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Combining Ability and Heterosis Studies in Bitter Guard (*Momordica charactia* L.)

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ABSTRACT

Keywords

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The present investigation was carried out during 2013-2015 at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India. Analysis of variance revealed highly significant variances among all the genotypes for 18 characters. The best three parents identified as general combiners over both the seasons and pooled over environment were US 33, VNR 28 and VNR 22 for earliness and yield characters. For earliness, the cross combinations VNR 28×US 33 (-3.31), VNR 22×PBIG 2 (-2.92) and VNR 28×MC 84 (-1.83) emerged as good specific combiners. For average fruit weight, MC 84× Pant Karela 3 (13.51), PDM ×VNR 28 (11.14) and Pant Karela 3× PBIG 2(10.80) were found with significant SCA effects. For number of fruits/plant and fruit yield/plant, the crosses VNR 28×Pant Karela 3(21.66), VNR 22×MC 84 (19.78), VNR 28×MC 84 (10.45), VNR22×Pant Karela 1(398.51g), US33×Pant Karela3 (346.95g) and MC84×Pant Karela 3(264.74g), respectively were found to have promising SCA effect. Maximum amount of standard heterosis for no. of fruits/plant and yield/plant were noted in crosses VNR22×MC 84 (139.44) and US33×Pant Karela3 (26.40). The best parents with desirable and significant gca effects may be used in hybrid breeding programme for developing high yielding hybrids in bitter gourd.

Introduction

Bitter Gourd (*Momordica charantia* L., 2n=2x=22) is a multipurpose herb belonging to family Cucurbitaceae. The crop is extensively grown in India, China, Japan, South East Asia, tropical Africa and South America. Asian *M. charantia* originated from tropical Africa (Schaefer and Renner, 2010), while its original place of domestication is unknown yet. Areas of Eastern India and Southern China have been proposed as places of origin (Dey *et al.*, 2006). Among the

cultivated cucurbits, bitter gourd has been identified as one of the potent vegetables for export by Agricultural Processed Food Products and Export Development Authority. In India, Uttar Pradesh, Bihar, West Bengal, Orissa, Karnataka, Maharashtra, Telangana, Tamil Nadu, Kerala and Chhattisgarh are the major bitter gourd growing states with Telangana being the leading producer followed by Chhattisgarh and Orissa One of the possible approaches for achieving the targeted production is to identify and develop suitable hybrids with high yield and good

quality. In spite of wide range of diversity very little work has been undertaken to exploit this naturally endowed diversity in the form of hybrid breeding. Hybrids in most of the vegetable crops offer opportunity of earliness, high yield, quality improvement besides better capacity to face biotic and abiotic stresses. The exploitation of heterosis is much easier in cross pollinated crops and bitter gourd being monoecious, provides ample scope for utilization of hybrid vigour on commercial scale. A wide range of variability in vegetative and fruit characters is available in bitter gourd so, the diversified parents from different locations with high yield and quality would also pave way for the development and release of hybrids having high yield, earliness and quality through heterosis breeding. Information on combining ability facilitates the choice of suitable parents for hybridization programme to develop promising F_1 hybrids. In actual plant breeding combining abilities have found their principle use in predicting the performance of parents and hybrid population. Diallel analysis is widely used to estimate combining ability effects of the parents and the crosses (Griffin, 1956). It is the most balanced and systematic experimental design to examine continuous variation. The genetic information related to parental population become available quite in early generation i.e. in F_1 and it is thus useful to define breeding strategy without losing much time. Diallel analysis provides reliable information on the components of variance, general combining ability (GCA), specific combining ability (SCA), variances and their effects (Singh and Narayanan, 1993) and also helps in formulating the breeding methodology for crop improvement.

The information usually needed for developing high yielding crop in particular species pertains to the extent of genetic variability for desirable traits in the available germplasm. Large variability ensures better chances to produce new forms. Though bitter

gourd is an important cucurbitaceous vegetable and lot of variation is present for characters, such information is inadequate. Keeping in view all the above standpoint in consideration, the present investigation was conducted to study the magnitude of heterosis and combining ability of parental lines and crosses.

Materials and Methods

The present investigation was carried out at the Vegetable Research Centre, G.B.Pant University of Agriculture and Technology, Pantnagar, U.S.Nagar, during spring-summer seasons of 2013-15. Pantnagar lies on 29° North latitude, 79.3° East longitude and at an altitude of 243.83 meters above mean sea level and comes under the Tarai belt of Shivalik ranges of Himalayas. The climate of Pantnagar is broadly humid and subtropical in nature with hot summers and cool winters. The soil of experimental field was calcareous and of miscellaneous type and it is generally 1.0 to 1.5 meter deep with good drainage and nearly neutral reaction (pH 6.0-7.5). High rainfall is generally received from June to September. The experimental material consisted of eight inbred lines of bitter gourd *viz.* PDM, VNR-28, VNR-22, MC-84, Pant Karela 1, US-33, Pant karela 3 and PBIG-2. Their 28 F_1 's developed by crossing in diallel fashion excluding reciprocals. The seeds of parental lines were obtained from cucurbits breeding programme of the department of Vegetable Science, G.B.Pant University of Agriculture and Technology, Pantnagar. The experiment was laid out in Randomized Block Design (RBD) with three replications. Each genotypes consisted of 10 plants. Row to row spacing was kept 3 m, while plant to plant was kept 80 cm, respectively. Initially, 3-4 seeds were sown per hill from which 2 plants were retained after thinning. The observations were recorded on five randomly selected plants and the average was computed for the following 24 morphological characters among first male

flower anthesis (days), first female flower anthesis (days), node number to first male flower, node number to first female flower, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit diameter (cm), L/D ratio, main vine length (m), number of primary branches per vine, internodal length (cm), leaf blade length (cm), leaf blade width (cm), petiole length (cm), leaf area (cm²), fruit yield /ha (q).

Statistical analysis

The data was statistically analyzed following the standard procedure as applicable to a typical randomized block design. Treatments were tested by 'F-test' (Snedecor and Cochran, 1967). Heterosis expressed as per cent increase or decrease in the performance of F₁ over mid-parent (average or relative) heterosis, better parent (heterobeltiosis) and check parent (standard heterosis).

Residual heterosis was calculated using similar formulas instead of F₁ mean was used for all the genotypes under study. The combining ability analysis for parental genotypes and their crosses were carried out following method 2 and Model I of Griffing (1956).

Results and Discussion

Combining ability analysis

Analysis of variance for combining ability

The analysis of variances of combining ability was done for the eighteen characters in bitter gourd (Table 1). The GCA variances were highly significant for all the characters for both the season and pooled over season except internodal length in pooled season. The SCA variances were also highly significant for all the characters. The GCA variances were higher and prominent than SCA variances for all the characters under study.

Estimates of general combining ability effects

The estimates of general combining ability (GCA) of the parents for various characters for both the season and pooled have been shown in Table 2a and 2b. For days to first male and female flower and node no. to first male and female flower, the negative gca and sca effects were considered to be desirable as it indicates earliness. The parent VNR-28 was recorded as the best general combiner for the traits first male flower anthesis, first female flower anthesis, node no. to first male flower and node no. to first female flower and US-33 for petiole length, leaf area, fruit length, fruit diameter, L/D ratio, average fruit weight, fruit yield per plant and fruit yield per ha. Whereas, the parent VNR-22 was found to be the best general combiners for main vine length and internodal length. These lines may be used in bitter gourd improvement programme for developing desirable genotypes. GCA effects would be more stable as compared to SCA effects. In general, additive effects are mainly due to polygenes producing fixable effects and indicate the capacity of variety in relation to all other varieties, it was crossed with. High GCA effects of a parent is a function of breeding value and hence due to additive gene effect and/or additive × additive interaction effect which represents the fixable components of genetic variance (Griffing, 1956). Apparently, parents with good GCA effects may be presumed to possess more favourable genes for the concerned traits. The findings were in proximity to those of the studies conducted by Srivastava and Nath (1983) and Bhatt *et al.*, (2017) who observed significantly high GCA and SCA effects were for days to flowering, fruit per plant, fruit weight and total yield per plant in majority of parents. Gopalkrishnan (1986) also evaluated 30 crosses and reported parent MDU-1 as best general combiner for weight, size, number of fruits per plant and total yield and the cross,

Priya × MDU-1 was reported to have high SCA effect. Vahab (1989) reported Priya, MC-66, and MC-84 as best general combiner for total yield. Devadas *et al.*, (1993) also reported *cv.* MC 13 as good general combiner for seeds per fruit and 100 seed weight and MC 84 for field emergence, seedling length and seedling dry weight. Gupta *et al.*, (2006) reported highly significant general combining ability (GCA) and specific combining ability (SCA) for yield and yield components indicating the presence of variability in combining ability of the parents. The similar sort of studies were also conducted by Tamilselvi *et al.*, (2015) identified the parents Kasi Harit, Vadhalagundu Local and CO2 as the best genotypes for improvement of earliness and yield characters

Specific combining ability studies

Specific combining ability effect which represents the predominance of non additive gene action is a major component that may be utilized in heterosis breeding (Table 3). Out of 28, cross combinations 3, 11 and 17 exhibited significant and desirable sca effects for days to first male anthesis during 2014, 2015 and pooled over analysis. The cross combination VNR-22 x US-33 had exhibited the highest significant sca effects for first male flower anthesis over all the season and pooled over analysis and VNR-22 x MC-84. For node no. of first female flower, the estimate of sca effect of crosses in first season were found significant negative effects in VNR 28× US 33 (-7.25), MC 84 ×US 33 (-3.82) and VNR 28 ×VNR 22 (-3.24). Similarly, for season II, the crosses revealed significant effects were VNR 28× US 33 (-5.46), MC 84 ×US 33 (-3.22) and MC 84 ×PBIG 2 (-3.16). For internodal length for the year 2014 and 2015, significant sca effects were observed in almost all the crosses. The highest sca effect was observed for the crosses Pant karela 1× Pant karela 3 (1.03 and 1.09), followed by VNR 28× VNR 22 (0.95 and 0.98) and VNR 22× US33 (0.74

and 1.14) in season I and II. For pooled season also similar crosses showed highest significant sca effects. Among 28 crosses, maximum positively associated values for sca effects for fruit length were recorded in cross combinations MC 84×PBIG 2 (4.82), VNR22×US 33 (4.35) and PDM ×VNR 28 (2.36) for season I and in cross combinations MC 84×PBIG 2 (5.53), VNR22×US 33 (3.25) and VNR 28×US 33 (3.25) for season II. For pooled season, crosses with maximum sca effect were MC 84× PBIG 2 (5.17), VNR 22× US 33 (3.71) and PDM ×Pant karela 1 (2.39).

For fruit weight, estimates of sca effects revealed that Pant karela 3×PBIG 2 (11.59 and 10.01), MC 84× Pant karela 3 (15.98 and 11.03) showed maximum value of sca for both the season, while PDM ×VNR 28 (12.52) in season I and VNR 28× US 33 (10.61) in season II. Pooled data showed similar crosses with highest values viz., Pant karela 3×PBIG 2 (10.80), MC 84× Pant karela 3 (13.51) and PDM ×VNR 28 (11.14). Whereas for number of fruits/plant, the perusal of results revealed highest value of 31.74, 20.27 and 19.54 for VNR 28×Pant karela 3, VNR 28× MC 84 and VNR 22×MC 84, respectively in 2014 season. VNR 28×Pant karela 3, VNR 22×MC 84 and PDM × Pant karela 1 (7.09) noted maximum value for season II. Similarly, VNR 28×Pant karela 3 (21.66), VNR 28× MC 84 (10.45) and VNR 22×MC 84 (19.78) showed significant highest sca effects. Fruit yield/ha showed maximum values of significant sca effects in crosses US 33× Pant karela 3 (14.46 and 14.48), VNR 22× Pant karela 1 (17.26 and 16.88) for both seasons. Whereas, US 33× PBIG 2 (13.32) in 2014 and MC 84×Pant karela 3 (10.44) in 2015 having highest sca effect. Pooled season showed US 33× Pant karela 3 (14.47), VNR 22× Pant karela 1 (17.07) and MC 84×Pant karela 3 (11.05) with maximum values.

Table.1 ANOVA for combining ability for various quantitative traits

Characters	2014			2015			Pooled					
	GCA	SCA	Error	GCA	SCA	Error	GCA	SCA	Env.	GCA*Env.	SCA*Env	Error
d.f.	7	28	70	7	28	70	7	28	1	7	28	140
1st Male Flower Anthesis (days)	45.72**	1.18**	0.36	30.51**	14.89**	0.35	49.53**	9.40**	74.16**	26.70**	6.66**	0.36
1st Female Flower Anthesis (days)	40.05**	4.90**	0.42	63.63**	8.32**	0.43	85.34**	5.61**	233.00**	18.34**	7.61**	0.43
Node No. of 1st Male Flower	27.18**	1.73**	0.03	31.23**	31.42**	0.03	47.58**	16.03**	24.81**	10.83**	17.11**	0.03
Node No. of 1st Female Flower	98.39**	7.08**	0.12	69.04**	8.94**	0.1	160.81**	12.33**	5.49**	6.62**	3.69**	0.11
Main Vine Length (cm)	1.06**	0.58**	0	0.41**	0.25**	0	0.85**	0.44**	2.85**	0.62**	0.39**	0
Primary Branches/ Plant	2.56**	14.44**	0.05	12.65**	4.16**	0.05	9.03**	9.69**	196.01**	6.18**	8.92**	0.05
Internodal Length (cm)	0.49**	0.48**	0.01	0.44**	0.60**	0.01	0.92**	1.06**	1.20**	0	0.02**	0.01
Leaf Length (cm)	8.28**	7.53**	0.02	9.96**	4.12**	0.02	17.15**	10.57**	7.12**	1.10**	1.08**	0.02
Leaf Width (cm)	2.52**	2.28**	0.02	3.72**	2.17**	0.02	5.87**	4.04**	0.80**	0.36**	0.41**	0.02
Petiole Length (cm)	1.59**	2.86**	0	5.23**	3.15**	0.01	4.24**	4.39**	33.70**	2.59**	1.62**	0.01
Leaf Area (cm²)	1620.78**	1412.75**	3.29	1710.50**	906.97**	2.86	3144.35**	2150.55**	951.81**	186.93**	169.17**	3.07
Fruit Length (cm)	45.62**	6.43**	0.05	38.72**	5.66**	0.05	81.85**	10.93**	9.96**	2.49**	1.16**	0.05
Fruit diameter (cm)	0.48**	0.09**	0	0.30**	0.09**	0	0.69**	0.13**	0.88**	0.10**	0.05**	0
Length/ diameter ratio	3.59**	0.43**	0.01	3.02**	0.36**	0.01	6.50**	0.70**	0.04*	0.12**	0.09**	0.01
Average Fruit Weight (g)	510.84**	128.72**	0.66	538.21**	121.89**	0.57	1015.59**	233.34**	223.29**	33.45**	17.28**	0.62
Fruits/ Plant	407.09**	131.41**	0.28	241.40**	61.03**	0.27	621.28**	161.17**	369.59**	27.21**	31.27**	0.27
Fruit Yield//Plant (g)	82731.06*	65283.28*	442.82	83106.71*	51911.91*	656.73	153485.25*	108280.39*	33139.22*	12352.51*	8914.80*	549.78
Fruit Yield/ hac	143.65**	113.36**	1.11	142.82**	91.46**	1.05	265.01**	189.37**	55.21**	21.46**	15.45**	1.08

Table.2a Estimates of GCA traits over pooled analysis

Source of variation	First male flower anthesis (days)	First female flower anthesis (days)	Node no. to first male flower	Node no. to first female flower	Main vine length (m)	No.of primary branch	Inter-nodal length (cm)	Leaf length(cm)	Leaf width (cm)
PDM	-0.23	-2.06**	2.71**	0.77**	0.03**	-0.51**	-0.20**	-0.11**	-0.25**
VNR-28	-2.32**	-3.46**	-2.55**	-4.74**	-0.26**	-0.34**	-0.20**	0.75**	0.18**
VNR-22	0.55**	0.43**	0.85**	0.71**	0.28**	-0.72**	0.46**	-0.68**	0.05
MC-84	0.48**	0.17	-0.63**	-2.50**	0.19**	-0.61**	-0.08**	-1.29**	-0.70**
PK-1	-1.65**	-0.64**	0.05	0.58**	-0.17**	0.15**	0.07**	0.60**	0.49**
US-33	2.93**	2.74**	0.81**	4.77**	-0.14**	0.35**	0.02	1.00**	0.81**
PK-3	0.02	2.28**	-0.97**	1.48**	0.22**	1.24**	0.05**	-1.11**	-0.74**
PBIG-2	0.22	0.54**	-0.27**	-1.08**	-0.15**	0.46**	-0.11**	0.84**	0.16**
CD for GCA									
Gi--Gj at 95%	0.37	0.41	0.11	0.21	0.03	0.14	0.05	0.09	0.08
Gi--Gj at 99%	0.49	0.54	0.15	0.27	0.04	0.18	0.07	0.12	0.11

Table.2b Estimates of GCA traits over pooled analysis

Source of variation	Petiole length (cm)	Leaf area (cm ²)	Fruit length (cm)	Fruit dia. (cm)	L/D ratio	Aver-age fruit weight (g)	No. of fruits /plant	Fruit yield /plant (g)	Fruit yield/ha (q/ ha)
PDM	-0.49**	-4.73**	1.21**	0	0.26**	7.66**	-6.34**	78.75**	3.27**
VNR-28	0.18**	5.81**	-4.27**	0.14**	-1.09**	-11.17**	11.55**	9.38	0.38
VNR-22	-0.16**	-6.58**	2.06**	-0.29**	0.78**	-7.05**	3.01**	-58.82**	-2.41**
MC-84	-0.45**	-15.09**	-0.41**	0.12**	-0.22**	0.49**	1.68**	57.07**	2.36**
PK-1	0.20**	7.96**	-0.09	-0.27**	0.21**	0.42*	-1.82**	-53.43**	-2.18**
US-33	0.83**	20.44**	2.09**	0.16**	0.48**	10.79**	-4.43**	128.50**	5.34**
PK-3	-0.41**	-15.34**	-0.23**	0	-0.19**	0.99**	-0.77**	-16.24**	-0.69**
PBIG-2	0.30**	7.54**	-0.37**	0.15**	-0.22**	-2.13**	-2.88**	-145.20**	-6.06**
CD for GCA									
Gi--Gj at 95%	0.05	1.1	0.14	0.04	0.06	0.49	0.33	14.66	0.65
Gi--Gj at 99%	0.06	1.45	0.19	0.05	0.07	0.65	0.43	19.36	0.86

Table.3 Three best hybrids in terms of specific combining ability, standard heterosis and heterobeltiosis

S. No.	Characters	Best Specific Combiners	Best Crosses (Standard Heterosis)	Best Crosses (Heterobeltiosis)
1.	1st Male Flower Anthesis (days)	VNR 22× US 33 (-4.35), VNR 28 × PBIG 4 (-3.39), VNR 22×MC 84 (-2.43)	VNR28×Pant Karela3(-18.55), PDM×VNR28(-14.85), VNR28× MC84 (-13.00)	VNR28×US33 (-20.91), VNR22×US33 (-19.70), VNR28× Pant Karela 3(-18.55)
2.	1st Female Flower Anthesis (days)	VNR 28 ×US 33 (-3.31), VNR 22×PBIG 2 (-2.92), VNR 28×MC 84 (-1.83)	PDM × VNR28 (-23.95), VNR 28×MC 84 (-21.95), VNR 28× US33 (-19.77)	VNR 28× US33 (-20.00), VNR28× Pant Karela 3(-15.60), VNR 28×MC84 (-13.19)
3.	Node No. of 1st Male Flower	PBIG3×PBIG4(-2.42) PBIG3×US33(-2.40), PDM ×PBIG 3 (-1.46)	VNR28×PBIG2 (-15.24), VNR28 × PantKarela3(13.83), Pant Karela1×Pant Karela 3(-7.40)	VNR28× US33 (-30.83), Pant Karela 1× US33(-27.76), VNR 28×VNR 22 (-26.88)
4.	Node No. of 1st Female Flower,	VNR 28×US 33(-6.35), MC 84 ×US 33 (-3.52), MC 84 ×PBIG 2(-2.04)	VNR 28× MC 84 (-36.72), VNR 28× US 33 (-36.51), VNR 28×PBIG 2 (-29.44)	VNR28×US33 (-55.87), MC84×US 33(-40.13), VNR 28×VNR 22(-26.08)
5.	Main Vine Length (cm)	MC 84 × PBIG 4(0.70), MC 84 ×US 33(0.68), PDM ×PBIG 2 (0.60)	MC 84× Pant Karela 3(49.54), VNR 22× Pant Karela 3 (44.14), MC 84×US 33 (36.03)	US33×Pant Karela 3 (33.33), VNR 22×Pant Karela 3 (21.22), Pant Karela 1×Pant Karela 3(17.10)
6.	Primary Branches/ Plant	MC 84× US 33(5.15), PBIG 4× PBIG2 (3.59), PDM ×PBIG 2 (3.44)	Pant Karela 3× PBIG 2(40.00), MC 84×US 33(36.92), US 33×Pant Karela 3 (33.84)	MC 84×US 33(50.85), PDM× PBIG 2(40.52), Pant Karela 3× PBIG 2(40.00)
7.	Internodal Length (cm)	Pant K 1× Pant K 3(1.09), VNR 28× VNR 22(0.98), VNR 22× US33 (1.14)	VNR 22× US 33 (30.43), Pant Karela 1× Pant Karela 3(26.95), VNR 22× Pant Karela 3 (23.48)	VNR 28×VNR 22 (30.36), VNR 22× Pant Karela 3 (23.48), VNR 22× US 33 (16.28)
8.	Leaf Length (cm)	PDM×VNR22(3.00), VNR 22×MC 84 (3.10), VNR 28× MC 84 (2.91)	VNR28×Pantkarela 1 (127.38), VNR28× MC84 (112.29), PDM × VNR22 (109.75)	VNR 22×MC 84 (39.69), MC 84× Pant Karela 3 (30.98), VNR 28× MC 84 (19.41)
9.	Leaf Width (cm)	VNR22×MC84(2.12) VNR28×MC 84(1.83), PDM×PantKarela 1(1.70)	PDM× Pant Karela 1(117.90), VNR 28×MC 84 (103.26), VNR 28× Pant Karela 1 (101.98)	MC 84×Pant Karela3 (38.28), VNR 22×MC84 (29.63), PDM ×VNR 22 (23.12)
10.	Petiole Length (cm)	PDM ×VNR 22(2.25), VNR 28×MC 84(2.76) PDM×Pant Karela 3(1.36)	-	MC84×Pant Karela 3 (69.88), VNR28×MC84(68.73), VNR22×MC 84 (50.58),
11.	Leaf Area (cm ²)	VNR 22× MC 84(44.90), VNR 28×MC 84(39.47), PDM ×VNR 22 (2.25)	VNR 28× MC84 (143.04), PDM× VNR 22 (113.62), VNR 28× Pant Karela 3 (98.15)	VNR 22× MC84 (85.29), MC 84 ×Pant Karela 3(81.09), VNR 28×MC 84 (42.96)
12.	Fruit Length (cm)	MC 84× PBIG 2(5.17), VNR 22× US 33(3.71), PDM ×PBIG 3 (2.39)	-	MC84× PBIG 2 (27.68), PDM ×US 33 (14.70), PDM ×PBIG 2 (14.06)
13.	Fruit Dia (cm)	VNR 28× PBIG 2 (0.72), VNR 22×Pant K1(0.45), PDM ×US 33 (0.44)	VNR 28× PBIG 2 (22.94), PDM ×US33 (10.40), PDM ×MC 84 (8.99)	VNR 22×Pant Karela 1 (14.79), VNR 28× PBIG 2 (9.47), PDM× Pant Karela 3 (7.80)
14.	Length/ Dia ratio	Pant Karela 3×PBIG 2(10.01), MC 84× Pant K 3(11.03)	-	MC 84×PBIG 2 (36.89)
15.	Average Fruit Weight	Pant Karela 3×PBIG 2(10.80), MC84× Pant Karela 3(13.51), PDM ×VNR 28 (11.14)	PDM×MC84 (5.63), MC 84×Pant Karela 3 (3.99), Pant Karela 1 ×US 33 (2.93)	US33× PBIG 2 (11.62), VNR 22× US 33 (5.73), MC 84×Pant Karela 3 (3.99)
16.	Fruits/ Plant	VNR 28×Pant Karela 3(21.66), VNR 28× MC 84(10.45), VNR 22×MC 84(19.78)	VNR 28×Pant Karela 3(160.55), VNR 22×MC 84 (130.26), VNR 28×MC 84 (127.27)	Pant Karela 1× Pant Karela 3 (57.42), VNR 22×MC 84 (50.02), VNR 28× Pant Karela 3 (29.02).
17.	Fruit Yield//Plant (gm)	US 33× Pant Karela 3 (346.95), VNR22× PantKarela1(398.51), MC 84×Pant Karela 3 (264.74)	US33×Pant Karela 3 (29.34), MC84× US 33 (21.97), PDM × US 33 (21.17)	US33×Pant Karela 3 (29.34), VNR 22× US33 (15.32), US 33× PBIG 2 (11.22)
18.	Fruit Yield/ hac	US 33× Pant Karela 3 (14.47) VNR 22× Pant Karela 1(17.07), MC 84×Pant Karela 3 (11.05)	US 33× Pant Karela 3 (29.34), MC 84 × US 33 (21.97), PDM × US 33(21.18)	US33×Pant Karela 3 (29.34), VNR 22× US 33(15.32), US 33× PBIG 2 (11.22)

The significance of SCA effects elucidates the presence of genetic diversity among parents tested and illustrates the contribution of dominance/ epistatic effect which represents the non fixable components of genetic variation related to heterosis. The crosses showing sca effects involving parent with good gca could be exploited as F₁ hybrid breeding, however if a cross having high sca has one of its parents as good general combiner and the other as poor or average combiner, such crosses are likely to give some segregants. These results were in the conformity with the results reported by Masmade and Kale (1986) who evaluated combining ability in seven cultivars of cucumber crossed in diallel fashion excluding reciprocals and found that both GCA and SCA variances were significant for all the characters. The hybrids Poona Khira X Japanese Long Green, White Long Cucumber X Poinsette, Kalyanpur Ageti X Panval and Poona Khira X Turkish Long Green were found to be most promising as having highest SCA effects. Jankiram and Sirohi (1988) also estimated components of SCA in bottle gourd hybrids. The F₁ hybrid S-46 X S-54 was the best specific combiner for fruit weight and total yield per plant. Vahab (1989) observed highest SCA effect for total yield and number of fruits per vine in cross, Arka Harit × MAC-79.

Heterosis

There is a good scope of exploiting heterosis in bitter melon because of the fact that it is a cross pollinated crop. In the present study, the extent of heterosis was studied in 28 F₁ hybrids of bitter melon developed by 8 parents in diallel design in two seasons. The estimates of heterobeltiosis (better parent) and standard heterosis (check parent) have been presented in table 3. For the characters days to 1st female flower anthesis and node number to 1st female flower, the negative heterosis was

considered to be desirable, as it indicates earliness. The parental genotype PBIG 4 (Pant Karela 3) was used as a check for standard heterosis. For days to first female flower, the heterobeltiosis ranged from -16.82 (MC84×PBIG2) to -4.18 (VNR22× US33). The highest negative values was obtained in crosses -16.82 (MC84×PBIG2), -14.74 (MC84×US33) and -14.60 (VNR 28×Pant karela 3). Standard heterosis was found maximum in MC 84×PBIG2 (-21.46), PDM×MC84 (-19.74) and PDM×VNR28 (-19.32) in season I. In season II, maximum negative heterobeltiosis, was found in crosses VNR28× MC84 (-24.93), VNR28× US33 (-24.25) and PDM× Pant karela 3 (-20.63). For heterosis over check parent, top crosses were VNR28× US33 (-28.94), VNR28× MC84 (-28.72) and PDM× VNR28 (-27.97). Pooled data revealed that crosses VNR 28× US33 (-20.00), VNR28× Pant karela 3 (-15.60) and VNR 28×MC84 (-13.19) had maximum value for heterobeltiosis. Over check parent the crosses PDM × VNR28 (-23.95), VNR 28×MC 84 (-21.95) and VNR 28× US33 (-19.77) showed heterotic effects. The magnitude of heterobeltiosis for node number to first female flower ranged from -47.86 to -0.02, out of which the top three crosses were VNR28 × VNR22 (-47.86), MC84 × US 33 (-40.96) and VNR 28 × Pant karela 1 (-34.75). Over the standard check (Pant karela 3), top three crosses havng maximum heterosis were VNR 28×VNR 22 (-40.20), VNR 28×US33 (-36.76) and VNR 28× MC84 (-32.35) in 2014. For year 2015, maximum value for heterobeltiosis was noted for crosses VNR28×US33 (-50.28), MC 84×US33 (-39.26) and VNR28×Pant karela 3 (-33.52). The magnitude of standard heterosis was found maximum for MC 84×PBIG2 (-44.87), VNR 28×MC84 (-40.37) and VNR 28×US33 (-36.30). For pooled season, maximum heterosis over better parent was found in crosses VNR28×US33 (-55.87), MC84×US 33 (-40.13) and VNR 28×VNR 22 (-26.08).

Standard heterosis was found maximum in crosses VNR 28× MC 84 (-36.72), VNR 28× US 33 (-36.51) and VNR 28×PBIG 2 (-29.44).

Out of all the 28 crosses, three crosses showed significant positive heterobeltiosis in season I viz., US 33×PBIG 2 (12.04), VNR 22× US 33 (5.25) and MC 84× Pant karela 3 (5.02) for fruit weight. Crosses which found to have significantly positive heterosis over standard check were US 33×PBIG 2 (9.17), VNR 22× US 33 and US 33 × Pant karela 3 (2.56) and Pant karela 1× US 33 (2.14). For season II, US 33 × PBIG 2 (11.18), Pant karela 1 ×US 33 (9.19) and VNR 22 ×Pant karela 1 (6.22) showed significant positive values for heterobeltiosis. Whereas for standard heterosis very little amount was noticed in crosses PDM× MC84 (9.45), Pant karela 1× US33 (3.66) and PDM× PBIG 2 (1.92) respectively. Pooled data revealed comparatively less than 10% of heterosis over better parent and standard check viz., US33× PBIG 2 (11.62), VNR 22× US 33 (5.73), MC 84×Pant karela 3 (3.99) and PDM×MC84 (5.63), MC 84×Pant karela 3 (3.99), Pant karela 1 ×US 33 (2.930), respectively. For number of fruits per plant, a significant amount of heterobeltiosis was observed among crosses VNR 28×Pant karela 3 (68.26), Pant karela 1× Pant karela 3 (54.31) and VNR 28×MC 84 (48.82) in season I. Crosses exhibiting highest amount over standard heterosis were VNR 28× Pant karela 3 (204.88), VNR 28× MC 84 (169.65) and VNR 28× Pant karela 1 (140.71). For next season, magnitude of heterobeltiosis was found maximum for Pant karela 1× Pant karela 3 (60.54), VNR 22× MC 84 (53.12) and PDM ×Pant karela 1 (19.64). For standard heterosis, highest significant positive values were obtained for crosses VNR 22×MC 84 (139.44), VNR 28×P ant Karela 3 (112.64) and VNR 28× MC 84 (81.46). On pooling data it was observed that the top three crosses

which were having significant positive amount of heterosis over better parent were Pant karela 1× Pant karela 3 (57.42), VNR 22×MC 84 (50.02) and VNR 28× Pant karela 3 (29.02). For heterosis over standard check, crosses found were VNR 28×Pant karela 3 (160.55), VNR 22×MC 84 (130.26) and VNR 28×MC 84 (127.27).

In 2014, the crosses which exhibited significant high magnitude of heterobeltiosis were US33×Pant karela 3 (32.29), US33×PBIG 2 (24.01) and VNR 22× US33 (18.65). Values for standard heterosis were found maximum for the crosses US33×Pant karela 3 (32.29), PDM× US 33 (31.60) and VNR 22× US33 (26.67). In 2015, the values for heterosis over better parent were found highest in crosses US33×Pant karela 3 (26.40), VNR 22×Pant karela 1 (13.98) and VNR 22× US33 (11.82), respectively. For standard heterosis, crosses US33×Pant karela 3 (26.40), MC 84 × US33 (24.41) and MC 84× Pant karela 3 (18.49) revealed highest values. Pooled data revealed that US33×Pant karela 3 (29.34), VNR 22× US 33 (15.32) and US 33× PBIG 2 (11.22) exhibited significant amount of heterobeltiosis. Maximum standard heterosis for fruit yield was found highly significant and positive for the crosses US 33× Pant karela 3 (29.34), MC 84 × US 33 (21.97) and PDM × US 33 (21.18).

The yields in F1 hybrids have been attributed to earliness, increased no. of fruits per plant and increase in fruit weight. The results of present investigation are similar to the findings of Tewari and Ram (1999) in studying heterosis for yield and other associated characters in bitter gourd using three F₁ hybrids from 3 promising genotypes (PBIG-1, PBIG-2 and PBIG-3) of diverse nature reported ample amount of heterosis for yield over local check and better parent. The best performing hybrid was PBIG-1 × PBIG-2 which showed 25.75 per cent heterosis over

better parent. Rajeswari and Natarajan (1999) evaluated 30 hybrids of bitter gourd in full diallel fashion and reported significant heterosis for sex ratio, fruit length, fruit girth, fruit weight, number of fruits per hill, yield per hill. The Hybrids, Preethi × MDU-1, Preethi × Co.1 and Arka Harit × Preethi had highest heterosis for yield per hill and fruit weight. Singh *et al.*, (2000) also evaluated seven parental lines (BG-4, BG-11, BG-23, BG-25; Pusa Do-Mausami, BG-29, BG-46 and BG-52) and their 21 F₁ hybrids of bitter gourd in half diallel fashion and they observed that BG-5, BG-23 and BG-11 were the three top performing parents for fruit yield per plant. Tamilselvi *et al.*, (2015) conducted an experiment to study the heterosis for earliness and yield characters. Evaluation of parents revealed that the parents Kashi Harit, Vadhalagundu Local, and CO₂ were identified as the best genotypes for improvement of yield and earliness

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