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Generation mean analysis of yield related traits and inheritance of fruit colour and surface in bitter gourd

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ABSTRACT

Analysis of generation means in P_1, P_2, F_1, F_2, B_1 and B_2 generations of bitter gourd cv. Pusa Do Mausami × DBG 43 was performed to determine the nature of gene action governing yield traits. Significant differences among parents and generations were observed for all traits, and the two parental lines differed significantly for fruit length, fruit diameter, fruit number and average weight per fruit. All the traits studied showed non allelic gene interaction indicating presence of epistatis gene action. Nature of gene action varied with the character and both additive and non-additive gene action was involved in expression of the characters having the duplicate type of epistasis. The traits were predominantly governed by dominance and dominance × dominance interaction effects and favors heterosis breeding for improvement. Chi-square tests was applied in the segregating generations of crosses Sel-1 × Pusa Do Mausami and Sel-1 × Pusa Vishesh revealed that green fruit colour of bitter gourd was governed by a single pair of nuclear genes and green colour is dominant over white fruit colour. The inheritance of ridgeness in cross Sel-1× Pusa Vishesh indicated that the fruit surface (discontinuous ridge) of bitter gourd was governed by a single dominant gene.

Key words: *Momordica charantia*, generation mean analysis, epistasis, fruit colour.

INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is an important cucurbit, which is consumed as a vegetable. Bitter gourd is well known for its antidiabetic and other medicinal properties. Since immature fruits are sliced during the preparation of various Asian meals, exceptional internal fruit quality and uniform green peel colour are desirable. Liu *et al*. (5) reported high heritability of fruit colour controlled by one pair of nuclear genes where green is dominant to white. Fruit colour governs its marketability as the colour preference differs from region to region. Green-fruited types are in high demand in southern China, while white-fruited types are preferred in central China. Similarly, dark green to glossy green fruits are favored in northern India, whereas, white fruits are preferred in southern India. In eastern parts of the country small and dark green fruited types are preferred.

Being cross-pollinated crop, its variations could be found on almost all characters including quantitative and qualitative traits like fruit colour and fruit surface. The genetic analysis of a large fruited (*M. charantia* var. *charantia* / *maxima*) × small fruited (*M. charantia* var. *muricata* / *minima*) population suggested that the small fruit was partially dominant over large fruit (Kim *et al*., 4), but that fruit length was incompletely dominant and controlled by a minimum of five genes (Zhang *et al*., 14). Fruit length, average fruit weight, and number of fruits per vine are controlled by additive factors, and have direct positive effects on fruit yield (Dey *et al*., 2). Consequently, simple selection strategies (e.g., backcrossing) focusing on flowering duration, harvesting span, fruit length and diameter, fruit rind thickness, average fruit weight, number of fruits per vine, dry fruit weight, dry matter per vine and harvest index could be used to improve bitter gourd yield. In contrast, genetic dominance and complementary gene action associated with some of these traits combined with their low narrow-sense heritability indicate that hybrid breeding would be an advantageous strategy when breeding for higher yield (Celine and Sirohi, 1).

The purpose of this investigation was to understand the nature and magnitude of gene actions involved in the inheritance of yield components in bitter gourd through generation mean analysis and inheritance of qualitative fruit traits based on chi square test.

MATERIALS AND METHODS

Two genetically diverse inbreds of bitter gourd Pusa Do Mausami {*Momordica charantia* var. *charantia*; medium long fruits (13 cm)} and DBG 43 {*Momordica charantia* var. *muricata*; small fruits (4 cm)} were used to develop F_1, F_2, B_1 and B_2 generations. A single F_1 plant from this initial mating was used as the paternal parent to produce B_1 (P_1 × F_1) and B_2 (P_2 × F_1) progeny, and was also self pollinated to generate F_2 progeny.

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In another experiment, P_1, P_2, F_1, F_2, B_1 and B_2 generations of cross Sel-1 (white fruit with continuous ridges) × Pusa Do Mausami (green fruit, continuous ridges) and Sel-1 (white fruit with continuous ridges) × Pusa Vishesh (green fruit with discontinuous ridges) were analyzed for fruit colour and fruit surface. Both the experiments were laid out in Randomized Block Design (RBD) with three replications during summer season of 2010. Seeds of the six generations for each family were sown in 50-cell plug-trays in the polyhouse at Division of Vegetable Science, IARI, New Delhi in January, 2010. An artificial soil medium with leaf mold was used as growing medium. The trays were regularly moistened to capacity after seeding and held in the polyhouse at temperature around 20°C. The transplants were moved to an open field at the field site for acclimatization one week before transplanting. The seedlings were transplanted by hand at the two-true-leaf stage.

Data were recorded on 10 plants of each parent, 20 plants each in F_1, B_1 and B_2 generations, respectively and 80 plants in F_2 per replication for four economic traits at marketable stage of fruit. For generation mean analysis, six-parameter model for estimation of various genetic components proposed by Hayman (3) including mean (m), additive effect (d), dominant effect (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) type for gene interaction were fitted to the data. The data were tested for the adequacy of the additive-dominance model using the ABC Scaling Test (Mather, 6). Generation means analyses were carried out on the original scale to determine the gene effects of fruit length, fruit diameter, average fruit weight and number of fruits per plant. For inheritance studies on fruit colour and surface, total number of plants falling into different classes were counted and subjected to chi-square analysis for goodness of fit to various classical Mendelian ratios as suggested by Panse and Sukhatme (7).

RESULTS AND DISCUSSION

Significant ($P \leq 0.05$) mean differences were detected between the two parental lines for all traits (Table 1). P_1 (*Momordica charantia* var. *charantia*) consistently possessed higher primary fruit length (13.12 ± 0.76 cm), fruit diameter (3.54 ± 0.09 cm) and average fruit weight (69.27 ± 5.77 g) than P_2 (*Momordica charantia* var. *muricata*). Individual B_1, B_2 and F_2 progeny were observed that reached or transgressed the phenotypic extremes of either parent for most traits. For most traits, F_1 generation means were higher than the mid-parent value. The F_1 generation was intermediate to parental lines for fruit diameter and performed equal to P_1 (commercial cultivar Pusa Do Mausami). B_1 and B_2 progenies resembled their respective recurrent parent with respect to all four traits and F_2 individuals varied dramatically for the yield-related characteristics examined.

The generation means of parents and crosses with respect to four important quantitative traits are presented in Table 2. Data for all characters did not adequately fit a simple additive-dominance model (three-parameter model). The non-weighted scaling test approach identified significant additive, dominance and nonallelic interactions for all characters. The sign of dominance (h) and dominance × dominance (l) components were opposite sign to each other indicating duplicate epitasis for all the characters studied. The results are in agreement with the reports of Celine and Sirohi (1) who recorded non allelic gene interaction for fruit length, fruit diameter, fruits per plant and fruit weight in bitter gourd.

The scaling test results showed that factor A was significant for fruit length, average fruit weight and number of fruits per plant. The factor B was significant for fruit length and average fruit weight. The factor D was significant for fruit length, fruit diameter and average fruit weight. The significance of factors reflected the role of epistatic gene action involved in the expression of quantitative parameters. Analysis of variance of different fruit characters showed significant differences between the parents and among generation means (Table 2).

The dominance (h) component of genetic variation was observed to be highly significant and positive in the inheritance of fruit length suggesting that dominance was in the direction of more fruit length. Regarding the epistatic gene effect, both additive × additive (i) and dominance × dominance (l) were highly significant for this trait. The absolute magnitude of

Table 1. Generation mean for different fruit traits in Pusa Do Mausami × DBG 43 cross of bitter gourd.

Character	P_1	P_2	F_1	F_2	B_1	B_2
Fruit length (cm)	13.12 ± 0.76	3.93 ± 0.12	12.01 ± 1.58	10.19 ± 0.52	10.35 ± 0.39	4.65 ± 0.27
Fruit diameter (cm)	3.54 ± 0.09	2.99 ± 0.09	3.48 ± 0.43	3.37 ± 0.14	3.40 ± 0.12	3.06 ± 0.19
Average fruit weight (g)	69.27 ± 5.77	17.50 ± 2.22	62.44 ± 3.71	55.50 ± 2.44	54.15 ± 2.85	14.51 ± 1.07
No. of fruits/plant	9.80 ± 1.05	25.20 ± 2.05	15.10 ± 1.81	17.67 ± 0.92	18.33 ± 1.51	23.27 ± 2.80

Table 2. Gene effects and standard error for different fruit traits in Pusa Do Mausami × DBG 43 cross of bitter gourd.

Character	A	B	C	D	m	d	h	i	j	l
Fruit length	-6.43** ±1.91	-8.64** ±1.67	-4.28 ± 3.85	5.39** ± 1.14	10.19** ± 0.51	5.69 ± 0.47	5.30** ± 2.79	-10.78** ± 2.28	1.10 ± 0.60	-25.86** ± 4.29
Fruit diameter	-0.15 ± 0.50	-0.45 ± 0.58	1.44 ± 1.03	1.02** ± 0.35	3.78** ± 0.13	0.42 ± 0.22	-1.73* ± 0.83	-2.05** ± 0.71	0.15 ± 0.23	2.66 ± 1.37
Average fruit weight	-33.41* ±11.19	-60.91** ± 8.29	-9.67 ± 19.27	42.33** ± 5.75	55.49** ± 2.44	39.63** ± 3.04	-55.60** ± 14.19	-84.66** ± 11.51	13.75** ± 4.33	178.99** ± 22.79
No. of fruits/ plant	11.76** ± 3.66	6.23 ± 6.22	5.50 ± 5.66	-6.25 ± 3.67	17.67** ± 0.92	-4.93** ± 0.17	10.10** ± 1.65	12.50 ± 7.35	2.76 ± 3.38	-30.50* ± 13.91

*, ** = Significant at 0.05 and 0.01 levels, respectively.

epistatic gene effects exceeded the additive (d) and dominance (h) gene effects. Duplicate epistatis was present for fruit length. Hence, heterosis breeding may be advantageous for achieving higher gain for fruit length. In main gene effects only dominance (h) component and in epistatic gene effect only additive × additive (i) component was significant for inheritance of fruit diameter. Among significant components, no one was in desire positive direction. The absolute magnitude of epistatic gene effects was greater than their respective estimates of additive (d) and dominance (h) effects.

Average fruit weight and number of fruits per plant had positive correlation with yield per plant in bitter gourd. In the present study, both additive (d) and dominance (h) gene effects were found to be highly significant for average fruit weight with higher absolute magnitude of dominance effects. The entire epistatic components, *i.e.* additive × additive (i), additive × dominance (j) and dominance × dominance (l) were highly significant. Among significant components, additive, additive × dominance and dominance × dominance components were in desire positive direction. The total epistatic effects exceeded the additive (d) and dominance (h) gene effects. Regarding number of fruits per plant both additive (d) and dominance (h) gene effects were highly significant but additive component was in negative direction. Among epistatic gene effect only dominance × dominance (l) component was significant. The absolute magnitude of epistatic gene effects exceeded the additive (d) and dominance (h) gene effects.

Duplicate epistatis with significant dominance component in favorable direction for fruit length and number of fruits per plant suggests heterosis breeding for these characters. The significant negative dominance gene effects for fruit diameter and average fruit weight suggests combination-breeding approach based on hybridization followed by selection like pedigree or back cross breeding and also recurrent selection with moderate selection intensity for improving these characters. These findings are in agreement with Sharma and Bhutani (9) who reported that fruit length and fruit weight were controlled by non additive type of gene action in bitter gourd. Celine and Sirohi (1) also reported greater involvement of dominance and dominance × dominance gene action for fruit length, fruit weight and number of fruits per plant in bitter gourd. However, they found that fruit diameter was controlled by additive and additive × additive gene action while Sirohi and Choudhury (10) noted greater involvement of dominance and dominance × dominance gene action for fruit length and diameter in bitter gourd. Tewari *et al*. (12) also reported similar results for fruit diameter. 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 in oriental pickling melon (Pornsuriya and Pornsuriya, 8). Additive gene effects were most important in governing primary branch number and fruit number per plant, while dominance and epistatic genetic effects mainly controlled days to anthesis, fruit weight per plant and average weight per fruit in melon (Zalapa *et al*., 13).

Inheritance pattern of fruit colour was investigated in bitter gourd in cross Sel-1 (white fruited line) × Pusa Do Mausami (green fruited line) and Sel-1 × Pusa Vishesh. In both crosses, the F_1 generations had all fruits of green colour, indicating that green colour was inherited as a dominant trait (Table 3). Out of total 80 plants in F_2 population of cross Sel-1 (white fruited line) × Pusa Do Mausami (green fruited line), 56 were green fruited and 24 plants had white fruits (Table 3). The observed frequency of F_2 plants fitted well in the expected ratio of 3 green: 1 white

Table 3. Single-locus goodness-of-fit test for fruit colour in bitter gourd.

Generation	Total	Green	White	Expected	χ^2	P value
Sel-1 × Pusa Do Mausami						
P_1	10	0	10			
P_2	10	10	0			
F_1	20	20	0			
F_2	80	56	24	3:1	1.06	0.50-0.30
B_1	20	12	8	1:1	0.80	0.50-0.30
B_2	20	20	0			
Sel-1 × Pusa Vishesh						
P_1	10	0	10			
P_2	10	10	0			
F_1	20	20	0			
F_2	80	59	21	3:1	0.06	0.90-0.75
B_1	20	11	9	1:1	0.20	0.75-0.50
B_2	20	19	1	1:0	0.05	0.90-0.75
Pooled						
P_1	20	0	20			
P_2	20	20	0			
F_1	40	40	0			
F_2	160	115	45	3:1	0.83	0.50-0.30
B_1	40	23	17	1:1	0.90	0.50-0.30
B_2	40	39	1	1:0	0.02	0.90-0.75

Table 4. Single-locus goodness-of-fit test for fruit surface (ridgeness) in bitter gourd.

Generation	Total	Discontinuous	Continuous	Expected	χ^2	P value
Sel-1 × Pusa Vishesh						
P_1	10	0	10			
P_2	10	10	0			
F_1	20	20	0			
F_2	80	57	23	3:1	0.60	0.50-0.30
B_1	20	8	12	1:1	0.80	0.50-0.30
B_2	20	20	0			

as evident from the non significant χ^2 values of 1.06 (P = 0.50-0.30). The B_1 population segregated into 12 green and 8 white fruited plants. The observed frequency of B_1 plants fitted well in the expected ratio of 1 green: 1 white fruited plant with non-significant χ^2 values of 0.80 (P value 0.50-0.30). In another cross Sel-1 (white fruited line) × Pusa Vishesh (green fruited line) the F_2 population segregated into green and white fruiting plants in the ratio of 59: 21 fitting well in the expected ratio of 3 green: 1 white fruited plants ($\chi^2 = 0.06$; P = 0.90-0.75; Table 3). Out of 20 plants in B_1, 11 showed green fruits and remaining 9 had white fruits. The observed frequency fitted well into expected ratio of 1 green: 1 white fruited plant ($\chi^2 = 0.20$; P = 0.75-0.50). The B_2 generation had one white fruit may be due to misclassification differences.

In pooled data analysis of both crosses, the F_2 generation segregated in ratio of 115: 45 (green: white fruited lines) fitting well in the expected ratio of 3 green: 1 white (χ^2= 0.83; P = 0.50-0.30). Out of 40 plants in B_1, 23 plants had green fruits and 17 had white fruits. Thus, this observed frequency is matching with expected ratio of 1 green: 1 white ($\chi^2 = 0.90$; P = 0.50-0.30). In B_2, 39 plants were green fruited and 1 white fruited (χ^2 = 0.02; P = 0.90-0.75, Table 3).

Inheritance pattern of fruit surface (ridgeness pattern) was investigated in bitter gourd in cross Sel-1 (continuous ridge) × Pusa Vishesh (discontinuous ridge). All F_1 plants showed discontinuous ridge, indicating that this was inherited as a dominant trait. Out of total 80 plants in F_2 population, 57 segregated as discontinuous ridge and 23 as continuous ridge fitting into the expected ratio of 3:1 (χ^2 = 0.60; P = 0.50-0.30; Table 4). The B_1 population segregated into 8 discontinuous and 12 continuous ridged fruited plants. The observed frequency of B_1 plants fitted well in the expected ratio of 1 discontinuous: 1 continuous ridged fruited plant (χ^2 = 0.80; P = 0.50-0.30; Table 4). Inheritance pattern of fruit colour and ridgeness depicts that they are inherited as single gene with green colour dominant over white and discontinuous ridge dominant over continuous ridge. This study confirmed the earlier report of Srivastava and Premnath (11) who stated that white immature fruit skin is controlled by the genotype *ww* for white epicarp that is recessive to the genotype *WW* for green epicarp.

A simplistic additive-dominance model did not adequately explain the observed variation for any of the traits examined herein, and was evident earlier that small fruit was partially dominant over large fruit (Kim *et al*., 4), but that fruit length was incompletely dominant and controlled by a minimum of five genes (Zhang *et al*., 14) with higher order epistatic interactions. Most of the traits examined exhibited the combined influence of substantial dominance and epistatic effects, which were mainly controlled by additive factors. Gene action and empirical estimates of genetic parameters governing trait expression have been useful in developing breeding strategies for incorporating genes for high fruit number and fruit weight. Altering the fruit setting habit of bitter gourd can provide for the development of high yielding genotypes. The alignment of desirable alleles conditioning such complex traits in bitter gourd could be enhanced by the identification of marker-trait associations for their subsequent use in marker assisted selection.

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