frequency of F_2 plants fitted well in the expected ratio of 3 straight: 1 curved as evident from the non significant χ^2 values of 2.30 (P = 0.30-0.10). The B_1 population segregated into 16 curved and 14 straight fruited plants. The observed frequency of B_1 plants fitted well in the expected ratio of 1 (straight): 1 (curved) with non-significant χ^2 values of 0.13 (P = 0.75-0.50). Inheritance pattern of tubercles and curviness of fruits reflected that they are inherited

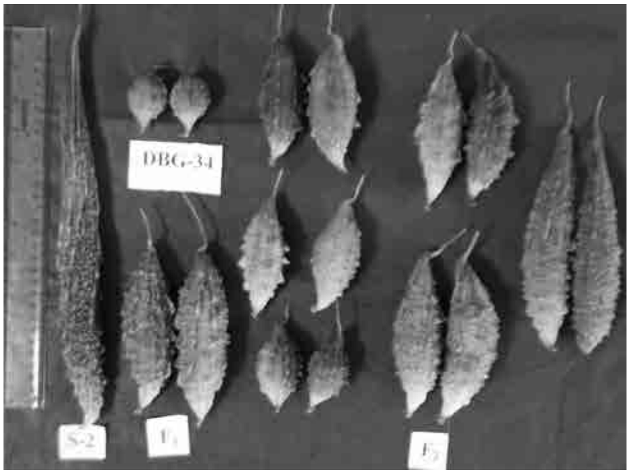

Fig. 1. Segregation of fruit length in F_2 population.

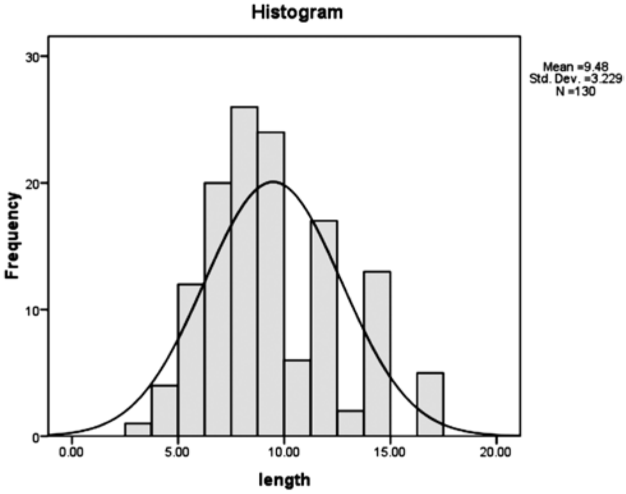

Fig. 2. Frequency distribution of fruit length in F_2 population.

Table 5. Single locus goodness of fit test for fruit tubercles in bitter gourd.

Generation	Total	Tubercle	Smooth	Expected	χ^2	P value
Sel-2 × Pusa Purvi						
P_1 (Sel-2)	15	0	15			
P_2 (Pusa Purvi)	15	15	0			
F_1 (Sel-2 × Pusa Purvi)	30	30	0			
F_2	130	102	28	3:1	0.83	0.50 - 0.30
B_1 (Sel-2 × Pusa Purvi) × Sel-2	30	17	13	1:1	0.53	0.50 - 0.30
B_2 (Sel-2 × Pusa Purvi) × Pusa Purvi	30	30	0			

Table 6. Single locus goodness of fit test for fruit curviness in bitter gourd.

Generation	Total	Curved	Straight	Expected	χ^2	P value
Sel-2 × Pusa Purvi						
P_1 (Sel-2)	15	15	0			
P_2 (Pusa Purvi)	15	0	15			
F_1 (Sel-2 × Pusa Purvi)	30	0	30			
F_2	130	25	105	3:1	2.30	0.30 - 0.10
B_1 (Sel-2 × Pusa Purvi) × Sel-2	30	16	14	1:1	0.13	0.75 - 0.50
B_2 (Sel-2 × Pusa Purvi) × Pusa Purvi	30	0	30			

as single gene with prominent tubercles dominant over non prominent type and straight fruits dominant over curved one. This was also supported by the study of Vahab (14).

Preponderance of non-additive gene action for fruit length and fruit weight was also reported by Sharma and Bhutani (11). Partial dominance of small fruit over large fruit was earlier evidenced by Kim *et al.* (6). Greater involvement of dominance (*h*) and dominance × dominance (*l*) gene action for fruit length was confirmed by the study of Celine and Sirohi (2) and Sirohi and Choudhury (12). Thus, in the present study, greater magnitude of dominance (*h*) gene effect with respect to additive (*d*) effect for most of the traits suggest that combination breeding approach based on hybridization followed by selection with moderate selection intensity may be more useful for improving these characters along with selection procedure for improvement in fruit length.

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