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Genetic analysis for yield and its attributes in bitter gourd (*Momordica charantia*)

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ABSTRACT

Genetic interaction and inheritance study in bitter gourd was carried out using six-generation mean analysis to determinate the types and magnitude of gene effects for yield and its attributes. The knowledge portioning to gene action and interaction, is tool for designing appropriate breeding strategy for developing varieties in bitter gourd. Four crosses, viz. DBGS-54 × DBGS-34, DBGS-2 × DBGS-34, PVGy-201 × Pusa Do Mousami and DBGS-2 × DBGS-3 were used for studying six generation (P_1, P_2, F_1, F_2, B_1 and B_2) model. The presence of non-allelic interaction were detected by both scaling test and joint scaling test and observed inadequacy of the additive-dominance model for all traits except vine length in cross PVGy-201 × Pusa Do Mousami.The results revealed the contribution of additive (d), dominance (h) and epistasis interaction (i, j, l) towards expression of all traits studied. In most of the characters magnitude of dominance gene effect was greater than additive gene effect suggested that recurrent selection or heterosis breeding would prove useful. Duplicate epistasis was prevalent in most of the traits like vine length, days to first female flower and fruit weight. Fruit epicarp colour and seed coat colour inheritance suggested these traits were controlled by monogenic.

Key words: Dominance effect, Epistasis interaction, Genetic studies, Generation Mean Analysis, *Momordica charantia*

Bitter gourd (*Momordica charantia* L.) 2n=2x=22 is one of the important vegetable cum medicinal plant belongs to the family Cucurbitaceae, which is widely cultivated in Asia, Africa, the Caribbean, and South America (Grover and Yadav 2004). Since from last two decades bitter gourd has occupied a special position among the vegetables because of its incomparable hypoglycemic action and nutraceutical values (Tan *et al.* 2016) and hence, bitter gourd is accepted as "Vegetable Insulin". Despite the presence of several valuable medicinal and nutritional attribute, the productivity of bitter gourd remain unsatisfactory to a large extent and are attributable to the limited research effort concentrated in this crop. Bitter gourd is predominantly cross-pollinated vegetable due to predominance of monoecious sex form and expresses very little inbreeding depression. Indian bitter gourd shows diverse morphological variation with respect to growth habit, maturity, fruit shape, size, colour, and surface texture and sex expression (Behera *et al*. 2006). Genetic improvement depends primarily on the effectiveness of selection among progenies that differ in genetic value.

The primary breeding objective of bitter gourd is to improve the yield and quality of the fruit. The yield trait is a complex character and governed by polygenic which have small and cumulative effect and expression of which is continuous in nature. Therefore, to attain the actual yield potential, the fundamental understanding of the genetics and inheritance that underlies the yield and its component characters are urgently required. Hence, adopting appropriate breeding and selection strategies for targeted trait improvement largely depend on the knowledge of gene action/effects operating in a particular breeding population. Generation mean analysis are being widely used for estimation of gene action and knowledge on gene action would benefit breeders in terms of illustrating the appropriate breeding methods and selection process for developing bitter gourd varieties .In bitter gourd, in addition to additive and dominance variation, epistasis may also be involved in the inheritance of many quantitative characters (Dey *et al*. 2010). The present investigation aims to elucidate the gene action involved in the inheritance of yield components in bitter gourd through generation mean analysis.

MATERIALS AND METHODS

Plant materials and experimental design: An experiment was conducted at experimental field of ICAR-Indian Agricultural Research Institute, New Delhi, India.

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The experimental materials comprised of six generations including parental lines (P_1& P_2), F_1, F_2, B_1 and B_2 from four crosses of bitter gourd namely, DBGS-54 × DBGS-34, DBGS-2 × DBGS-34, PVGy-201 × Pusa Do Mousami and DBGS-2 × DBGS-3. The F_1's were developed during rainy season (June-October, 2015), and raising of F_1's to develop F_2 and backcross progenies (B_1 and B_2) was done during spring-summer of 2016-17 under insect proof net house condition. The evaluation trial of above said six generations (P_1, P_2, F_1, F_2, B_1 and B_2) was organized in the open field conditions during March-July-2018 in a completely randomized block design with three replications .The data was recorded from 20 plants in each parent, 40 plants of F_1, B_1 and B_2 generations and 110 (DBGS-54×DBGS-34), 170 (DBGS-2×DBGS-34),285(DBGS-2×DBGS-3) and 165 (PVGy-201×PDM) plants in F_2 for five economical traits.

Statistical and Genetic Analysis: The Generation Mean Analysis (GMA) was performed as suggested by Hayman (1958). Before estimating the different parameters, ABCD scaling tests of Hayman and Mather (1955) were performed to detect the presence of non-allelic interactions (epistasis). The means of different generations were utilized to calculate the above said scales. To test the significance of the scales, student 't' test was used for each scale.

In addition to scaling test data was further subjected to joint scaling test because sometime scaling test remain inadequate to fully explain the additive-dominance model (Deb and Khaleque 2009). Hence joint scaling test was performed which integrates multiple scaling tests and to test the competence of simple additive–dominance model or to detect epistasis for all the measured traits using χ^2 test. In instance, where χ^2 and ABCD scaling test is inadequate, six-parameter model or digenic interaction model (Hayman 1958) was used to estimate the gene effects. These parameters represent mean effect [m], genetic effects including additive [d] and dominance [h], and gene interaction effects comprising additive × additive [i], additive × dominance [j] and dominance × dominance [l]. The square roots of respective variances were used for the computation of standard error which were used to calculate the 't' values for testing significance of the corresponding gene effects.

The type of epistasis was determined only when dominance (h) and dominance × dominance (l) effects were significant, when these effects had the same sign, the effects were complementary while different signs indicated duplicate epistasis (Kearsey and Pooni 1996).

The chi-square (χ^2) test suggested by Panse and Sukhatme (1985) was subjected to study the inheritance of fruit color and seed coat color in bitter gourd. These traits are expected as controlled by single gene. The χ^2 value was calculated as:

$$\text{Chi} - \text{squarare } (X^2) = \frac{(\text{Observed number - Expected number})^2}{\text{Expected number}}$$

RESULTS AND DISCUSSION

The success of the plant breeder lies in the steady improvement of genetic constitution of crop plant for the development of superior genotypes with all desirable traits. To achieve this, knowledge of the genetic mechanism of the control of various traits is the first pre-requisite. The mean performance of F_1 surpassed the better parent for early flowering (DBGS-2×DBGS-3 and yield per plant in all four crosses. The superior performance of F_1 over better parent indicated over-dominance of these traits and need to be exploited through heterosis breeding. These findings are in agreement with the results obtained by Dey *et al*. (2012) and Al-Mamuna *et al*. (2016). There was reduction in mean performance of F_2 population than F_1 for vine length in three crosses except DBGS-2 × DBGS-34, late flowering in all the four crosses, and fruit weight in all four crosses. This apparently indicated influence of inbreeding depression. Angadi (2015) and Rao (2017) in bitter gourd obtained similar results. The backcross generations (B_1 and B_2) means were near to their respective parents. The mean effect (m) was significant for all studied traits among three crosses, indicated that the traits were quantitatively inherited.

Adequacy of the genetic model: Data (Table 1) showed non-significance of scaling test and joint scaling χ^2 test for vine length in PVGy-201×PDM, indicating the absence of digenic non-allelic interaction (epistasis) in these cases. In the other crosses, the significance results of A, B, C, D and χ^2 test suggested these traits do not fit to an additive-dominance model hence improvement of these traits would be moderately difficult due to existence of non-allelic gene interaction, as compared to the situation best fitting to an additive-dominance model. The presence of non-allelic gene interactions involved in expression of quantitative characters in bitter gourd was reported by Rani *et al*. (2013) and Kumari *et al*. (2015). The result revealed (Table 1) that mean effect of F_2 performance (*m*) was highly significant for all the studied traits in four crosses.

Genetic studies using generation mean analysis: In the present study, scaling test and joint scaling χ^2 test were found to be significant for most of the traits. This indicates presence of inter-allelic interaction, which plays an important role in the expression of a trait, and additive-dominance alone will not be sufficient to deal with such traits. Hence, six-parameter model was employed according to Jinks and Jone (1958) to estimate six components of genetic variation, viz. m, d, h, i, j and l. The sign associated with additive effect (d) and dominance effect (h) indicates the parents who possess the highest number of positive alleles for increasing the characters. The significant and positive d was observed for vine length, days to first female appearance in cross DBGS-2×DBGS-34, while average fruit weight showed significant and positive values in all four crosses, indicates that additive effect of the genes is predominant and selection of these traits should be delayed to later generations.

The significant and positive values of h was recorded for vine length in cross DBGS-54×DBGS-34 and DBGS-2×DBGS-3, days to first female flower appearance in cross DBGS-2×DBGS-34, DBGS-2×DBGS-3,PVGy-201×PDM and yield per vine (in cross DBGS-2×DBGS-34, DBGS-

Table 1 Estimations of gene effects and epistasis for yield and its attributes in four crosses of bitter gourd

Vine length (cm)												
SBGS-2 × DBGS-34	-96.43** ± 14.31	-59.67** ± 13.36	-37.32** ± 27.43	59.44** ± 13.38	99.03**	251.32** ± 5.73	68.87** ± 6.92	-193.14** ± 27.81	-118.89** ± 26.71	-68.38** ± 9.35	374.99** ± 38.97	D
SBGS-54 × DBGS-34	-2.63 ± 9.49	-6.07 ± 9.01	-23.36* ± 11.73	-7.33 ± 6.46	4.18**	168.88** ± 1.92	-15.23** ± 5.20	27.01* ± 13.67	14.66 ± 12.93	1.72 ± 6.24	-5.96 ± 23.88	D
SBGS-2 × DBGS-3	-69.76** ± 25.02	44.68** ± 23.39	-70.62** ± 36.06	-22.74* ± 15.37	91.03**	337.13** ± 4.84	-44.97** ± 6.06	59.39** ± 24.55	66.14** ± 22.85	-93.83** ± 16.7	-63.31** ± 35.85	D
PVGy-201 × PDM	-12.07 ± 14.33	16.33 ± 15.81	-2.04 ± 21.32	-3.15 ± 10.36	2.17	208.09** ± 3.33	-43.00** ± 7.94	-3.90 ± 22.33	6.30 ± 20.72	-14.2 ± 9.76	-10.57 ± 38.24	C
Days to first female flower appearance												
SBGS-2 × DBGS-34	-3.43* ± 1.66	18.27** ± 1.98	6.81* ± 3.08	-4.01* ± 1.47	105.52**	55.78** ± 0.55	7.30** ± 0.97	7.08* ± 3.13	8.03* ± 2.94	-10.85** ± 1.12	-22.86** ± 4.94	D
SBGS-54 × DBGS-34	5.52* ± 2.61	-2.68 ± 2.49	-0.24 ± 2.40	-1.54 ± 1.75	6.37**	31.81** ± 0.36	0.50 ± 1.59	1.23 ± 3.62	3.08 ± 3.49	4.10* ± 1.74	-5.91 ± 6.81	D
SBGS-2 × DBGS-3	1.18 ± 1.48	0.52 ± 2.09	-28.04** ± 3.63	-14.87** ± 1.62	88.74**	67.66** ± 0.71	-7.27** ± 0.86	18.49** ± 3.50	29.74** ± 3.31	0.33 ± 1.12	-31.44** ± 5.01	D
PVGy-201 × PDM	15.12** ± 3.78	10.28** ± 2.59	-11.42** ± 2.94	-18.41** ± 2.22	83.06**	40.19** ± 0.44	-8.53** ± 2.04	29.22** ± 4.60	36.82** ± 4.45	2.42 ± 2.21	-62.22** ± 8.64	D
Fruit weight (g)												
SBGS-2 × DBGS-34	-50.33** ± 4.62	5.83 ± 3.17	-63.68** ± 4.53	-9.59** ± 3.11	283.19**	34.79** ± 0.88	25.29** ± 2.56	1.13 ± 6.37	19.18** ± 6.21	-28.08** ± 2.67	25.32* ± 11.18	C
SBGS-54 × DBGS-34	13.18 ± 8.89	-10.31** ± 2.24	-24.45** ± 6.86	-13.66* ± 5.19	34.15**	35.87** ± 1.46	42.96** ± 4.29	36.14** ± 10.53	27.32** ± 10.37	11.74* ± 4.51	-30.18 ± 18.48	D
SBGS-2 × DBGS-3	-1.00 ± 6.40	-7.74 ± 10.06	-91.80** ± 9.41	-41.53** ± 6.59	99.03**	88.13** ± 1.91	4.80 ± 5.37	81.88** ± 13.47	83.06** ± 13.19	3.37 ± 590	-74.32** ± 23.45	D
PVGy-201 × PDM	-9.36 ± 5.23	-36.40** ± 4.73	-17.74* ± 6.50	14.01** ± 3.82	61.49**	59.17** ± 1.23	6.48** ± 2.392	-18.84** ± 7.93	-28.02** ± 7.64	13.52** ± 3.45	73.79** ± 13.35	D
No. of fruits/vine												
SBGS-2 × DBGS-34	-5.40* ± 2.54	-2.60 ± 6.09	-12.35* ± 4.92	-2.18 ± 3.53	8.98**	38.21** ± 0.94	-20.60** ± 2.99	14.95* ± 7.24	4.35 ± 7.07	-1.40 ± 3.22	3.65 ± 12.83	C
SBGS-54 × DBGS-34	-11.38** ± 5.78	-5.78 ± 4.10	-4.70 ± 4.38	6.23* ± 2.59	15.34**	36.75** ± 0.74	-21.00** ± 2.12	-10.62* ± 5.42	-12.47** ± 5.18	-2.80 ± 2.42	29.63** ± 9.53	D

Contd.

Table 1 (*Concluded*)

SBGS-2 × DBGS-3	-5.55** ± 1.49	-3.75 ± 2.11	-8.92** ± 2.45	0.19 ± 1.03	16.48**	14.45** ± 0.24	-0.30 ± 0.91	0.57 ± 2.35	-0.38 ± 2.07	-0.90 ± 1.12	9.68 ± 43.30	C
PVGy-201 × PDM	-9.77** ± 3.51	-7.80** ± 2.76	-23.35** ± 3.69	-2.89 ± 2.15	40.39**	21.39** ± 0.53	1.47** ± 1.81	11.93** ± 4.56	5.78 ± 4.30	-0.98 ± 2.05	11.78 ± 8.34	C
Yield/vine (kg)												
SBGS-2 × DBGS-34	-0.87** ± 0.13	0.49 ± 0.25	-0.91** ± 0.19	-0.26 ± 0.16	58.72**	1.30** ± 0.04	0.09 ± 0.13	1.33** ± 0.32	0.52 ± 0.31	-0.68** ± 0.14	-0.14 ± 0.57	D
SBGS-54 × DBGS-34	-0.42** ± 0.10	-0.31* ± 0.11	-0.20 ± 0.24	0.27* ± 0.11	23.37**	1.27** ± 0.05	0.43** ± 0.05	0.44 ± 0.23	-0.53 ± 0.22	-0.05 ± 0.06	1.27 ± 0.31	C
SBGS-2 × DBGS-3	-0.67 ± 0.13	-0.60** ± 0.17	-2.47** ± 0.21	-0.60** ± 0.08	185.17**	1.22** ± 0.02	0.07 ± 0.07	1.29** ± 0.19	1.20** ± 0.16	-0.03 ± 0.09	0.06 ± 0.36	C
PVGy-201 × PDM	-0.91** ± 0.16	-1.36** ± 0.14	-1.97** ± 0.31	0.15 ± 0.12	120.18**	1.23** ± 0.03	0.20** ± 0.08	0.36 ± 0.23	-0.3 ± 0.21	0.22 ± 0.03	2.57** ± 0.39	C

2×DBGS-3) indicates predominance of dominant gene effect and for these traits selection should be delayed until heterozygous is reduced in population. The traits with high magnitude of dominance and additives can be improved by pedigree or bulk methods. Among the interaction effects additive × additive (i) gene effect was found highly significant and in desired direction for days to first female flower appearance and the values are higher than dominance (h) effect, indicates predominance of additive × additive gene interactions suggest that simple selection procedure can be adopted for improvement of these traits. Complementary type of epistasis was observed for vine length in cross DBGS-2×DBGS-34. Fruit weight in cross DBGS-2×DBGS-34, number fruits/vine in all crosses except cross DBGS-54 × DBGS-34 and yield per vine in all crosses expect cross DBGS-2 × DBGS-34. The complementary epistasis indicated that parents selected for crossing were diverse for that particular trait; hence it is possible to realize enhanced genetic gain in breeding programme. Inheritance pattern of fruit colour was studied using cross of DBGS-2 (Green fruits) × DBGS-3 (White fruit) and the results (Table 2) reflect that green fruits colour was dominant over white colour and controlled by monogenic trait. The results confirmed earlier report of Hu *et al.* (2002) who explained fruit colour was controlled by one pair of nuclear gene with white recessive and green dominant in nature. In contrary, immature fruit colour in bitter gourd shows continuous distribution from white to dark green pointing this trait

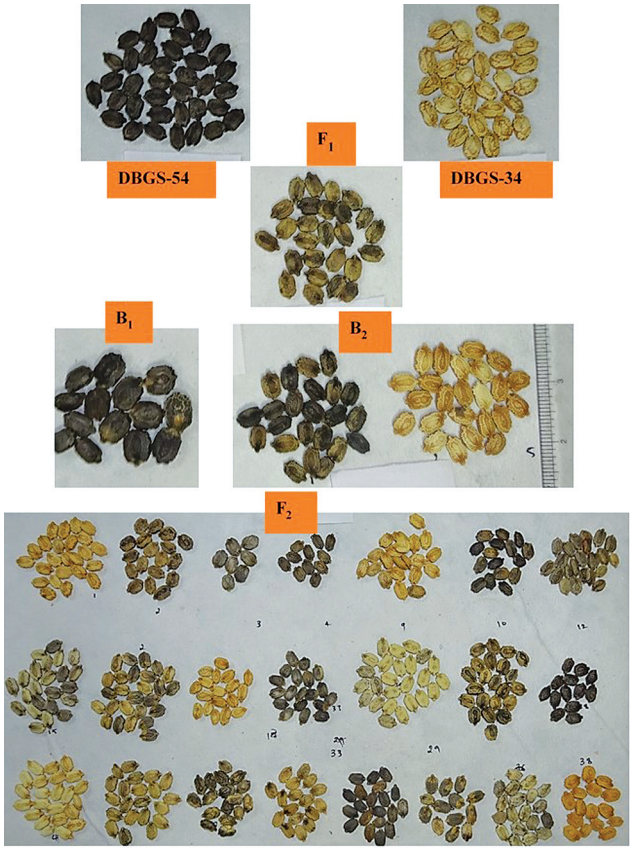

Fig 1 Inheritance of seed coat colour in bitter gourd.

Table 2 Inheritance pattern of fruit epicarp color and seed color in bitter gourd

Epicarp color in cross DBGS-2 × DBGS-3						
Population	Total	Observed		Expected ratio	$\chi 2$ value	P value
		Green fruit	White fruit			
Pooled Data (2017 and 2018)						
DBGS-2	20	20	0	-	-	-
DBGS-3	20	0	20	-	-	-
F_1	40	40	0	-	-	-
F_2	285	214	71	3:1	0.001	0.97
B_1	60	60	0	-	-	-
B_2	60	33	27	1:1	0.60	0.45
Seed coat color in bitter gourd in cross DBGS-54 × DBGS-34						
		Black seed	Light black	Yellow		
DBGS-54	20	20	0	0		
DBGS-34	20	0	0	20		
F_1	40	0	40			
F_2	110	24	58	28	1:2:1	0.62	0.73
B_1	30	30	0			
B_2	20	16	-	14	1:1	0.80	0.37

was controlled by quantitative genes (Huang and Hsieh 2017). The inheritance of seed coat colour was studied in cross DBGS-54 (Black seed) × DBGS-2 (Brown seed), all the progenies in F_1 bore light black seeds (Table 2). In F_2 population the seed colour segregate in the ratio of 1 black: 2 light black: 1 yellow seed coat (Fig 1), which indicates the seed coat colour is controlled by major semi dominant gene. Kole *et al.* (2012) reported that seed coat colour in bitter gourd is controlled by digenic (9:7) gene, in contrary Srivastava and Premnath (1972) reported dark brown seed colour was dominant over light colour and suggested trait is governed by single gene.

The yield and its attributing traits showed presence of both additive and non-additive gene interactions. Therefore, recombination breeding could be used, followed by selection in later generations. For improvement of quantitative traits in bitter gourd, standard selection methods may be used to exploit additive gene action. Simultaneously, dominant gene effects should be concentrated. The traits governed by additive gene effect could be improved through pedigree method. The traits pretended by non-additive gene interaction (dominance effect) could be improved by recurrent selection for specific combining ability or heterosis breeding. The traits controlled by both additive and non-additive gene effects would be improved by using inter se or bi-parental mating followed by cyclic selection such as diallel mating or reciprocal recurrent selection.

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