DOI : 10.5958/0974-0112.2015.00042.0

Indian J. Hort. 72(2), June 2015: 218-222

Inheritance of gynoecism and genetics of yield and yield contributing traits through generation mean analysis in bitter gourd

Smaranika Mishra, T.K. Behera[*], A.D. Munshi, C. Bharadwaj[**] and A.R. Rao[***]
Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi 110012

ABSTRACT

The phenotypic ratio of 3:1 (monoecious vs gynoecious) in bitter gourd confirmed the monogenic recessive inheritance of gynoecism trait. Further investigation on gene action in the cross DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami by generation mean analysis revealed duplicate epistasis for most of the traits including node at which first female flower appear, days to first flowering, days to first harvestable maturity, fruit length, fruit diameter, fruit weight and yield suggesting the possibilities of obtaining transgressive segregants in later generations. Moreover, significant additive and non-additive gene effect for traits like node at which first female flower appear, days to first flowering, days to first harvestable maturity and fruit diameter indicates use of reciprocal recurrent selection or bi-parental mating for improvement of these traits. Non-additive gene action was significant for number of fruits per plant, fruit length, weight and yield inferring heterosis breeding as the best option for obtaining higher gain in these characters.

Key words: *Momordica charantia*, gynoecism, inheritance, generation mean analysis.

INTRODUCTION

Exploitation of hybrid vigour (heterosis) is always the prime goal of a breeder for achieving high yield, uniformity and earliness. Breeders search for effective genetic mechanisms like self-incompatibility, male sterility, gynoecism etc. that facilitate the easy and economic way for hybrid seed production. In bitter gourd, the recent sex form, *i.e.* gynoecy can serve as a best option in this regard. The physiology and genetics of gynoecious sex expression in cucumber has been extensively studied (Staub *et al*., 10) and it has been commercially exploited in heterosis breeding. In bitter gourd, exploitation of this genetic mechanism is a recent approach for hybrid seed production and now more emphasis is given on introgression of this gene into commercial inbreds. Previous research reports published so far with respect to inheritance of gynoecism in bitter gourd have distinct findings: (i) gynoecism was monogenic recessive (Behera *et al*., 1; Ram *et al*., 8), and (ii) gynoecism was partially dominant (Iwamoto and Ishida, 4). The inheritance study was attempted here to confirm earlier reports by utilizing new genetic background. Hybrids produced by using this gynoecious line were reported to be better for their earliness in yield and high yielding ability.

Prevalence of additive component was more than that of the dominance effects for days to first female flower anthesis and days to first fruit set in bitter gourd was reported by Singh and Ram (9). Choudhury and Sikdar (2), however, reported that fruit length, fruit flesh weight and total fruit number per plant shows dominant effects of genes. Therefore, the present study was carried out to obtain information about gene action on yield and its components in two crosses involving monoecious and gynoecious line of bitter gourd.

MATERIALS AND METHODS

Two crosses namely DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami were selected from Line × Tester analysis based on their better yield performance. The parents involved in these crosses were different in their sex form, DBGy 201 is a completely gynoecious line and S-2 and Pusa Do Mausami are monoecious. The experiment was conducted in the experimental field of Division of Vegetable Science, IARI, New Delhi during growing season of bitter gourd in India (spring-north summer season).

The seeds of the parents were planted and crossing of parent was done in 2010 and 2011. F_1 is selfed to produce seeds of F_2 and back crossed to parents, *i.e.* P_1 (DBGy 201) and P_2 (Pusa Do Mausami) to get B_1 and B_2, respectively. The plants of parent P_1 (DBGy 201) was converted in to hermaphrodite by spaying silver thio-sulphate (6 mM) twice before using as male parent. Six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of both crosses were evaluated separately in randomized complete block design (RCBD) with three replications. All plants were observed for the presence of pistillate and

---

[*] Corresponding author's E-mail: tusar@rediffmail.com
[**] Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110012
[***] ICAR-Indian Agricultural Statistics Research Institute, New Delhi 110012

staminate flowers throughout the growing season. Based on flowering habit, individual F_2 plants were classified as gynoecious or monoecious. The data from the F_2 populations were analyzed using the χ^2 test to determine the inheritance of gynoecism as suggested by Panse and Sukhatme (5).

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 traits like node bearing first female flower, days to first female flower opening, days to first harvestable maturity, number of fruits per plant, fruit length and breadth, single fruit weight and fruit yield per plant. Generation mean analysis, six parameter model for estimation of genetic components was adopted and prior to that adequacy of the additive-dominance model was estimated by using the ABCD scaling test. The significance of any one of the scales was taken to indicate the presence of non-allelic interactions. The estimates of mean gene effects, *i.e.* mean (m), additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) were obtained for yield and its attributes. Statistical analysis was carried out using Generation Mean Analysis (OPSTAT, CCS HAU, Hisar, Haryana).

RESULTS AND DISCUSSION

For inheritance study, seeds of the parental lines, DBGy 201, Pusa Do Mausami, S-2 and the F_1 and the F_2 populations were sown and observation was taken for sex behaviour of the plants. All the F_1 plants in both the crosses were found monoecious, while the F_2 populations segregated for gynoecism. In the F_2 generation of the cross DBGy 201 × S-2, 57 plants were monoecious and the other 23 were gynoecious. The χ^2 value indicated a good fit to a 3:1 ratio (χ^2 = 0.41 and P = 00.52, Table 1). In the B_1 generation also monoecious and gynoecious plants were 11 and 9 respectively and fitting to a 1: 1 ratio model with a χ^2 value of 0.06 and P=0.81. In the second cross (DBGy 201 × Pusa Do Mausami), 61 plants produced both male and female flowers and the other 19 gave only female flowers. As with the earlier cross, the χ^2 analysis indicated a good fit to a 3:1 ratio (χ^2 = 0.01 and P = 0.92). Again in B_1 generation, 8 and 12 monoecious and gynoecious lines were obtained giving a ratio of 1: 1 (χ^2 = 0.46, P = 0.50). Inheritance pattern of a trait determines the breeding methodologies to be followed for improvement of the trait. In our study, χ^2 analysis for goodness of fit indicated that gynoecism in the line DBGy 201 is under the control of a single recessive gene (*gy-1*). This study confirmed the earlier report of (Behera *et al.*, 1; Ram *et al.*, 8), which stated single recessive control of gynoecious sex form in bitter gourd. Poole and Grimball (6) reported the similar inheritance pattern of gynoecism in melon. In contrast, Iwamoto and Ishida (4) reported that gynoecism in bitter gourd was partially dominant.

Significant ($P \leq 0.05$) mean differences were detected between the two parental lines of each of these crosses DBGy 201 × S-2 and DBGy 201 × Pusa Do Mausami for the traits like node bearing first female flower, days to 1st flowering, days to first harvestable maturity, number of fruits/plant, fruit length, fruit diameter, fruit weight and yield/plant (Tables 2 & 4). DBGy 201 was found superior over the other parent (S-2) for the traits like node at which first female flower appear, earliness in flowering and fruiting, number of fruits per plant and total yield. For most of the traits, F_1 generation mean is higher than the mid parent value except for node at which first female flower appears (7.86), days to first flowering (99.12) and days to first harvestable maturity (108.21). B_1 and B_2 exhibited mean values

Table 1. Chi square (χ^2) analysis of F_2 population for studying inheritance pattern of gynoecism in bitter gourd.

Cross	Monoecious plant(s)	Gynoecious plant(s)	Expected ratio	χ^2 value	P - value
DBGy 201	0	10	-		
S-2	10	0	-		
Pusa Do Mausami	10	0	-		
DBGy 201 × S-2 (F_1)	20	0	-		
DBGy 201 × Pusa Do Mausami (F_1)	20	0	-		
(DBGy 201 × S-2) × DBGy 201 (B_1)	11	9	1:1	0.06	0.81
(DBGy 201 × Pusa Do Mausami) × DBGy 201 (B_1)	8	12	1:1	0.46	0.50
(DBGy 201 × S-2) × S-2 (B_2)	20	0	-		
(DBGy 201 × Pusa Do Mausami) × Pusa Do Mausami (B_2)	20	0	-		
DBGy 201 × S-2 (F_2)	57	23	3:1	0.41	0.52
DBGy 201 × Pusa Do Mausami (F_2)	61	19	3:1	0.01	0.92

Table 2. Generation mean for different traits in the bitter gourd cross DBGy 201 × S-2.

Trait	P_1	P_2	MP	F_1	F_2	B_1	B_2
Node at which first female flower appear	4.40 ± 0.48	20.40 ± 0.95	12.40	7.86 ± 0.67	7.62 ± 0.27	8.13 ± 0.47	10.35 ± 0.62
Days to first flowering	92.83 ± 1.50	109.50 ± 1.06	101.16	99.120 ± 1.07	104.57 ± 0.90	96.66 ± 0.48	109.17 ± 0.62
Days to first harvestable maturity	106.00 ± 0.00	118.36 ± 0.95	112.18	108.21 ± 1.09	114.98 ± 0.70	106.81 ± 0.65	118.71 ± 0.61
No. of fruits/plant	17.13 ± 1.15	9.40 ± 0.67	13.26	16.90 ± 1.04	14.57 ± 0.58	15.50 ± 1.17	11.93 ± 0.74
Fruit length (cm)	7.61 ± 0.17	18.83 ± 1.24	13.22	14.46 ± 0.87	11.29 ± 0.21	11.56 ± 0.36	8.94 ± 0.34
Fruit dia. (cm)	3.76 ± 0.06	4.04 ± 0.34	3.90	4.28 ± 0.22	4.15 ± 0.14	3.81 ± 0.10	4.24 ± 0.17
Av. fruit wt. (g)	55.07 ± 1.19	91.36 ± 2.90	73.21	96.76 ± 1.71	79.22 ± 2.85	60.62 ± 3.19	75.46 ± 2.51
Yield/plant (g)	942.30 ± 66.33	851.66 ± 55.53	896.98	1641.80 ± 110.33	1147.25 ± 60.73	940.03 ± 87.14	906.08 ± 69.43

those were close to their recurrent parent (Table 2). Genetic variance among F_2 plants was found to be significantly diverse for all the traits studied. In the cross DBGy 201 × Pusa Do Mausami, a significant difference among the parents was noted in mean performance for all the traits. Pusa Do Mausami was found superior to DBGy 201 for traits like fruit length, fruit diameter and fruit weight. But for all other traits P_1 (DBGy 201) was better than P_2 (Pusa Do Mausami). For most of the values F_1 was not found competent with mid parent value except for traits like node at which first female flower appears (7.66), fruit length (12.22), average fruit weight (99.73) and yield per plant (1037.63) (Table 4). For days to first flowering and days to first harvestable maturity F_2, B_1 and B_2 means were close to the P_2.

In our experiment for node at which first female flower appear, additive (d), additive × additive (i) and additive × dominance (j) gene action were found significant in the cross DBGy 201 × S-2 but in the cross DBGy 201× Pusa Do Mausaami, additive (d), additive × dominance (j) and dominance × dominance (l) gene interactions were found significant. Duplicate type of epistasis was observed in both the crosses for this trait suggesting the possibilities of obtaining transgressive segregants in later generations (Table 3 and 5).

Days to first flowering and harvestable maturity were found to be governed by additive (d), dominance (h), additive × additive (i) and additive × dominance (j) type of gene action in the cross of DBGy 201 × S-2 with complementary type of epistasis. Use of reciprocal recurrent selection or bi-parental mating is suggested for improving the characters when additive and non-additive gene effects are involved in the expression of traits, whereas duplicate type of epistasis govern the trait days to first flowering and days to first first harvestable maturity in the cross of DBGy 201 × Pusa Do Mausami indicating selection at later generation. Singh and Ram (9) were of the opinion that additive component was more than that of the dominance for days to first female flower anthesis and days to first fruit set in bitter gourd, but Sundharaiya and Arumugam (11) reported non-additive gene action for the trait number of days to first female flowering and node number of the first female flower in bitter gourd.

Number of fruits per plant showed complimentary epistasis with predominance of dominant × dominant (l) interaction in DBGy 201 × S-2 indicating hybridization to be followed for its improvement but a duplicate type of epistasis with significant additive × dominance (j) interaction was noted in DBGy 201 × Pusa Do Mausami. The result corroborates with Choudhury and Sikdar (2). A duplicate type of epistasis with additive × dominance (j) and dominance × dominance (l) type of gene action was noted for fruit length in both the crosses. Dalamu *et al.* (3) reported greater involvement of dominance and dominance × dominance gene action for fruit length, fruit weight and number of fruits per plant in bitter gourd. Duplicate epistasis for fruit diameter was also observed in both the crosses. It is governed by all the three epistatic interaction (i, j, l) in DBGy 201 × S-2 but only j and l in DBGy 201 × Pusa Do Mausami. Therefore, selection should be delayed and after several generations (single seed descent) when a

Table 3. Scaling test, gene effects and SE for different traits in the cross DBGy 201 × S-2 of bitter gourd.

Trait	A	B	C	D	m	D	h	i	j	l
Node at which first female flower appear	-4.00* ± 0.72	7.57* ± 0.98	10.03* ± 1.19	-3.23* ± 0.55	7.63* ± 0.16	- 2.217* ± 0.446	1.93 ± 1.21	6.47* ± 1.10	11.57* ± 1.08	-2.90 ± 2.14
Days to first flowering	-1.38 ± 1.15	-9.71 * ± 1.13	-17.74* ± 2.62	3.33 * ± 1.14	104.57* ± 0.52	-12.500* ± 0.458	-8.70* ± 2.41	-6.65* ± 2.28	-8.33* ± 1.35	-4.44 ± 3.20
Days to first harvestable maturity	0.58 ± 0.98	-10.85* ± 1.10	-19.13* ± 2.14	4.43* ± 0.97	114.98* ± 0.41	-11.900* ± 0.515	-12.83* ± 2.05	-8.87* ± 1.93	-11.43* ± 1.17	-1.40 ± 2.97
No. of fruits/plant	3.03 ± 1.63	2.43* ± 1.12	2.03 ± 1.97	1.72 ± 1.05	14.58* ± 0.34	3.567* ± 0.804	0.20 ± 2.22	-3.43 ± 2.11	-0.60 ± 1.79	8.90* ± 3.78
Fruit length (cm)	-1.06* ± 0.66	15.41* ± 0.96	10.21* ± 1.33	2.07* ± 0.38	11.29* ± 0.12	2.623* ± 0.290	-2.90* ± 0.98	-4.14* ± 0.75	16.46 ± 0.93	18.49* ± 1.77
Fruit dia. (cm)	0.44 ± 0.17	-0.16* ± 0.31	-0.25* ± 0.47	0.26* ± 0.20	4.16* ± 0.08	-0.435* ± 0.115	-0.15* ± 0.44	-0.53* ± 0.41	-0.60* ± 0.31	0.808* ± 0.66
Av. fruit wt. (g)	30.60* ± 3.87	37.20 ± 3.49	23.10 ± 7.11	22.35 ± 4.04	79.22* ± 1.65	-14.850* ± 2.342	-21.15 ± 8.19	-44.70 ± 8.08	6.60* ± 5.02	112.50 ± 11.76
Yield/plant (g)	704.03* ± 125.10	681.30* ± 107.31	488.57* ± 195.95	448.33* ± 95.16	1147.25* ± 35.06	33.950 ± 64.331	-51.95 ± 202.25	-896.77 ± 190.33	-2.73 ± 138.02	2282.10* ± 323.44

*indicates significance at 5% level

Table 4. Generation mean for different traits in the cross DBGy 201 × Pusa Do Mausami of bitter gourd.

Trait	P_1	P2	MP	F_1	F_2	B_1	B_2
Node at which first female flower appears	4.37 ± 0.43	13.67 ± 0.99	9.02	7.67 ± 0.56	6.23 ± 0.27	5.18 ± 0.28	7.30 ± 0.68
Days to first flowering	91.07 ± 1.35	107.97 ± 1.05	99.52	105.38 ± 0.57	104.50 ± 0.90	106.93 ± 0.51	107.53 ± 0.60
Days to first harvestable maturity	106.00 ± 0.00	117.90 ± 1.03	111.95	115.10 ± 0.72	114.75 ± 0.70	116.83 ± 0.70	119.07 ± 0.61
No. of fruits/plant	17.40 ± 1.03	9.50 ± 0.67	13.45	10.40 ± 0.47	10.64 ± 0.84	12.63 ± 0.73	10.35 ± 0.80
Fruit length (cm)	7.61 ± 0.17	14.81 ± 0.09	11.21	12.22 ± 0.19	10.20 ± 0.35	7.20 ± 0.22	12.55 ± 0.20
Fruit dia. (cm)	3.03 ± 0.33	4.54 ± 0.21	4.23	3.31 ± 0.15	3.39 ± 0.27	4.02 ± 0.23	3.30 ± 0.25
Av. fruit wt. (g)	53.63 ± 1.40	84.89 ± 0.91	69.26	99.74 ± 1.01	76.58 ± 2.85	52.13 ± 0.67	83.56 ± 0.44
Yield/plant (g)	929.87 ± 56.10	806.47 ± 57.68	868.17	1037.63 ± 48.31	810.74 ± 74.24	658.18 ± 39.03	864.62 ± 66.49

high level of gene fixation is attained subsequent crossing between promising lines may be done to accumulate favourable genes. Rajeswari and Natarajan (7), and Choudhury and Sikdar (2) were also of the same opinion.

In both the crosses duplicate type of epistasis with predominance of additive × dominance gene action was observed for average fruit weight. Yield per plant showed duplicate type of epistasis in both the cross and dominance of dominance × dominance type of interaction (l) was recorded. Similar result for fruit weight was also reported by Choudhury and Sikdar (2) but it negates the finding of Sundharaiya and Arumugam (11) who have found significant additive effect for fruit weight, whereas the total yield per plant was in accordance with their result.

The results of this study demonstrated that the trait gynoecism is under the control of a recessive gene (*gy* 1) in both the crosses but gene effects obtained by generation mean analysis differed with the different genetic backgrounds of the inbred crosses. Further, the involvement of epistasis in

Table 5. Scaling test, gene effects and standard error for different traits in the cross DBGy 201 × Pusa Do Mausami.

Trait	A	B	C	D	m	d	H	i	j	l
Node at which first female flower appears	6.73* ± 1.02	1.67* ± 0.52	8.47* ± 1.09	-0.03 ± 0.52	6.23* ± 0.15	2.12* ± 0.42	-1.28 ± 1.14	0.07 ± 1.04	-5.07* ± 1.05	8.33* ± 2.01
Days to first flowering	-1.72 ± 0.96	-37.42 ± 29.43	-8.20* ± 2.41	-15.47 ± 14.75	104.50* ± 0.52	-9.40 ± 14.71	36.80 ± 29.51	30.93 ± 29.50	- 35.70 ± 29.45	-70.07 ± 58.90
Days to first harvestable maturity	-5.13* ± 1.01	-12.67* ± 1.59	-4.90* ± 1.91	6.45* ± 1.17	114.75* ± 0.40	2.18* ± 0.84	16.05* ± 2.40	12.90* ± 2.34	-7.53* ± 1.79	-30.70* ± 3.88
No. of fruits/plant	-0.80 ± 1.04	2.53* ± 1.06	5.15* ± 2.14	-1.71 ± 1.15	10.64* ± 0.49	-2.28* ± 0.62	0.37 ± 2.35	3.42 ± 2.31	3.33* ± 1.44	-1.68 ± 3.29
Fruit length (cm)	1.92* ± 0.26	5.43* ± 0.29	6.07* ± 0.84	0.64* ± 0.44	10.20* ± 0.20	5.35* ± 0.17	-0.27 ± 0.88	-1.28* ± 0.88	3.51* ± 0.36	8.63* ± 1.09
Fruit dia. (cm)	-0.25* ± 0.33	0.81* ± 0.34	1.64* ± 0.68	-0.54 ± 0.37	3.39* ± 0.16	-0.73* ± 0.20	0.12 ± 0.75	1.09 ± 0.74	1.06* ± 0.46	-0.54* ± 1.05
Av. fruit wt. (g)	17.50 ± 0.94	49.11* ± 1.26	31.67* ± 6.76	17.47 ± 3.32	76.58* ± 1.65	31.44* ± 0.46	-4.46 ± 6.69	-34.94 ± 6.65	31.61* ± 1.33	101.55 ± 7.01
Yield/plant (g)	114.87 ± 88.21	651.13* ± 62.08	57.63* ± 19.18	98.68 ± 96.60	810.74* ± 42.87	206.44* ± 44.51	-27.90 ± 196.57	-197.30 ± 193.192	536.27* ± 100.39	963.37* ± 257.62

*indicates significance at 5% level

genetic control of all the traits studied was confirmed. The selection of high-yielding bitter gourd genotypes is complicated by often occurrence of duplicate epistasis. The different types of gene effect estimates provided a test for gene action and are useful for analyzing the genetic architecture of the crop so as to further improve the desirable traits. The estimates obtained from each cross may be unique to that cross and may not be applicable to the parental population.

REFERENCES

1. Behera, T.K., Dey. S.S., Munshi, A.D., Gaikwad, A.B., Pal, A. and Singh, I. 2009. Sex inheritance and development of gynoecious hybrids in bitter gourd (*Momordica charantia* L.). *Scientia Hort.* **120**: 130-33.
2. Choudhury, A.R. and Sikdar, B. 2005. Genetic analysis for nine fruit characters in relation to five parental diallel crossing of bitter gourd. *J. Life Earth Sci.* **1**: 31-34
3. Dalamu, Behera, T.K., Satyavati, C.T. and Pal, A. 2012. Generation mean analysis of yield related traits and inheritance of fruit colour and surface in bitter gourd. *Indian J. Hort.* **69**: 65-69.
4. Iwamoto, E. and Ishida, T. 2006. Development of gynoecious inbred line in balsam pear (*Momordica charantia* L.). *Hortic. Res. (Japan)*, **5**: 101-04.
5. Panse, V.G. and Sukhatme, P.V. 1985. *Statistical methods for Agricultural Workers*. ICAR, New Delhi, India, 359 p.
6. Poole, C.F. and Grimball, P.C. 1939. Inheritance of new sex forms in *Cucumis melo* L. *J. Hered.* **30**: 21-25.
7. Rajeswari, K.S. and Natarajan, S. 2000. Genetics and inheritance of yield and its components in bitter gourd. *South Indian Hort.* **50**: 82-90.
8. Ram, D., Kumar, S., Singh, M., Rai, M. and Kalloo, G. 2006. Inheritance of gynoecism in bitter gourd (*Momordica charantia* L.). *J. Hered.* **97**: 294-95.
9. Singh, D.K. and Ram, H.H. 2003. Genetics of quantitative traits in bitter gourd (*Momordica charantia* L.). *Prog. Hort.* **35**: 189-91.
10. Staub, J.E., Robbins, M.D. and Wehner, T.C. 2008. Cucumber. **In**: Prohens, J., Nuez, F. (Eds.). *Handbook of Plant Breeding: Vegetable I*. Springer Science, New York, USA, pp. 241-82.
11. Sundharaiya, K. and Arumugam, S. 2006. Gene action studies in bitter gourd (*Momordica charantia* L.). *Adv. Plant Sci.* **19**: 249-52.

Received : January, 2014; Revised : October, 2014;
Accepted : January, 2015