# Breeding bitter gourd (*Momordica charantia* L.) for simultaneous improvement in yield, nutritional quality and downy mildew disease tolerance

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## ABSTRACT

Six phenotypically diverse bitter gourd (Momordica charantia L.) parents were crossed in a full-diallel mating design to determine the extent of heterobeltiosis, mode of gene action and combining ability effects for 17 quantitative traits. Field experiments were carried out at C Block Farm, Kalyani, Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal in two consecutive seasons in 2019. The predictability ratio indicated the preponderance of non-additive gene action for most of the traits. Based on general combining ability and mean performance, two genitors BCBG-1 and BCBG-11 were identified as potential parents. Based on mean performance, heterosis, and specific combining ability effects, the crosses BCBG-10 × BCBG-14 and BCBG-3 × BCBG-10 were identified as most promising. This investigation also suggested that bitter gourd breeders to include reciprocal crosses in hybridization programs as significant effect was noticed in the present study. Promising hybrids could also be exploited in segregating generations to identify pure lines with desirable traits. Commercially exploitable bitter gourd hybrids tolerant to downy mildew disease could be developed with involvement of a single parent tolerant to this disease. The results also suggested that commercial production of bitter gourd hybrids is a possible way to enhance the productivity, fruit quality and tolerance to downy mildew disease in bitter gourd.

**Keywords**: Momordica charantia, full diallel, combining ability, gene action, heterobeltiosis, downy mildew

## INTRODUCTION

Bitter gourd (*Momordica charantia* L.) is very popular as vegetable and extensively used in folk medicine. It contains a variety of bioactive compounds including alkaloids, polypeptides, vitamins, and minerals. Qualitatively and quantitatively inherited phenotypic variation is present over a wide range in bitter gourd (Behera, 2004). This advantage has not been fully utilized to develop improved genotypes for suitability in tropical and subtropical regions of the world. Improvement in this crop can be achieved by assessing and exploiting genetic variability. But continuous market-oriented breeding led to narrow the genetic base of the crop. However, great opportunity exists to create diverse and rich gene pool with the involvement of diverse parental lines. The gynoecious and out crossing nature of bitter gourd hold promises to exploit heterosis with a range from 27 to 86 per cent depending on genotype (Behera, 2004). But monoecious is the primitive sex form found in bitter gourd and these are suitable for growing under open field conditions as they require pollination for fruit set. This facilitates easy and economic method of hybrid seed production as compared to gynoecious cultivars which require protected condition. Monoecious hybrids of bitter gourd have high potential for commercial cultivation with respect to yield, earliness and other important traits.

Considerable heterosis has been reportedfor greater vigour, faster growth and development, earliness in maturity, increased productivity and better quality in bitter gourd (Mallikarjunarao *et al.*, 2018). Heterosis of low magnitude for individual yield contributing characters may have an additive or synergistic effect on the end product (Talekar *et al.*, 2013). Identification of inbred lines with good general combining ability (GCA) and specific combining ability (SCA) is the prime source to promote heterosis in hybrids. The productivity of bitter gourd is low in India due to use of local cultivars and heavy infestations of insect-pests and diseases, particularly fungal and viral diseases. Efforts are necessary to improve host plant

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tolerance against fungal diseases, for downy mildew (*Pseudoperonospora cubensis*) diseases. Studies of genetic bases of resistance to *Pseudopernospora cubensis* resulted in identification of single-gene-mediated and polygenically inherited (Olczak-Woltman*et al.*, 2011; Das *et al.*, 2020). Early infection of downy mildew (within 20 days after sowing) is more damaging to crops leading to crop loss up to 60 per cent (Wallace *et al.*, 2014). The investigation was undertaken to determine the extent of heterosis and nature of gene action for yield, fruit quality and downy mildew disease severity traits in bitter gourd.

## MATERIALS AND METHODS

The investigation was carried out at the Research Farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, West Bengal, India, situated at 23.5° N latitude and 89° E longitude at a mean sea level of 9.75 m. Based on the wide genetic background and phenotypic diversity, six widely divergent inbred lines BCBG-1, BCBG-2, BCBG-3, BCBG-10, BCBG-11 and BCBG-14 were collected from different sources and were selected based on divergence analysis (Kundu, 2020). Parents were sown (April, 2019) in 3.00 m × 1.00 m sized plots and eight plants in each plot trained over low trellis. The cultural practices were followed for growing a good crop. The parents were crossed in a diallel fashion with reciprocals during summer season, 2019.A day before anthesis, mature male and female flower buds that were likely to open on the next day, were covered using butter paper bags in the afternoon. On thenext day, between 6 a.m. and 8 a.m., pollen grains of bagged male flowers were collected and dusted on stigmatic surfaces of female flowers ofthe female parent. The pollinated female flowers were re-covered with butter paper bags. The $F_1$ seeds were extracted; sun dried and kept in a desiccator. Selfing of parental lines was done in the same way. During the rainy season (June–September 2019), seeds of 30 $F_1$s along with six parents, after treated with Thiram @ 3 g/kg of seed were sown separately in plots at a spacing of 3 m × 1.00 m accommodating eight plants per plot following randomized block design with three replications. The soil type was sandy loam (pH 6.8). Before sowing seeds were soaked in water overnight for getting uniform germination. Three presoaked seeds were sown in each hill by dibbling method. Weak seedlings were thinned out leaving only one healthy seedling per hill after three weeks of sowing. Allplants in each plot were supported with trellises made with bamboo poles.Five randomly selected plants from 30 hybrids and six parental lines were considered to record the observations on internode length (cm), length of leaf (cm), leaf breadth (cm), length of ovary (cm), days to first female flower, days to first male flower, days to 50% female flowering, node at which first female flower appears, days to first fruit harvest, fruit length (cm), fruit diameter (cm), days to marketable fruit maturity, number of fruits per plant, fruit weight (g), fruit yield per plant (g), ascorbic acid content of fruit of marketable maturity (mg/100 g fresh) and PDI of downy mildew disease. The data were taken as per documented descriptors (ECPGR, 2008) Samples of 15 randomly selected fruits of marketable maturity were used to measure the physical and biochemical parameters from each genotype/replication. Ascorbic acid was estimated by 2,6 dichlorophenolindophenol method (Sadasivam and Manickam, 2008). Severity of downy mildew disease was recorded periodically starting from 15 days after sowing (DAS) up to 90 DAS from all plants from each plot in each replication during early morning. The spread of the disease was studied through visual observation from initiation of the disease till final harvest. The disease severity was recorded by using disease rating scale (0-9) as proposed by Yangn *et al.* (2007). The PDI was calculated from numerical ratings (Wheeler, 1969). The Percent Disease Index (PDI) was expressed as percentage from all eight plants in a replication through visual evaluation. Data were statistically analyzed using Gomez and Gomez (1984). Following the analysis of variance to test the significance for each character, the combining ability analyses were carried out as per the procedure given by Griffing's (1956) fixed effect model. The relative importance of additive and non-additive genetic effects for characters was reflected by the predictability ratio; that is, additive genetic variance expressed as a proportion of total genetic variance (Baker, 1978). The predictability ratio close to unity (greater than 0.8), indicates predominance of additive gene effects for the trait. Statistical analyses were done with Windostat (ver. 8.0, Indostat Services, Hyderabad, India).

## RESULTS AND DISCUSSION

### Analysis of variance and nature of gene action

Analysis of variance in the present study was significant for all variables (Table 1). These highly divergent parental lines indicated the suitability for developing promising hybrids. Parents vs. hybrids variance was also significant for most characters except node at which first female flower appears, days to marketable fruit maturity and fruit weight.Analysis of variance for combining ability based on Griffing's Model 1 and Method 2 exhibited significant GCA and SCA values for fruit yield per plant along with most traits in the $F_1$generation (Table 2). This indicated that inheritance of fruit yield per plant and most of the yield components, fruit quality traits and PDI of downy mildew were apparently controlled by additive and non-additive gene action. If both the GCA and SCA values are not significant for certain characters, epistatic gene effects may play a remarkable role in determining these characters (Fasahat *et al.,* 2016). The relative importance of GCA and SCA variances in determining progeny performance is better assessed by the predictability ratio proposed by Baker (1978). A greater magnitude of SCA than GCA variances, and lower predictability, ratios were observed for length of ovary, days to first male flower, days to 50% female flowering, days to first harvest and fruit diameter supported the predominant role of non-additive genetic effect in expression of these traits (Table 2). Days to marketable fruit maturity was controlled by both additive and non-additive gene action as the predictability ratio was intermediate. In contrast, predictability ratio was higher than unity for node at which first female flower appears indicating additive genetic control for the conditioning of this trait.

Most of the traits are governed by non-additive gene action. Hence, direct selection will bring no or slow genetic improvement for these traits. Heterosis breeding is the best possible option for improving these traits in bitter gourd. While a population improvement approach in the form of diallel selective mating (Radha Rani *et al.,* 2013) or mass selection with concurrent random mating (Redden and Jensen, 1974) or restricted recurrent selection by intermating the most desirable segregates followed by selection

(Shende *et al.,* 2012) could be followed for the exploitation of both additive and non-additive gene action for days to marketable fruit maturity. Due to the predominance of additive gene action for the trait node at which first female flower appears, selection should be done in later generation when the effects of non-additive gene action are minimized and the additive gene action effects will be fixed.

### Identification of good combiners

The *gca* effects of the parents used in the present study for seventeen quantitative traits are given in Table 3. It appeared that the parents differed in their *gca* effects for all the characters. No single parent was found to be a good combiner for all the traits. Among the parents, the maximum significant *gca* effects in desired directions were recorded by BCBG-1 for fruit yield per plant followed by PDI of downy mildew, ascorbic acid content, days to first female flower appearance and days to 50% female flowering. The parent BCBG-11 was the second best in the order of merit. Rest of the parents exhibited desired significant *gca* effect but in low magnitude.

Thus, BCBG-11 and BCBG-1 were found most promising genitors because they produced the maximum frequency of high yielding hybrids with appreciable downy mildew disease tolerance when crossed with other genitors. These two genitors could be considered for future utilization. Progress in improving desired traits will be slow if parental selection is based on mean performance alone. For continued improvement, selection of parents should be based on average performance and combining ability (Mukherjee, 2020). Significant and positive *gca* effects were also reported for fruit yield per plant, number of fruits per plant, ascorbic acid content of fruit, fruit length, fruit weight and fruit diameter in bitter gourd by previous workers (Mallikarjunarao *et al.,* 2018; Acharya *et al.,* 2019;).

### Identification of specific combiners

Significant *sca* effects in desired direction were recorded in four normal crosses and seven reciprocal crosses for fruit yield per plant; eight normal crosses and eleven reciprocal crosses for PDI of downy mildew; six normal crosses and

Table 1: Analysis of variance response for parents, hybrids and their interaction for different characters of bitter gourd

| Source of variation | d.f. | LL[a] | LO | DFFF | DFMF | D50FF | NFFFA | DFH | FD | DMMF | NFPP | FW | ASCA | PDI DM | FYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 0.103** | 0.075 | 1551.083 | 744.52 | 945.814 | 391.686 | 746.58** | 0.371 | 17.444 | 186.218** | 22.121 | 349661.57 | 58.129 | 0.799 |
| Parent (P) | 5 | 5.393** | 0.572** | 95.60** | 101.60** | 163.700** | 34.103 | 40.800** | 0.495* | 16.400* | 641.285** | 206.518** | 828523.09** | 961.823** | 346.968** |
| Hybrid (H) | 29 | 5.269** | 0.723** | 184.03** | 174.07** | 142.475** | 16.686 | 102.482** | 0.578** | 28.910** | 200.916** | 252.496** | 401361.65** | 427.135** | 134.615** |
| P ×H | 1 | 0.682* | 0.748** | 170.016** | 410.81** | 204.118** | 4.683 | 106.666** | 1.120* | 11.266 | 154.668** | 1.277 | 176562.97* | 377.387** | 13.252** |
| Error | 70 | 0.152 | 0.072 | 9.483 | 13.242 | 7.357 | 15.338 | 3.411 | 0.194 | 5.730 | 17.423 | 38.343 | 40254.06 | 40.064 | 0.642 |

Table 2: Analysis of variance response for combining ability (Griffing's Model 1 and Method 2

| Source of variation | d.f[a] | LL[a] | LO | DFFF | DFMF | D50FF | NFFFA | DFH | FD | DMMF | NFPP | FW | ASCA | PDI DM | FYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GCA | 5 | 1.739** | 0.196** | 44.888** | 47.522** | 19.013** | 9.202 | 9.655** | 0.085 | 14.755** | 211.588** | 69.281** | 324925.96** | 213.315** | 91.872** |
| SCA | 15 | 1.134** | 0.271** | 41.868** | 48.924** | 50.445** | 5.009 | 27.462** | 0.206** | 3.251 | 81.512** | 45.285** | 138394.79** | 185.774** | 60.483** |
| Error | 70 | 0.050 | 0.024 | 3.161 | 4.414 | 2.452 | 5.112 | 1.137 | 0.064 | 1.910 | 5.807 | 12.781 | 13418.02 | 13.354 | 0.214 |
| $\alpha^2 a$ | | 0.281 | 0.028 | 6.954 | 7.184 | 2.760 | 0.681 | 1.419 | 0.003 | 2.140 | 34.296 | 9.416 | 33.326 | 15.276 | 51917.99 |
| $\alpha^2 na$ | | 1.08 | 0.246 | 38.707 | 44.510 | 47.992 | -0.103 | 26.326 | 0.141 | 1.341 | 75.704 | 32.504 | 172.419 | 60.269 | 124976.77 |
| $\frac{\alpha^2 a}{\alpha^2 a + \alpha^2 na}$ | | 0.206 | 0.104 | 0.152 | 0.138 | 0.054 | 1.178 | 0.051 | 0.023 | 0.614 | 0.311 | 0.224 | 0.293 | 0.162 | 0.202 |

*\*\* Significant at P ≤ 0.01*
*[a]LL= Leaf length(cm); LO = Length of ovary(cm); DFFF = Days to first female flower; DFMF= Days to first male flower; D50FF= Days to 50% female flowering; NFFFA= Node at which first female flower appears; DFH= Days to first harvest; FD= Fruit diameter(cm); DMMF=Days to marketable maturity of fruit; NFPP= Number of fruits per plant; FW=Fruit weight(g); ASCA= Ascorbic acid content(mg/100g); PDI DM= Percent disease index of downy mildew(%)at 90 DAS; FYPP= Fruit yield per plant(g).*
*$\alpha^2 a$ = Additive genetic variance.*
*$\alpha^2 na$ = Non-additive genetic variance.*
*$\alpha^2 a / \alpha^2 a + \alpha^2 na$ = Ratio of additive genetic variance to total genetic variance.*

nine reciprocal crosses for ascorbic acid content of fruit; three normal crosses and six reciprocal crosses for fruit weight; three normal crosses and seven reciprocal crosses for number of fruits/plant; single normal cross and two reciprocal crosses for fruit diameter; three normal crosses and four reciprocal crosses for fruit length; six normal crosses and five reciprocal crosses for days to 50% female flowering. Other normal and reciprocal crosses exhibited significant *sca* effects for rest of the characters but their magnitude were low (Table 3). Among normal crosses, four cross combinations BCBG-1 × BCBG-2, BCBG-3 × BCBG-10, BCBG-10 × BCBG-11 and BCBG-10 × BCBG-14 exhibited significant *sca* effects in desired direction for fruit yield per plant along with PDI of downy mildew and other desirable traits. However, the crosses BCBG-1 × BCBG-2 and BCBG-10 × BCBG-11 involved one of the parents as good general combiner for fruit yield per plant along with percent disease index of downy mildew, indicated that these cross combinations are expected to produce segregants with high yield and better tolerance to downy mildew disease in subsequent generations through simple pedigree method (Table 3).

Among the reciprocal crosses, the most promising cross was BCPG-14 × BCPG-1 followed by BCPG-14 × BCPG-10 which exhibited desired significant *sca* effects for fruit yield/plant, PDI of downy mildew along with other desirable traits. The cross BCPG-14 × BCPG-1 can further be exploited for generating superior lines. Interestingly, the most promising normal cross BCBG-1 × BCBG-2 did not exhibit significant *sca* effects for fruit yield/plant and other desirable traits in reverse combination. The same trend was noticed in the most promising reciprocal cross BCPG-14 × BCPG-1(Table 3).The significant difference between normal and reciprocal cross depicted the maternal effect. The results clearly reflects that in cross pollinated crop like bitter gourd, reciprocal cross also played a significant role which justifies the proposition of full diallel mating design in the present study. No normal cross exhibited significant *sca* effects for node at which first female flower appears which agreed well with the findings of Acharya *et al.*,(2019).

Based on *sca* effects and *per se* performance, three cross combinations namely,

BCBG-1 × BCBG-2 followed by BCBG-10 × BCBG-11 and BCBG-10 × BCBG-14 could be identified as good specific combiners for future breeding of bitter gourd. Based on *gca* effects, the promising heterotic crosses involved three types of combinations namely, Good × Poor, Poor × Good and Poor × Poor, where good denotes significant *gca* effect of parent in desired direction and poor stands for non-significant *gca* effect of the parent (Table 4).Good × Poor cross combinations (BCBG-2 × BCBG-1)for length of internode and length of ovary; BCBG-11 × BCBG-14 for days to marketable fruit maturity or Poor × Good crosses (BCBG-14 × BCBG-2 for leaf breadth; BCBG-2 × BCBG-3 for days to first female flower appearance and days to first harvest; BCBG-10 × BCBG-11 for fruit length involved at least one parent with significant *gca* effect which indicated that predominant additive effect in good combiner and possibly complementary epistatic effect in poor combiner and these two gene actions acted in complementary fashion to maximize the expression. In crosses involving poor × poor category (e.g.,BCBG-10 × BCBG-14 for fruit yield/plant; BCBG-3 × BCBG-10 for PDI of downy mildew and fruit yield per plant), *sca* effects played a very important role and high performance was due to non-additive gene action (Bhutia *et al.*, 2015). Heterosis breeding in such case would be effective for improvement of traits.

**Extent of heterosis**

Manifestation of heterosis is very common in cross pollinated species like bitter gourd. Gynoecy is also reported in this crop which could be a useful tool to exploit heterosis on commercial scale. Currently, hybrid seed is produced by hand pollination without emasculation (Behara, 2004).Three crosses 'BCBG-10 × BCBG-14','BCBG-3 × BCBG-10' and 'BCBG-10×BCBG-3' which showed the maximum significant heterobeltiosis for fruit yield per plant along with significant heterosis in desired direction over better-parent for PDI of downy mildew, number of fruits per plant, days to 50% female flowering (Table 4) can be considered for exploitation. Downy mildew is one of the most dreaded foliar diseases of bitter gourd whose early infection cause 60% yield reduction (Wallace *et al.*, 2014). In India, it is

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Table 3: Estimates of general- and specific-combining ability effects of parents and hybrids for growth, and flowering traits of bitter gourd

| Parent | Leaf length | Length of ovary | Days to first female flower | Days to first male flower | Days to 50% female flowering | Node at which first female flower appears | Days to first harvest | Fruit diameter | Days to marketable maturity | No. of fruits /plant | Fruit weight | Fruit yield/plant | Ascorbic acid content | % disease index of downy mildew at 90 DAS |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BCBG-1 | -0.222** | -0.097* | -1.861** | -0.222 | -1.731** | -0.415 | -0.111 | -0.005 | 1.444** | 6.959** | 0.093 | 261.149** | 6.435** | -4.371** |
| BCBG-2 | 0.561** | 0.186** | 0.389 | 1.194* | 0.157 | 1.162 | 0.889** | 0.063 | 0.528 | -2.907** | 4.292** | 4.567 | -3.956** | 0.477** |
| BCBG-3 | -0.547** | -0.122** | -1.444** | -2.889** | -0.676 | -1.227* | -1.111** | 0.074 | -0.639 | -2.610** | -2.655** | -195.052** | -1.560 | 1.144** |
| BCBG-10 | 0.236** | 0.103* | 1.139* | 0.861 | 0.602 | 0.071 | 0.722* | -0.158* | 0.278 | 0.293 | -1.353 | -24.239 | -1.952* | 2.419** |
| BCBG-11 | -0.064 | 0.036 | 3.139** | 2.611** | 1.991** | 0.803 | 0.639* | 0.034 | -1.806** | 2.515** | -1.051 | 93.954** | -3.023** | -2.256** |
| BCBG-14 | 0.036 | -0.106* | -1.361** | -1.556** | -0.343 | -0.394 | -1.028** | -0.008 | 0.194 | -4.249** | 0.675 | -140.379** | 4.055** | 2.587** |
| SE (gi) | 0.153 | 0.105 | 1.204 | 1.423 | 1.061 | 1.532 | 0.722 | 0.173 | 0.936 | 1.633 | 2.422 | 78.469 | 2.476 | 0.313 |
| **Hybrid (Direct cross)** | | | | | | | | | | | | | | |
| BCBG-1 × BCBG -2 | -0.394* | 0.531** | 2.444* | 4.056** | 2.981** | 0.647 | 2.444** | -0.079 | 0.639 | 2.407 | 8.425** | 315.156** | -9.149** | -2.829** |
| BCBG -1 × BCBG -3 | 0.564** | -0.061 | -3.722** | -3.361* | -2.685* | 0.691 | -0.056 | 0.395* | 1.806* | -2.390 | -2.184 | -87.182 | 0.970 | 1.647** |
| BCBG -1 × BCBG -10 | 0.281 | 0.064 | 4.694** | 1.389 | 4.204** | 2.207 | 3.611** | 0.027 | -0.111 | -1.293 | 5.675* | 104.687 | -14.108** | -2.957** |
| BCBG -1 × BCBG -11 | 0.531** | -0.069 | -6.806** | -8.361** | -6.352** | -0.464 | -5.806** | 0.300 | 0.472 | -5.015** | -1.367 | -202.089* | 8.318** | 2.632** |
| BCBG -1 × BCBG -14 | 0.281 | -0.078 | 1.194 | 7.806** | 2.481* | -0.481 | 0.361 | -0.478** | -0.528 | -0.751 | 0.077 | 36.037 | 5.865* | -1.136** |
| BCBG -2 × BCBG -3 | 0.231 | -0.394** | -1.472 | -2.778* | -1.074 | 0.764 | -3.056 *** | 0.242 | -0.778 | 0.227 | -1.862 | -15.373 | -0.814 | -1.034 ** |
| BCBG -2 × BCBG -10 | 0.747** | 0.231* | -0.056 | -1.028 | 1.648 | 1.305 | -0.389 | 0.059 | -0.694 | -6.676** | -1.808 | -312.065** | 2.512 | 3.554** |
| BCBG -2 × BCBG -11 | -1.403** | 0.147 | 2.444* | 3.722** | 5.759** | -2.741 | 2.694** | -0.518** | -0.611 | -7.648** | -2.240 | -393.867** | 5.264* | 2.728** |
| BCBG -2 × BCBG -14 | 0.947** | -0.261* | 1.944 | -3.611* | -0.907 | 0.371 | 2.861** | 0.129 | 0.889 | 0.616 | -1.472 | -13.603 | 12.471** | 3.436** |
| BCBG -3 × BCBG -10 | -0.344* | -0.511** | -8.722** | -4.444** | -7.019** | -1.070 | -5.389** | -0.117 | 1.472 | 12.777** | -1.977 | 243.308** | 8.507** | -10.498** |
| BCBG -3 × BCBG -11 | -0.244 | -0.094 | 5.778** | 1.806 | 4.593** | 0.818 | 4.694** | 0.136 | -0.944 | -4.112* | -1.952 | -141.193 | -4.764* | 1.819** |
| BCBG -3 × BCBG -14 | -0.394* | 0.297** | -2.222 | -0.028 | -3.074** | -1.385 | -2.639** | 0.278 | 0.556 | -2.681 | 0.155 | -73.919 | -13.285** | 7.815** |
| BCBG -10 × BCBG-11 | -0.778** | 0.331** | -0.806 | -0.944 | -5.685** | -1.445 | -2.139** | -0.002 | 2.139* | 3.152* | 5.500* | 249.304** | 12.279** | -4.743** |
| BCBG -10 × BCBG-14 | -0.528** | -0.428** | -1.306 | -5.278** | -1.852 | -0.133 | -1.472* | 0.284 | -0.861 | 3.666* | -0.437 | 178.048* | -1.718 | -2.182** |
| BCBG -11 × BCBG-14 | -0.028 | -0.261* | -1.806 | -2.028 | -2.241* | -0.480 | -2.389** | 0.028 | -1.278 | -0.306 | -5.264* | -158.482* | 0.193 | -0.601* |
| SE (sij) | 0.291 | 0.201 | 2.292 | 2.708 | 2.018 | 2.914 | 1.374 | 0.329 | 1.781 | 3.106 | 4.608 | 149.296 | 4.710 | 0.596 |
| **Hybrid (Reciprocal cross)** | | | | | | | | | | | | | | |
| BCBG -2 × BCBG -1 | -0.850** | -0.400** | -2.500* | -2.000 | -2.500* | -1.365 | -4.000** | 0.445* | -2.000* | -2.500 | 2.200 | -46.283 | 0.335 | 1.298** |
| BCBG -3 × BCBG -1 | -0.700** | 0.00 | -2.500* | 0.500 | 3.000** | 1.610 | -0.500 | 0.00 | 5.000** | 7.000** | 1.495 | 275.627** | 1.260 | -2.868** |
| BCBG -10 × BCBG -1 | 0.700** | -0.250* | 5.500** | 6.000** | 5.167** | -2.597 | 3.000** | 0.210 | -1.000 | 1.000 | -10.165** | -230.548** | 8.460** | 0.477 |
| BCBG -11 × BCBG -1 | -0.550** | -0.150 | -1.000 | 0.00 | 2.000 | 0.325 | 1.500* | -0.065 | 2.500** | 4.500** | 7.075** | 346.375** | 9.665** | -1.120** |
| BCBG -14 × BCBG -1 | 2.300** | 0.00 | 9.500** | 15.000** | 11.500** | 0.870 | 8.000** | -0.755* | -1.500 | 5.000** | 10.765** | 430.582** | 7.560** | -3.358** |
| BCBG -3 × BCBG -2 | 0.050 | 0.150 | -12.000** | -4.500** | -1.731** | -2.900* | -8.500** | 0.065 | 3.500** | 5.750** | -3.085 | 167.937* | -2.525 | -4.125** |
| BCBG -10 × BCBG -2 | -0.250 | 0.300** | 6.000** | 1.000 | 5.500** | 1.020 | 4.000** | -0.380* | -1.500 | 0.750 | 3.310 | 61.631 | 7.980** | -6.092** |
| BCBG -11 × BCBG -2 | -1.700** | -0.050 | -1.500 | -2.500 | 1.000 | 0.065 | 0.00 | 0.315 | 1.500 | 2.000 | -5.660* | 10.215 | 9.660** | -0.367 |
| BCBG -14 × BCBG -2 | -0.450** | -0.300** | -4.500** | 2.000 | -5.000** | 0.350 | -1.500* | 0.190 | 3.000** | 4.500** | 7.935** | 295.663** | 16.385** | -9.785** |
| BCBG -10 × BCBG -3 | -1.250** | -0.350** | -3.500** | -6.500** | 1.000 | -2.915* | -3.000** | -0.235 | -1.500 | 13.500** | -13.685** | -0.188 | 6.290* | -0.027 |
| BCBG -11 × BCBG -3 | -0.650** | -0.100 | -2.000 | -7.500** | -2.000 | -0.575 | -3.000** | 0.550** | -1.000 | 0.167 | 4.498 | 83.953 | 9.732** | -3.658** |
| BCBG -14 × BCBG -3 | -0.300** | -0.250* | -8.500** | -1.500 | -4.000** | -2.135 | -6.000** | 0.160 | 2.500** | 2.500 | -5.965* | 30.372 | -8.155** | -2.045** |
| BCBG -11 × BCBG-10 | -0.700** | 0.850** | -10.000** | -10.500** | 0.00 | -0.170 | -8.000** | 0.100 | -3.000** | 0.00 | 9.845** | 266.710** | 11.570** | -0.858** |
| BCBG -14 × BCBG-10 | -1.450** | -0.050 | -4.000** | 0.00 | -3.500** | -0.075 | -1.000 | -0.145 | 3.000** | 6.250** | 7.985** | 400.497** | 0.840 | -7.660** |
| BCBG -14 × BCBG-11 | 1.450** | 0.450** | 5.500** | 1.000 | 3.500** | 3.770* | 4.000** | -0.350* | -1.500 | -2.000 | 9.180** | 117.625 | 3.360 | -3.005** |
| SE (sij) | 0.291 | 0.201 | 2.292 | 2.708 | 2.018 | 2.914 | 1.374 | 0.329 | 1.781 | 3.106 | 4.608 | 149.296 | 4.710 | 0.596 |

*, ** Significant at P≤ 0.05 and P≤ 0.01, respectively

infecting bitter gourd all ecosystems except high altitude temperate zone in the Himalaya (Kumar and Pathak, 2018).

The significant difference between direct and reciprocal cross depicted that hybrid performance for related traits is dependent on the cross direction (Machida *et al.*, 2010). Principally reciprocal differences are attributable to maternal and non-maternal effects in which maternal effect is caused by cytoplasmic genetic factors, while non-maternal effect is explained by the interaction between nuclear genes and cytoplasmic gene effects (Dermail, 2018). In practical breeding terms, the choice of the female parent in a single cross hybrid may influence agronomic performance and yields in case of major contribution of maternal effect. Reciprocal cross effects significantly impact heterosis (both mid-parent and better-parent) for most traits observed. Considering both high heterosis percentage and significant reciprocal effects on fruit yield and other desirable horticultural traits, superior hybrids were potentially derived from bitter gourd $F_1$ hybrids tested. The reciprocal effects may be due to cytoplasmic inheritance and maternal effect (Mahanta and Barua, 2020). This investigation suggests bitter gourd breeders to include reciprocal crosses in their mating design.

Table 4: List of most promising cross combinations, their corresponding *per se* performance, *gca* effects and type of cross combination

| Character | Promising crosses with heterobeltiosis (%) in desired direction and *per se* performance | Parents with *gca* effects and *per se* performance | Type of cross combination |
|---|---|---|---|
| Leaf length | BCBG-1 × BCBG-14  (31.71 **, 10.80 cm) | BCBG-1 (-0.222 **,6.70 cm), BCBG-14 (0.036,8.20 cm) | Poor × Poor |
| Length of ovary | BCBG-2 × BCBG-1 (40.91 **, 3.10 cm) | BCBG-2 (0.186 **, 2.20 cm), BCBG-1 (-0.097 *,1.50 cm) | Good × Poor |
| Days to first female flower appearance | BCBG-2 × BCBG-3 (-36.07 **, 39.00) | BCBG-2 (0.389, 49.00), BCBG-3 (-1.444 **, 61.00) | Poor × Good |
| Days to 50% female flowering | BCBG-10 × BCBG-11 (-30.99 **, 49.00) | BCBG-10 (0.602, 71.00), BCBG-11 (1.991 **, 69.00) | Poor × Poor |
| Node at which first female flower appears | BCBG-14 × BCBG-11 ( -40.57 **, 14.30) | BCBG-14 (-0.394, 19.46), BCBG-11 (0.803, 24.06) | Poor  ×Poor |
| Days to first harvest | BCBG-2 × BCBG-3 (-22.54 **, 55.00) | BCBG-2 (0.889 **, 64.00), BCBG-3 (-1.111 **, 71.00) | Poor  ×Good |
| Days to marketable fruit maturity | BCBG-11 × BCBG-14 ( -40.00 **, 9.00) | BCBG-11 (-1.806 **, 10.00), BCBG-14 (0.194, 15.00 ) | Good × Poor |
| Number of fruits/plant | BCBG-3 × BCBG-10 (275.00 **, 45.00) | BCBG-3 (-2.610 **, 12.00), BCBG-10 (0.293, 10.00 ) | Poor ×  Poor |
| | BCBG-10 × BCBG-14 (125.00 **, 27.00) | BCBG-10 (0.293, 10.00 ), BCBG-14 (-4.249 **, 12.00) | Poor × Poor |
| Fruit weight | BCBG-10 × BCBG-1 (87.10 **, 52.07 g) | BCBG-10 (-1.353, 27.83 g), BCBG-1 (0.093, 27.05 g) | Poor × Poor |
| Ascorbic acid content of fruit | BCBG-2 × BCBG-11 (72.53 **, 62.18 mg) | BCBG-2 (-3.956 **, 36.04 mg), BCBG-11 (-3.023 **, 26.90 mg) | Poor × Poor |
| PDI of downy mildew at 90 DAS | BCBG-3 × BCBG-10 (-68.16 **, 13.37 ) | BCBG-3 (1.144 **, 22.87), BCBG-10 (2.419 **, 41.997) | Poor × Poor |
| Fruit yield/plant | BCBG-10 × BCBG-14 (124.10**, 1196.84 g) | BCBG-10 (-24.239, 271.153 g), BCBG-14 (-140.379 **, 534.07 g) | Poor × Poor |
| | BCBG-3 × BCBG-10 (72.69**, 806.74) | BCBG-3 (-195.052 **, 467.16 g), BCBG-10 (-24.239, 271.15 g) | Poor × Poor |

*,** Significant at P≤ 0.05 and P≤ 0.01, respectively*

For yield attributes, some crosses were non-heterotic, which may be ascribed to internal cancellation of positive and negative effects exhibited by the parents involved in a cross combination and can also happen when the dominance is not unidirectional.The superiority of the $F_1$ hybrids over the better parent *vis-a-vis* the standard hybrid can profitably be exploited

for commercial production. More than 30 % heterobeltiosis over better parent could reduce the cost of hybrid seed (Reddy *et al.*, 2013). Thus, the crosses showing more than 30 % heterobeltiosis may be exploited for hybrid bitter gourd production. In the present study, the moderate extent of heterobeltiosis, as observed for yield and yield components, could be attributed to its cross-pollinated nature.

The preponderance of non-additive gene action is witnessed for fruit yield per plant and other attributing components. Heterosis breeding is the best strategy for improvement of traits in bitter gourd. Two genitors BCBG-1 and 'BCBG-11 could be used as parents for the development of high yielding and downy mildew tolerant recombinants. The high magnitude of heterobeltiosis of promising hybrids BCBG-10 × BCBG-14 and BCBG-3 × BCBG-10 could be commercially exploited.

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