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RESEARCH ARTICLE

Genetics of Yield and Fruit Quality Traits in Bitter Gourd (*Momordica charantia* L.)

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Abstract

Utilization of genetic resources in crop breeding requires a basic understanding of the economic traits they are recognized for. Determination of genetics of traits helps to decide the appropriate breeding strategy for developing improved varieties. Segregating populations developed using *Momordica charantia* var. *charantia* and *M. charantia* var. *muricate* genotypes were used for generation mean analysis (GMA) to work out the gene effects controlling yield and fruit quality traits in bitter gourd. The study confirmed the role of non-allelic interactions and predominance of dominance gene effect (h) for most economic traits, which indicates the suitability of recurrent selection or heterosis breeding for the improvement of these traits. Segregation analysis indicated the single dominant gene control of fruit epicarp color, tubercle nature and fruit ridges. The predominance of complementary type of epistasis for most traits implies the genetic divergence between the parents used and the possibility of realizing a greater genetic gain in the breeding programme using these genetic resources.

Keywords: Dominance effect, Epistasis interaction, Generation mean analysis, Genetic studies, *Momordica charantia*.

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Introduction

Momordica charantia L. (Syn. bitter gourd, balsam pear) (2n = 22) is a traditional vegetable and medicinal crop of tropics and subtropics of Asia, South America and East Africa (Heiser, 2016). Bitter gourd belongs to Cucurbitaceae family and is known for its distinctive bitter flavor and high nutritional value, specifically ascorbic acid and iron (Behera, 2004). As a medicinal crop, it is widely known for its anti-diabetic, anti-HIV and anti-tumor properties (Behera *et al.*, 2008). Bitter gourd is a highly cross-pollinated crop due to its monoecious sex form, which results in wide variability. Mainly, Indian bitter gourd gene pool exhibits high morphological variation in growth habit, maturity, fruit shape, size, color, surface texture and sex expression (Behera *et al.*, 2006). This genetic variability is vital in developing varieties as per consumer demand. Market preference for bitter gourd varieties varies from region to region with respect to its fruit quality traits, such as fruit color, length, shape, and tubercles (Rathod *et al.*, 2019). For instance, dark green to glossy green fruits are preferred in northern India. White fruits are ideal in the south Indian market, whereas in eastern parts of the country, small and dark green fruits are desired (Behera *et al.*, 2010). Hence to exploit the existing genetic variation in order to develop varieties suitable for various market segments, elucidating genetics of these traits is crucial. To successfully determine trait genetics, populations derived from diverse parents should be used for genetic analysis. The generated knowledge through this

Table 1: Generation means for earliness and yield traits in cross PVGy-201 × PDM and CBM-12 × DBG-4 of bitter gourd

Traits	*Cross*	*P1*	*P2*	*F1*	*F2*	*B1*	*B2*
Node to first female flower	PVGy-201 × PDM	3.05 ± 0.29	11.400 ± 0.72	5.62 ± 0.36	6.57 ± 0.16	4.83 ± 0.23	9.78 ± 0.31
	CBM-12 × DBG-4	12.60 ± 0.77	7.400 ± 0.64	7.82 ± 0.39	7.95 ± 0.40	9.91 ± 0.26	6.01 ± 0.28
Days to first female flower	PVGy-201 × PDM	26.80 ± 0.57	45.250 ± 1.01	32.10 ± 0.38	35.17 ± 0.46	30.36 ± 0.32	36.90 ± 4.33
	CBM-12 × DBG-4	79.45 ± 1.08	78.450 ± 1.60	63.450 ± 1.60	71.34 ± 0.68	69.46 ± 0.48	66.33 ± 0.74
Node to first male flower	PVGy-201 × PDM	-	-	-	-	-	-
	CBM-12 × DBG-4	9.05 ± 0.39	4.15 ± 0.38	4.45 ± 0.26	7.12 ± 0.33	6.30 ± 0.20	4.16 ± 0.17
Days to first male flower	PVGy-201 × PDM	-	-	-	-	-	-
	CBM-12 × DBG-4	64.20 ± 1.34	65.95 ± 1.39	55.82 ± 0.89	68.67 ± 0.80	61.66 ± 0.62	66.33 ± 0.74
Fruit length (mm)	PVGy-201 × PDM	113.87 ± 3.30	180.39 ± 2.27	165.48 ± 1.78	144.30 ± 2.71	140.53 ± 1.42	170.78 ± 1.39
	CBM-12 × DBG-4	54.19 ± 1.16	165.35 ± 1.90	109 ± 0.90	99.52 ± 1.79	73.01 ± 0.83	128.62 ± 0.91
Fruit weight (gm)	PVGy-201 × PDM	89.47 ± 4.26	145.27 ± 2.89	139.84 ± 1.352	120.46 ± 2.30	128.29 ± 1.12	147.39 ± 1.15
	CBM-12 × DBG-4	17.38 ± 0.68	96.85 ± 1.79	56.65 ± 0.93	47.32 ± 1.65	29.89 ± 0.60	70.25 ± 0.92
Fruit diameter (mm)	PVGy-201 × PDM	42.82 ± 0.81	38.97 ± 0.72	44.46 ± 0.57	40.79 ± 0.35	42.91 ± 0.45	38.06 ± 0.46
	CBM-12 × DBG-4	34.56 ± 0.94	41.55 ± 0.91	38.12 ± 0.44	38.49 ± 0.53	34.83 ± 0.35	39.483 ± 0.29
Number of fruits per plant	PVGy-201 × PDM	20.70 ± 0.84	13.20 ± 0.56	22.52 ± 0.64	19.01 ± 0.45	23.95 ± 0.51	18.05 ± 0.57
	CBM-12 × DBG-4	24.30 ± 1.54	13.50 ± 1.03	25.37 ± 0.87	18.47 ± 0.50	19.85 ± 0.61	16.33 ± 0.43
Fruit yield per plant (gm)	PVGy-201 × PDM	1,505.0 ± 100.9	1,775.7 ± 97.9	2,746.5 ± 94.1	1,556.2 ± 61.2	2,682.7 ± 74.9	2,261.1 ± 84.1
	CBM-12 × DBG-4	431.7 ± 35.4	1,308.5 ± 105.7	1,427.7 ± 43.8	843.5 ± 35.8	682.9 ± 22.5	1,288.1 ± 38.3

Table 2: Test of significance of A, B, C, and D scales earliness and yield traits in cross PVGy-201 × PDM and CBM-12 × DBG-4 of bitter gourd

Traits	*Cross*	*A*	*B*	*C*	*D*
Node to first female flower	PVGy-201 × PDM	-1.09* ± 0.46	-2.54* ± 0.72	3.39* ± 0.88	-3.51** ± 0.36
	CBM-12 × DBG-4	0.59 ± 0.72	3.19* ± 0.66	4.2* ± 1.447	-0.22 ± 0.62
Days to first female flower	PVGy-201 × PDM	-1.83* ± 0.67	3.55* ± 0.98	-4.468* ± 1.635	3.09** ± 0.75
	CBM-12 × DBG-4	3.96* ± 1.53	9.23** ± 1.91	-0.57 ± 3.278	6.88** ± 1.15
Node to first male flower	PVGy-201 × PDM	-	-	-	-
	CBM-12 × DBG-4	0.90* ± 0.44	0.26 ± 0.41	-6.39** ± 1.08	3.77** ± 0.50
Days to first male flower	PVGy-201 × PDM	-	-		-
	CBM-12 × DBG-4	-3.30* ± 1.44	-10.89** ± 1.57	-32.90** ± 2.93	9.35** ± 7.06
Fruit length (mm)	PVGy-201 × PDM	-1.71 ± 3.33	4.302 ± 2.84	48.02** ± 8.57	-22.71** ± 4.09
	CBM-12 × DBG-4	6.20** ± 1.59	6.15* ± 1.99	17.56* ± 5.49	-2.60 ± 2.68
Fruit weight (gm)	PVGy-201 × PDM	-27.26** ± 3.53	-9.67* ± 2.79	32.56** ± 7.71	-34.75** ± 3.45
	CBM-12 × DBG-4	4.25** ± 1.18	2.98 ± 1.94	18.23** ± 5.04	-5.49* ± 2.46
Fruit diameter (mm)	PVGy-201 × PDM	-1.53 ± 0.95	4.31** ± 0.92	1.54 ± 1.50	0.62 ± .067
	CBM-12 × DBG-4	3.01* ± 0.89	0.71 ± 0.832	-1.61 ± 1.87	2.67* ± 0.82
Number of fruits per plant	PVGy-201 × PDM	-4.67** ± 1.04	-0.37 ± 1.01	2.89 ± 1.73	-3.97** ± 0.84
	CBM-12 ×DBG-4	7.97** ± 1.52	4.20** ± 1.13	10.64** ± 2.29	0.768 ± 0.88
Fruit yield per plant (gm)	PVGy-201 × PDM	-1,113.8** ± 144.0	-0.14 ± 152.9	2,548.6** ± 239.9	-1,831.3** ± 117.6
	CBM-12 × DBG-4	293.66** ± 5.75	-40.06 ± 0.41	821.63** ± 5.76	-284.01** ± 4.7

(*, ** indicated significant effect at p = 5 and 1%)

study will help in better utilization of these germplasm in crop improvement through appropriate breeding methods.

Momordica charantia is the most widely grown species among the seven *Momordica* species found in India (Joseph & Antony 2010). Bitter gourd cultivars in India fall into two botanical groups, *M. charantia var. charantia*, which produces large fusiform fruits and *M. charantia var. muricata* (wild), which bears small and disc-shaped fruit with numerous tubercles on its surface (Chakravarty 1990). These two recognized botanical varieties show striking morphological

Table 3: Estimates of genetic effects for earliness and yield traits in cross PVGy-201 × PDM and CBM-12 × DBG-4 of bitter gourd

Traits	*Cross*	[m]	[d]	[h]	[i]	[j]	[l]	χ2	*Epistasis*
Node to first female flower	PVGy-201 × PDM	5.57** ± 0.11	4.90** ± 0.278	5.42** ± 0.818	7.02** ± 0.725	-1.45 ± 0.784	-10.65** ± 1.423	94.37**	D
	CBM-12 × DBG-4	7.85** ± 0.283	3.90** ± 0.274	-1.72 ± 1.335	0.45 ± 1.256	2.60* ± 0.897	3.32** ± 1.815	24.72*	C
Days to first female flower	PVGy-201 × PDM	35.17** ± 0.325	-6.53** ± 0.382	-10.11** ± 1.588	-6.18** ± 1.509	5.38** ± 1.122	7.90* ± 2.236	38.69**	D
	CBM-12 × DBG-4	71.34** ± 0.484	3.13** ± 0.628	-29.27** ± 2.659	-13.77** ± 2.306	5.26* ± 1.857	26.97** ± 4.129	47.61**	C
Node to first male flower	PVGy-201 × PDM	-	-	-	-	-	-	-	-
	CBM-12 × DBG-4	7.12** ± 0.234	2.13** ± 0.188	-9.70*8 ± 1.043	-7.55** ± 1.008	-0.63 ± 0.541	8.72** ± 1.317	57.01**	C
Days to first male flower	PVGy-201 × PDM	-	-	-	-	-	-	-	-
	CBM-12 × DBG-4	68.67** ± 0.565	-4.66** ± 0.688	-27.95*8 ± 2.807	-18.70** ± 2.647	-7.58* ± 1.943	4.50 ± 4.022	140.0**	-
Fruit length (mm)	PVGy-201 ×PDM	144.30** ± 1.92	-30.25** ± 1.40	63.77** ± 8.40	45.43** ± 8.18	6.01 ± 4.0	-42.84** ± 10.25	36.96**	C
	CBM-12 × DBG-4	99.52** ± 1.268	-55.60** ± 0.873	-6.52* ± 5.465	5.20 ± 5.362	-0.04 ± 2.355	7.16** ± 6.506	25.38**	D
Fruit weight (gm)	PVGy-201 × PDM	120.46** ± 1.63	-19.10** ± 1.140	91.98** ± 7.213	69.51** ± 6.913	17.59** ± 4.299	-106.45** ± 8.96	148.4**	C
	CBM-12 × DBG-4	47.32** ± 1.169	-40.36** ± 0.784	0.52 ± 5.024	10.99* ± 4.934	-1.26 ± 2.076	-3.75 ± 5.942	21.92**	-
Fruit diameter (mm)	PVGy-201 × PDM	40.79** ± 0.249	4.85** ± 0.457	-0.67 ± 1.463	-1.24 ± 1.351	5.85** ± 1.195	4.02 ± 2.363	28.30**	-
	CBM-12 × DBG-4	38.49** ± 0.377	-4.64* ± 0.326	-5.28** ± 1.737	-5.34** ± 1.644	-2.30* ± 1.136	9.072** ± 2.288	18.84**	D
Number of fruits per plant	PVGy-201 × PDM	19.01** ± 0.324	5.90** ± 0.549	13.52** ± 1.794	7.94** ± 1.699	4.30* ± 1.311	12.99** ± 2.799	35.57**	C
	CBM-12 × DBG-4	18.47** ± 0.355	3.51** ± 0.534	2.94 ± 1.992	-1.53 ± 1.776	-3.76* ± 1.695	13.71** ± 3.135	35.11**	C
Fruit yield pe plant (gm)	PVGy-201 × PDM	1,556.2** ± 43	421.5** ± 79.6	4,768.7** ± 249	3,662.6** ± 235	1,113.7** ± 187	4,776.6** ± 398	297.5**	C
	CBM-12 × DBG-4	843.53** ± 25.3	-605.2** ± 31.4	925.6** ± 129.4	568.0** ± 119.3	-333.7* ± 100.8	314.4** ± 190.1	66.82**	C

(*, ** indicated significant effect at p = 5 and 1%)

differences and exhibit remarkable diversity for economic traits. Hence, using these two botanical types in breeding programs is essential for effective bitter gourd improvement.

Yield is a complex polygenic trait, determined by the cumulative effects of several yield-contributing traits such as fruit length, weight, number of female flowers, etc. Earliness is another important trait that is directly correlated with yield. Farmers prefer early varieties due to its suitability to multiple cropping systems and ability to fetch high prices in the early season market (Dey *et al*., 2012). To breed high-yielding early varieties, basic understanding of the genetics of component traits and knowledge of gene action/effects functioning in a particular breeding population is essential (Vinay *et al*., 2023). Keeping above facts in mind, current generation mean analysis study was conducted to estimate the various genetic components of economic traits in bitter gourd using population derived from genetically diverse parental lines. The results of this study will lay the foundation for development of novel early-high yielding varieties and hybrids of bitter gourd to boost the production.

Material and Methods

Present investigation was conducted at experimental field of ICAR-Indian Agricultural Research Institute, New Delhi, India. For genetic analysis, two cross combinations PVGy-1 × Pusa Do Mausami (PDM) and CBM-12 × DBG-4, were used to develop populations (F1, F2, B1 and B). PVGy1, PDM and DBG-4 lines belong to *M. charantia* var *charantia* where as CBM-12 belongs to *M. charantia* var *muricata* group. The F_1 progenies were developed during rainy season (June-October, 2018), F_2 and backcross progenies (B_1 and B_2) were genertaed from F_1 plants during the spring-summer of 2019 under the insect-proof net house. Final trial for evaluation was laid out with six generations (P_1, P_2, F_1, F_2, B_1 and B_2) under natural/open field conditions during August- October of 2019 in a completely randomized block design with three replications. The data was recorded from 10 plants in each parent, 20 plants of F_1, 30 plants of B_1 and B_2 generations and 118 (PVGy-1 × Pusa Do Mausami) and 102 (CBM-12 × DBG-4) plants in F_2 progenies. The phenotypic observations were recorded for four earliness-related traits, namely, node to first female flower (NFFF), days to first female flower (DFFF), node to first male flower (NFMF) and days to first male flower (DFMF) and five yield traits *viz.* namely, fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant and fruit yield/plant (g). Two male flower-related parameters (NFMF, DFMF) were not considered in first cross (PVGy-1 × PDM) since the female parent (PVGy-1) was a gynioecious line. Spacing, nutrition, irrigation, cultural practices and plant protection measures were followed as per recommendations to raise a successful crop in the experimental plots.

Generation mean analysis (GMA) was performed as suggested by Hayman (1958) to estimate genetic

Table 4: Inheritance pattern of fruit epicarp color, tubercle nature and ridgeness in bitter gourd in PVGy-201 × PDM and CBM-12 × DBG-4 of bitter gourd

Fruit epicarp colour in cross - CBM-12 × DBG-4						
Population	*Total*	*Observed*		*Expected ratio*	*χ2 value*	*p-value*
	Green fruits	White fruits				
P1(CDM-12)	10	10	-	-		
P2 (DBG-4)	10	-	10	-		
F1(CBM-12 × DBG-4)	20	20	-	-		
F2	102	80	22	3:1	0.64	0.43
B1(F1 × CBM-12)	30	30	-	-		
B2(F1 × DBG-4)	30	17	13	1:1	0.53	0.47
Fruit tubercle nature in cross - CBM-12 × DBG-4						
Population	*Total*	*Observed*		*Expected ratio*	*χ2 value*	*p-value*
	Conspicuous	Non-conspicuous				
P1(CDM-12)	10	10	-	-		
P2 (DBG-4)	10	-	10	-		
F1(CBM-12 × DBG-4)	20	20	-	-		
F2	102	74	28	3:1	0.33	0.57
B1(F1 × CBM-12)	30	30	-	-		
B2(F1 × DBG-4)	30	16	14	1:1	0.13	0.72
Fruit ridgeness in cross - PVGy-201 × Pusa Do Mausami (PDM)						
Population	*Total*	*Observed*		*Expected ratio*	*χ2 value*	*p-value*
	Dis-continuous	Continuous				
P1(PVGy-201)	10	10	-	-		
P2 (PDM)	10	-	10	-		
F1(PVGy-1 × PDM)	20	20	-	-		
F2	118	84	34	3:1	0.92	0.34
B1(F1 × PVGy- 201)	30	17	13	1:1	0.53	0.47
B2(F1 × PDM)	30	30	-	-		

components. At first, using means of different generations, ABCD scales (Hayman and Mather, 1955) were tested to check for the presence of non-allelic interactions (epistasis) and then the data was subjected to joint scaling test which integrates multiple scaling tests to examine the competence of simple additive–dominance model or to detect epistasis using χ2 test. The six-parameter or di-genic interaction model (Hayman, 1958) was used to estimate the gene effects whenever the χ2 and ABCD scaling test is inadequate. 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]. Student 't' test was used to declare the significance of the estimated scales (ABCD) and gene effects (m, d, h, i, j, l). The type of epistasis was determined as per Kearsey and Pooni, 1996.

To study the genetic inheritance of fruit traits *viz*. fruit epicarp color, ridgeness, tubercle nature, chi-square (χ2) test suggested by Panse and Sukhatme (1985) was done. These traits are expected as controlled by single gene.

Results and Discussion

The mean values (Table 1) of F_1 for fruit length, fruit weight and fruit diameter (in CBM-12 × DBG-4) were greater than the mid-parent values (average of the two parents) which indicate average heterosis, whereas F_1 mean values of number of fruits per plant and yield per plant and fruit diameter (in PVGy-201 × PDM) was higher than better parent values which indicated over dominance/heterobeltotis. Similarly, for earliness-related traits, in both cross combinations mean values of F_1 implied negative average heterosis which is desirable. These results suggest the scope for improvement yield and earliness through heterosis breeding. There was decline in mean values of yield traits of F_2 population than corresponding F_1 in all yield traits. This apparently indicated influence of inbreeding depression. These findings are in agreement with the results obtained by Dey *et al*. (2012) in bitter gourd. The mean effect (m) was significant for all studied traits among three crosses, indicated that the traits were quantitatively inherited.

Significance of one or more scales (A, B, C, D) as shown in Table 2 and joint scaling χ2 (Table 3) test for all the traits under study in both crosses implies presence of digenic non-allelic interaction (epistasis). Hence, the simple additive-dominance model cannot satisfactorily explain the genetics of these traits. Therefore, according to Jinks and Jones (1958), the six-parameter model was employed to estimate six components of genetic variation, *viz*. m, d, h, i, j and l. The presence of non-allelic gene interactions involved in genetic control of quantitative yield traits in bitter gourd was previously reported by Kumari *et al*. (2015).

Higher magnitude and highly significant values of dominance effect (h) in desired direction was obtained for earliness-related traits like days to first female flower (both cross), node to first male flower (CBM12 × DBG-4) and day to first male flower (CBM12 × DBG-4). Additive × additive (i) type of non-allelic interaction was highly significant and negative for these traits. Similarly, higher magnitude significant-positive values of 'h' was observed for major yield parameters, number of fruits per plant and fruit yield per plant in both crosses, which indicates predominance of dominant gene effect. To add to this, of the three non-allelic interactions dominance × dominance (l) gene interaction was found to be positive and significant for these yield related traits. Hence, while breeding for improvement of earliness and yield traits selection should be delayed until heterozygosity is reduced in population. According to result of our study, hybrid development through heterosis breeding would be the most appropriate breeding method to evolve early and high-yielding hybrids using these cross combinations. For fruit length and fruit weight traits in cross PVGy-201 × PDM, additive effect (d) was positively significant with higher magnitude than dominance effect (h). In addition to this, additive × additive (i) type of non-allelic interactions was found to be highly significant. This clearly implies the suitability of simple selection procedure for the improvement of these traits. Complementary epistasis was observed for most earliness and yield traits under study, which implies that parents selected for crossing were diverse for that particular trait and desirable alleles for the traits are distributed among the parents. Hence, it is possible to realize greater genetic gain in a breeding programme. Our results are supported by the findings of Dey *et al*. (2012) in Bitter gourd.

The inheritance pattern of fruit epicarp color and tubercle nature was studied using cross of CBM-12 (green fruits with conspicuous tubercle) × DBGS-4 (white fruit with non-conspicuous tubercle). The analyzed result presented in Table 4 implies monogenic nature of both traits. Green fruit epicarp color is dominant over white, and conspicuous tubercles nature was dominant over non-conspicuous. Similar monogenic dominant nature of inheritance of fruit color was earlier reported by Hu *et al*. (2002) in bitter gourd. Our result of genetics of tubercle nature is supported by earlier studies (Rao *et al*., 2022). Phenotypic data obtained from cross PVGy-201 (dis-continuous) × PDM (continuous) was utilized to study the genetics of fruit ridgeness. The segregation pattern of fruit ridgeness in filial and backcross generations supported the single dominant gene hypothesis of genetic control. Discontinuous ridgeness was dominant over continuous ridgeness. Our study's result is supported by Rao *et al*.'s findings, 2022.

Conclusion

The genetic analysis for estimation of gene effects controlling economic traits in bitter gourd was done using diverse parental lines. Both additive and non-additive gene interactions control the economically important earliness and yield traits in bitter gourd. Therefore, recombination breeding with selection in later generations would be the most suitable way to improve these quantitative traits. Simple selection can give desired results when additive gene action is predominant. At the same time, dominant gene effects should be concentrated for better results. The traits governed by additive gene effect can be effectively improved through pedigree method. On the other hand, traits regulated by non-additive gene interaction (dominance effect) could be improved by heterosis breeding and through recurrent selection for specific combining ability. The traits with high magnitude of dominance and additives gene effects can be improved by pedigree or bulk methods or reciprocal recurrent selection methods. From the present study and most of the earlier reports, it is now clear that the fruit quality traits (color, tubercles and ridgeness) are qualitatively inherited *i.e.* by single dominant gene. Simple genetics of these fruit traits will permit the bitter gourd breeder to incorporate these traits in hybrids. The predominance of complementary epistasis for most economic traits studied implies the genetic divergence between the parents used and the possibility to realize greater genetic gain in breeding programme using these genetic resources. The study also implies the importance of populations derived from diverse genetic resources for the effective genetic analysis of phenotypic expressions in bitter gourd.

References

Behera TK (2004) Heterosis in bitter gourd. In: Singh PK, Dasgupta SK and Tripathi SK (ed) The Haworth Press. New York, USA, pp 217-221.

Behera TK, Behera S, Bharathi LK, John KJ, Simon PW and Staub JE (2010) Bitter gourd: botany, horticulture, Breeding. *Hortic. Rev.* **37**: 101.

Behera TK, Staub JE, Behera S and Simon PW (2008) Bitter gourd and human health. *Med. Aromat. Plant Sci. Biotechnol.* **1(2)**: 224-226.

Behera TK. Dey SS, and Sirohi PS (2006) DBGy-201and DBGy-202: two gynoecious lines in bitter gourd (*Momordica charantia* L.) isolated from indigenous source. *Indian. J. Genet. Plant.*

Breed. **66**: 61–62.

Chakravarty HL (1990) Cucurbits of India and their role in the development of vegetable crops In: Bates DM, Robinson RW and Jeffrey C (ed) Biology and Utilization Of Cucurbitaceae Cornell University Press, Ithaca, New York, pp 325-34.

Dey SS, Behera TK, Munshi AD, Rakshit S and Bhatia R (2012) Utility of gynoecious sex form in heterosis breeding of bitter gourd and genetics of associated vegetative and flowering traits. *Indian J. Hortic*. **69(4)**: 523–29.

Hayman BI (1958) The separation of epistatic from additive and dominance variation in generation means. *Heredity,* **12**: 371–90.

Hayman BI (1960) Maximum likelihood estimation of genetic components of variation. *Biometrics,* **16(3)**: 369-381.

Hayman BI, Mather K (1955) The description of genetics of interaction in continuous variation. *Biometrics*, **51**: 69–82.

Heiser CB (2016) The gourd book. University of Oklahoma Press, 248p.

Hu KL, Fu QM and Wang GP (2002) Study on the heredity of fruit color of *Momordica charantia*. *China Veg*. 11– 12.

Jinks JL, Jones RM (1958) Estimation of the components of heterosis. *Genetics,* **43**: 223-34.

Joseph JK and Antony VT (2010) A taxonomic revision of the genus *Momordica* L. (Cucurbitaceae) in India. *Indian J, Plant Genet. Resour*. **23**: 172–184.

Kearse MJ and Pooni HS (1996) *The genetic analysis of quantitative traits*, Chapman and Hall, London.

Kumari M, Behera TK, Munshi AD and Talukadar A (2015) Inheritance of fruit traits and generation mean analysis for estimation of horticultural traits in bitter gourd. *Indian. J. Hortic*. **72(1)**: 43–48.

ND, Vinay., Matsumura, H., Munshi, A.D., Ellur, R.K., Chinnusamy, V., Singh, A., Iquebal, M.A., Jaiswal, S., Jat, G.S., Panigrahi, I. and Gaikwad, A.B., (2023). "Molecular mapping of genomic regions and identification of possible candidate genes associated with gynoecious sex expression in bitter gourd. Frontiers in Plant Science, **14**.

Panse VG and Sukhatme PV (1985) Statistical methods for Agricultural Workers. ICAR, New Delhi, India, 359 p.

Rao PG, Behera TK, Munshi AD and Jat GS (2022) Genetic inheritance of fruit traits and seed coat colour in bitter gourd (*Momordica charantia*). *Indian J. Agric. Sci.* **92(3)**: 357–361.

Rathod V, Behera TK, Gaikwad AB and Hussain Z (2019) Genetic analysis and tagging of gene controlling fruit tubercles and fruit ridgeness pattern in bitter gourd using SSR markers. *Indian J. Genet. Plant. Breed.* **79(04)**: 749-755.