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Generation mean analysis of important yield traits in bitter gourd (*Momordica charantia*)

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ABSTRACT

Generation mean analysis study in bitter gourd was undertaken using six basic generations viz. P_1, P_2, F_1, F_2, B_1 and B_2 population were developed from gynoecious (IIHRBTGy- 491) × monoecious (IIHR Sel -19 -1 and IIHR Sel-78-4) crosses. The gynoecious parent was superior for node for first female flowering, number of fruits and yield/plant whereas the monoecious parents were superior for fruit length, fruit diameter and fruit weight. F_1 showed superior performance over mid parent for number of fruits, fruit length, fruit weight and yield per plant. F_2 plants were significantly diverse. B_1 and B_2 population exhibited mean value closer to their recurrent parents. Significance of one or more scaling tests, i.e. A, B, C and D in most of the traits revealed the presence of epistasis in both the crosses except for node bearing 1st male flower. Days to 1st female flower opening, node bearing 1st female flower, fruit diameter and yield showed presence of duplicate epistasis whereas days to 1st male flower opening, number of fruits per plant, fruit length and fruit weight showed complimentary epistasis in IIHRBTGy - 491 × IIHR Sel -19 -1 cross. Node bearing 1st female flower, fruit length, fruit diameter and yield showed presence of duplicate epistasis whereas days to 1st female flower opening, days to 1st male flower opening, number of fruits and fruit weight showed complimentary epistasis in IIHRBTGy - 491× IIHR Sel-78-4 cross. Additive gene action may be predominant for inheritance of node bearing 1st male flower.

Key words: Bitter gourd, epistatic interactions. gene action and scaling test.

INTRODUCTION

Bitter gourd is an economically important vegetable crop and considered as one of the most nutritious gourds, grown for its fruit and leaves. It is a good source of phytonutrients like carbohydrates, minerals like iron, calcium, phosphorus and vitamin B, vitamin C, and also contains vitamin A (Behera *et al*., 2010). The primary centre of diversity is India, and China is considered as the secondary centre of diversity. It is grown widely throughout India. The primary breeding goal for bitter gourd is to increase fruit yield and quality. This gynoecious sex form has been commercially exploited worldwide in cucumber for increased number of fruits, earliness, uniformity and mechanical harvesting. It is mostly useful for hybrid development as it avoids manual emasculation and pollination. So simply by isolating from other genotypes and with a desirable parent we can go for hybrid development. Yield is a complicated trait influenced by polygenes with small but cumulative effects. Therefore, detailed understanding of the genetics and inheritance that underpins yield and its component traits is required in order to achieve the actual yield potential by adopting appropriate breeding and selection strategies. Generation mean analysis has proven to be a useful tool for estimating various genetic parameters. Hayman (1960) proposed the concept of generation mean analysis for estimating various genetic components. This method gives data on several genetic parameters as well as epistatic interactions. It is beneficial to have a precise understanding of the nature and magnitude of gene action of various characters to maximise the use of genetic potential by choosing of effective breeding methods.

MATERIALS AND METHODS

The sib-mated seeds of gynoecious bitter gourd germplasm, IIHRBTGy–491 and two monoecious lines IIHR Sel -19 -1 and IIHR Sel-78-4 used as parents to develop, F_1, F_2 and back cross generations during 2018–2021 at Vegetable Research Block VIII of Division of Vegetable Crops, ICAR–Indian Institute of Horticultural Research, Bengaluru. The IIHRBTGy–491gynoecious plant was maintained by sib matting and through the pollens from silver nitrate 250 ppm induced hermaphrodite flowers in the gynoecious plant. The data was recorded on 10 competitive plants in parents and F_1, 100 plants in F_2 and 20 plants in backcrosses laid out in a randomized complete block design in three replications. The observations were recorded for 9 economical characters viz., days to first female flower opening,

Table 1. Generation means for different characters

Character	Cross	P_1	P_2	MP	F_1	F_2	B_1	B_2
Days to 1st female flower opening	1	29.10 ± 0.73	37.23 ± 0.93	33.16	37.96 ± 0.84	35.25 ± 0.43	33.66 ± 1.62	38.00 ± 0.90
	2	28.93 ± 0.67	38.13 ± 0.85	33.53	39.10 ± 0.71	34.47 ± 0.43	30.10 ± 0.67	36.66 ± 1.02
Days to 1st male flower opening	1	0.00 ± 0.00	29.23 ± 0.68	14.61	27.53 ± 0.75	24.25 ± 1.49	17.63 ± 5.71	31.06 ± 0.60
	2	0.00 ± 0.00	28.93 ± 0.83	14.46	25.20 ± 0.48	25.07 ± 1.46	15.56 ± 5.03	33.16 ± 0.75
Node bearing 1st male flower	1	0.00 ± 0.00	5.80 ± 0.47	2.90	4.33 ± 0.26	3.77 ± 0.24	2.50 ± 0.82	5.26 ± 0.32
	2	0.00 ± 0.00	6.96 ± 0.30	3.48	5.33 ± 0.24	4.25 ± 0.26	2.60 ± 0.85	5.83 ± 0.26
Node bearing 1st female flower	1	4.26 ± 0.31	12.40 ± 0.74	8.33	9.83 ± 0.72	9.40 ± 0.37	8.46 ± 1.09	13.00 ± 0.53
	2	4.26 ± 0.31	13.26 ± 0.86	8.76	11.86 ± 0.44	9.95 ± 0.38	7.73 ± 1.20	13.33 ± 0.50
Number of fruits per plant	1	42.10 ± 1.53	26.56 ± 1.03	34.33	37.73 ± 1.19	37.57 ± 0.77	41.96 ± 3.11	29.56 ± 0.85
	2	42.10 ± 1.53	24.49 ± 0.83	33.29	35.43 ± 1.09	38.01 ± 0.78	46.26 ± 1.83	30.56 ± 0.94
Fruit length (cm)	1	12.23 ± 0.33	22.91 ± 0.28	17.57	17.70 ± 0.26	14.42 ± 0.47	13.53 ± 0.21	21.15 ± 0.37
	2	12.23 ± 0.33	17.89 ± 0.30	15.06	16.57 ± 0.47	12.14 ± 0.46	13.13 ± 0.38	18.52 ± 0.30
Fruit diameter (cm)	1	4.18 ± 0.11	4.57 ± 0.15	4.37	4.31 ± 0.15	4.26 ± 0.04	4.09 ± 0.14	4.63 ± 0.15
	2	4.18 ± 0.11	5.02 ± 0.08	4.61	4.39 ± 0.12	4.39 ± 0.04	4.12 ± 0.11	4.72 ± 0.13
Fruit weight (g)	1	79.56 ± 1.38	106.00 ± 2.04	92.78	96.63 ± 3.55	98.19 ± 3.39	77.93 ± 1.82	103.46 ± 1.27
	2	79.56 ± 1.38	117.34 ± 3.18	98.36	109.43 ± 3.81	103.21 ± 3.41	83.69 ± 1.24	120.63 ± 1.42
Yield/ plant (kg)	1	3.54 ± 0.12	2.72 ± 0.13	3.13	3.26 ± 0.21	3.10 ± 0.16	3.28 ± 0.26	2.18 ± 0.11
	2	3.54 ± 0.12	2.87 ± 0.18	3.18	3.22 ± 0.21	3.06 ± 0.16	3.31 ± 0.35	2.37 ± 0.29

1: IIHRBTGy - 491× IIHR Sel -19 -1; 2: IIHRBTGy - 491× IIHR Sel -78-4

days to 1st male flower opening, node bearing 1st male flower, node bearing 1st female flower, number of fruits per plant, fruit length (cm), fruit diameter (cm), single Fruit weight (g) and fruit yield/ plant (g). Data from three replications was pooled to calculate mean values for all of the attributes investigated for the parents (P_1 and P_2), F_1's ($P_1 \times P_2$), F_2's (F_1's selfed) and their first-generation backcrosses (B_1's = $F_1 \times P_1$ and B_2's = $F_1 \times P_2$). The ABCD scaling tests of Mather and Jinks (1982) were employed to detect the presence of non-allelic interactions before calculating the different parameters. In addition to scaling test data was further subjected to joint scaling (Deb and Khaleque 2009). The parameters for the various gene effects employed in this investigation are the same as those used by Hayman (1960) namely, mean (m), additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The OPSTAT software was used to perform the generation mean analysis.

RESULT AND DISCUSSION

The information regarding gene action, interaction and inheritance study is the key factor for designing appropriate breeding strategy for improvement of any crop. The gynoecious parent IIHRBTGy – 491 was superior for node for first female flowering, number of fruits and yield/plant whereas the monoecious parents were superior for fruit length, fruit diameter and fruit weight. The mean performance of F_1 surpassed the mid parent for number of fruits, fruit length, fruit weight and yield per plant (Table - 1) in both the crosses (IIHRBTGy - 491 × IIHR Sel -19 - 1 and IIHRBTGy - 491× IIHR Sel-78-4). The superior performance of F_1 over mid parent indicated that these traits can be exploited through heterosis breeding. These findings are consistent with the findings of Dey *et al*. (2012) and Mishra *et al* (2015). The reduction in mean performance of F_2 population than F_1 for fruit length and yield in both crosses was observed, implying influence of inbreeding depression. Rathod *et al*. (2021) also obtained similar results in bitter gourd.

Days to 1st female flower opening

In IIHRBTGy - 491 × IIHR Sel -19 -1cross, C scale was significant (4.25) (Table - 2) and dominance component (h) was also significant (7.12) (Table - 3). The opposite sign of h (7.12) and l (-3.38) indicates presence of duplicate epistasis. Mishra *et al* (2015) reported similar gene interaction for the trait days to first flowering in the cross of DBGy 201 × Pusa Do Mausami indicating selection at later generation. However, in IIHRBTGy - 491× IIHR Sel-78-4 all four scales were significant which indicate the inadequacy of simple additive-dominance model to estimate the gene effects. The similar sign of h (2.20) and l (16.09) indicates presence of complementary epistasis. Kumari *et al*. (2015) reported additive gene effect and Rani *et al*. (2014) reported presence of dominance and epistasis for the trait.

Days to 1st male flower opening

In IIHRBTGy - 491 × IIHR Sel-19-1 cross, B (2.63) and C (3.27) scale and dominance component (21.29) were significant. The similar sign of h (21.29) and l (2.52) indicates presence of complementary epistasis. Similarly, in IIHRBTGy - 491× IIHR Sel-78-4 cross, A (4.06) and B (-2.20) scales were significant which indicate the inadequacy of simple additive-dominance model to estimate the gene effects. The similar sign of h (17.89) and l (4.70) indicate presence of complementary epistasis. Kumari *et al*. (2015) and Thangamani (2016) reported additive gene effect for days to 1st male flowering.

Node bearing 1st male flower

In both the crosses all the scaling tests, namely, A, B, C and D were insignificant for node bearing 1st male flower. It was determined that the additive–dominance model is sufficient to explain the effects. The sufficiency of the simple additive–dominance model implies that nonallelic interaction is absent and generation means are solely dependent on the additive–dominance effect of the gene. Additive gene action may be predominant for inheritance and selection should be delayed to later generations for this trait. Similar result reported by Thangamani (2016).

Node bearing 1st female flower

In IIHRBTGy - 491 × IIHR Sel -19 -1 cross, C (4.72) and D (-2.66) scale and dominance (9.82) component were significant. Non-additive component has a significant role in the inheritance of this trait. The opposite sign of h (9.82) and l (-5.92) indicates presence of duplicate epistasis. Similarly, in IIHRBTGy - 491× IIHR Sel-78-4 cross, C (3.44) and D (-2.15) scales were significant. The opposite sign of h (8.40) and l (-5.17) indicates presence of duplicate

Table 2. Scaling test

Character	Cross	A	B	C	D
Days to 1st female flower opening	1	-0.26 ± 1.98	-0.80 ± 1.27	4.25 ± 1.54**	-1.16 ± 1.18
	2	7.83 ± 0.96**	3.90 ± 1.34**	7.37 ± 1.44**	2.18 ± 0.86**
Days to 1st male flower opening	1	0.26 ± 6.61	2.63 ± 0.91**	3.27 ± 3.57**	-0.18 ± 3.73
	2	4.06 ± 5.81**	-2.20 ± 1.03**	-0.97 ± 3.47	1.42 ± 3.39
Node bearing 1st male flower	1	-0.66 ± 0.96	-0.40 ± 0.48	-0.61 ± 0.70	-0.22 ± 0.58
	2	0.13 ± 0.99	0.63 ± 0.37	0.63 ± 0.69	0.06 ± 0.59
Node bearing 1st female flower	1	0.16 ± 1.34	-0.76 ± 0.86	4.72 ± 1.29**	-2.66 ± 0.82*
	2	-0.33 ± 1.42	-0.53 ± 0.81	3.44 ± 1.14**	-2.15 ± 0.87*
Number of fruits per plant	1	8.90 ± 3.76**	8.16 ± 1.34**	13.82 ± 2.50**	1.62 ± 2.06
	2	1.00 ± 2.38	11.76 ± 1.35**	14.36 ± 2.42**	-0.80 ± 1.49
Fruit length (cm)	1	2.75 ± 0.34*	6.19 ± 0.48**	12.63 ± 1.17**	-2.84 ± 0.60*
	2	2.54 ± 0.55*	1.52 ± 0.47	10.79 ± 1.22**	-3.36 ± 0.60**
Fruit diameter (cm)	1	-0.02 ± 0.20	-2.10 ± 0.21*	-3.15 ± 0.23**	0.01 ± 0.13
	2	0.04 ± 0.16	2.49 ± 0.17*	4.66 ± 0.19**	-0.06 ± 0.11
Fruit weight (g)	1	47.32 ± 3.04**	-11.63 ± 2.88**	24.03 ± 8.95**	5.82 ± 4.13**
	2	43.12 ± 3.15**	-5.00 ± 3.30**	30.41± 9.25**	3.85 ± 4.16**
Yield/ plant (kg)	1	2.61 ± 0.34*	0.63 ± 0.20	2.79 ± 0.46*	0.73 ± 0.25
	2	2.44 ± 0.34*	0.80 ± 0.21	3.93 ± 0.46**	0.65 ± 0.25

*, ** significant at 5 and 1% probability respectively

1: IIHRBTGy - 491 × IIHR Sel - 19 - 1; 2: IIHRBTGy - 491 × IIHR Sel - 78 - 4

epistasis. Similar result obtained by Mishra *et al*. (2015) and additive gene action for the trait reported by Thangamani (2016).

Number of fruits per plant

In both the crosses, B and C scales were significant and dominance component, dominance × dominance components were significantly higher compared to additive component which indicate the inadequacy of simple additive-dominance model to estimate the gene effects. The similar sign of h and l indicates presence of complementary epistasis in both the cross. Similar result reported by Mishra *et al*. (2015) in DBGy 201 × Pusa Do Mausami cross and complementary epistasis observed in DBGy 201 × S-2 cross. Shukla *et al*. (2014) reported insignificant χ^2 value for number of fruits/plant, internodal length, seeds/fruit and yield/ plant in Gy333 × DRAR-1 cross indicating the absence of non-allelic interaction.

Fruit length

In IIHRBTGy - 491 × IIHR Sel -19 -1 cross, all the scaling tests, namely, A, B, C and D were significant and dominance component was higher compared to additive component. The similar sign of h (3.71) and l (5.26) indicates presence of complementary epistasis. However, in IIHRBTGy - 491× IIHR Sel-78-4cross, A, C and D scales were significant and dominance, additive × additive components were in positive direction indicating their significant role in inheritance

Table 3. Estimates of components of generation mean for different yield related character in bitter gourd

Character	Cross	m	d	h	i	j	l	Epistasis
Days to 1st female flower opening	1	35.25 ± 0.24	-4.33 ± 1.07**	7.12 ± 2.44**	2.32 ± 2.36*	-0.53 ± 2.25	-3.38 ± 4.56**	D D
	2	34.47 ± 0.25	-6.56 ± 0.70**	2.20 ± 1.81*	-4.36 ± 1.73**	-3.93 ± 1.55**	16.09 ± 3.18**	C C
Days to 1st male flower opening	1	24.25 ± 0.87	-13.43 ± 3.31**	21.29 ± 7.49**	0.37 ± 7.43	2.36 ± 6.64*	2.52 ± 13.74*	C C
	2	25.07 ± 0.84	-17.60 ± 2.93**	17.89 ± 6.79**	-2.84 ± 6.78*	-6.26 ± 5.89**	4.70 ± 12.24**	C C
Node bearing 1st male flower	1	3.77 ± 0.14	2.77 ± 0.50*	1.89 ± 1.18	0.45 ± 1.16	0.27 ± 1.05	-1.52 ± 1.09	- -
	2	4.25 ± 0.15	3.23 ± 0.51*	1.72 ± 1.20	-0.13 ± 1.19	0.50 ± 2.17	0.90 ± 2.15	- -
Node bearing 1st female flower	1	9.40 ± 0.21	-4.53 ± 0.70**	9.82 ± 1.72**	5.32 ± 1.65**	-0.93 ± 1.48	-5.92 ± 3.10**	D D
	2	9.95 ± 0.21	-4.60 ± 0.75**	8.40 ± 1.78**	4.30 ± 1.74**	-0.20 ± 1.59	-5.17 ± 3.22**	D D
Number of fruits per plant	1	37.57 ± 0.44	3.82 ± 1.86**	10.40 ± 4.22**	-3.24 ± 4.13**	-0.73 ± 3.87	20.30 ± 7.85**	C C
	2	38.01 ± 0.45	4.25 ± 1.19**	15.70 ± 3.10**	1.60 ± 2.99	10.76 ± 2.59**	11.16 ± 5.35**	C C
Fruit length (cm)	1	14.42 ± 0.27	-3.62 ± 0.24**	3.71 ± 1.22**	3.68 ± 1.21**	3.44 ± 0.55**	5.26 ± 1.53**	C C
	2	14.14 ± 0.26	-5.39 ± 0.28**	6.19 ± 1.24**	6.73 ± 1.20**	-1.02 ± 0.62	-2.66 ± 1.66*	D D
Fruit diameter (cm)	1	4.26 ± 0.02	2.05 ± 0.12*	2.26 ± 0.28*	-1.02 ± 0.26	-2.07 ± 0.27*	-5.10 ± 0.54**	D D
	2	4.35± 0.71	-1.20 ± 0.10	-3.15 ± 0.24**	2.13 ± 0.23*	4.44 ± 0.21**	11.40 ± 0.44**	D D
Fruit weight (g)	1	108.19 ± 1.95	-48.21 ± 1.33**	7.19 ± 8.55**	-11.65 ± 8.27**	-58.96 ± 3.03**	47.34 ± 10.43**	C C
	2	107.21 ± 1.97	-54.70 ± 1.33**	1.52 ± 8.67	-7.71 ± 8.32**	-48.12 ± 3.34**	45.84 ± 10.68**	C C
Yield/ plant (kg)	1	4.10 ± 0.09	-0.90 ± 0.17	-4.48 ± 0.52**	-1.46 ± 0.50	-1.97 ± 0.35	4.71 ± 0.82**	D D
	2	4.06 ± 0.09	-0.90 ± 0.17	-3.67 ± 0.52**	-1.31 ± 0.50	-1.63 ± 0.36	4.56 ± 0.82**	D D

*, ** significant at 5 and 1% probability respectively
1: IIHRBTGy - 491× IIHR Sel -19 -1; 2: IIHRBTGy - 491× IIHR Sel -78-4
C: Complementary epistasis, D: Duplicate epistasis

of the trait. Presence of duplicate epistasis is noticed. Similar result obtained by Mishra *et al*. 2015 for fruit length in both DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami) whereas incomplete dominance effect for fruit length reported by Kumari *et al*. (2015).

Fruit diameter

In both the crosses, B and C scale were significant. In IIHRBTGy - 491× IIHR Sel -19 -1 cross additive (2.05) and dominance (2.26) components were significant while in IIHRBTGy - 491× IIHR Sel -78-

4 cross dominance × dominance (11.40) component was significant. The opposite sign of h and l indicates presence of duplicate epistasis in both the crosses. In such circumstances, available populations must be carried to future generations in order to arrive at the best-fit model (Mather and Jinks 1982). The opposite signs of h and l neutralize each other, resulting in reduced heterosis for the trait. Similar result obtained by Mishra *et al*. (2015).

Fruit weight

In both the crosses, all the scaling tests, namely, A, B, C, D were significant and dominance × dominance (l) component was significantly higher. Non-additive component has significant role in the inheritance of this trait. The similar sign of h and l indicates presence of complementary epistasis. In contrary to the result, duplicate epistasis with predominance of additive × dominance gene action reported by Mishra *et al*. (2015) in both the crosses *i.e* DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami and Thangamani (2016) reported presence of additive gene action for fruit weight.

Yield/plant

In both the crosses, A and C scales were significant and dominance × dominance (l) component was higher and in positive direction. Non-additive component has a significant role in the inheritance for yield per plant. The opposite sign of h and l indicates presence of duplicate epistasis. Similar result obtained by Mishra *et al*. (2015) in both the crosses namely DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami and Shukla *et al*. (2014) in Cross Gy323 × DRAR-1. The opposite signs neutralize each other. It also shows reduced variability in segregating generations, which prevents the selection and makes them challenging to use in breeding programmes (Parihar *et al*. 2016).

CONCLUSION

The mean performance of F_1 surpassed the mid parent for number of fruits, fruit length, fruit weight and yield per plant in both the crosses indicating that these traits can be exploited through heterosis breeding. The reduction in mean performance of F_2 population than F_1 for fruit length and yield in both crosses was observed which apparently indicated influence of inbreeding depression. Significance of one or more scaling tests, i.e. A, B, C and D in most of the traits revealed the presence of epistasis in both the crosses except for node bearing 1st male flower where additive gene action was predominant. Characters showing complimentary epistasis have the possibility of considerable amount of heterosis for the trait and characters showing duplicate epistasis have the possibilities of obtaining transgressive segregants in later generations in the particular cross.

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