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Identification of heterobeltosis for quantitative traits in mungbean

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Abstract

Diallel analysis was performed using ten mungbean genotypes and their 45 F_1 hybrids. The experiment was laid down in Randomized Block Design (RBD) with three replications during *kharif* 2012 at Centre of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar, Gujarat. The observations were recorded both as visual assessment (days to flowering and days to maturity) and measurement on randomly selected five competitive individual plants (plant height, number of branches per plant, pods per plant, pod length, seeds per pod, 100-seed weight, seed yield per plant and protein content). The hybrid K 851 x Meha, registered significant positive heterobeltiosis for seed yield per plant. Heterosis in seed yield per plant was reflected mainly through component trait pods per plant.

Keywords: Mungbean, heterosis, heterobeltosis, yield

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek.] Commonly known as greengram is the most important pulse crop in India. This is an important seed legume which have prime role in meeting the quantitative and qualitative requirement of food and protein in India and other Asian countries. According to Vavilov (1926) [15], the mungbean have been originated in Hindustan region of Asia *i.e.*, Indian sub-continent. Genus *Vigna* belongs to tribe Phaseoleae of the family Fabaceae (Leguminosae) and it contains 104 accepted species (ILDIS, 2013) [5]. *Vigna radiata* (L.) R. Wilczek is having two synonyms *i.e.*, *Phaseolus aureus* Roxb and *Phaseolus radiatus* L. and the species also prescribed having two botanical varieties as *Vigna radiata* var. *radiata* (L.) R. Wilczek and *Vigna radiata* var. *sublobata* (Roxb.) Verdc. Pulses contribute as a major source of dietary protein for the large portion of vegetarian population of the world. Per capita availability of pulses is only 36 g/person/day in India against the World Health Organization recommendation of 80 g/person/day. The seed contains, protein (22.88 to 24.65%), carbohydrates (62.6%), crude fibre (4.30 to 4.80%) and lipids (1.53 to 2.63%). Like other pulses, the protein of mungbean is rich in lysine, an essential amino acid that is absent in cereal grains (Saleem *et al*., 1998) [11]. The diploid chromosome number of mungbean is 2n = 22 (Karpechenko, 1925 and Krishnan and De, 1965) [7, 8]. Mungbean is self-pollinated crop. Improved varieties have been developed in Taiwan and India. Genetic improvement in this crop has been made primarily through conventional techniques such as selection from local material and pedigree method of breeding. Heterosis has been reported in this crop. However, its commercial exploitation has not been possible till now because of cleistogamous nature of flower. Therefore, the development of pure lines and stable populations developed following pedigree method has been the main approach pursued by plant breeders working on this crop.

The yield level of this crop has been increased through genetic improvement such as incorporation of early and uniform maturity, better fertilizer response, photo thermo insensitivity, reduced vegetative growth, wider adaptability and resistances to disease and pest after selection from hybrid progenies, multiple-parent crosses; repetitive intercrossing (Dahiya and Singh, 1985) [4]. Most early varieties were developed by pureline selection from native germplasm. Hybridization is the most important breeding procedure for crops like wheat and mungbean (Poehlman, 1991) [10]. Taiwan deals with breeding of mungbean and maintains global gene pool. In India around one hundred varieties have been released in mungbean under the project AICRP MULLaRP, which includes popular cultivars like Pusa Baisakhi and K-851.

Yield of mungbean is low as compared to cereals. Like other pulses, this crop is cultivated for hundreds of years under marginal conditions of moisture stress and low soil fertility. Under these conditions of poor crop management, natural selection has had a much greater role in determining the plant type and other characteristics of this crop than human selection. The genes for agronomic characteristics responsible for high yield have been eroded from mungbean like other marginal crops, which had relatively little value under the competitive and stress conditions of a wild habitat or primitive agriculture (Tiwari *et al.,* 1993) [14]. Diallel analysis provides a systemic approach for identification of superior parent and crosses which is the basic material on which the success of a breeding programme depends. The advantage of the diallel analysis is that, it gives better picture of genetic information of the material under investigation in a single generation. Genetic information regarding heterosis provides a clue for selecting the most suitable parents for hybridization. The presence of heterosis can only be utilised in highly self-pollinated pulse crops for the development of high yielding pureline varieties (Singh 1971) [13].

Material and Methods

Location and Climatic Condition

The present investigation was conducted at the Centre of Excellence for Research on Pulses, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar, and Gujarat State during the year 2012-13. Geographically, Sardarkrushinagar is situated at 24°-12’N latitude and 72°-19’E longitude having an altitude of 154.52 metres above mean sea level. It has typical semi-arid climate with moderate rainfall during June to October. The soil of the experimental plot was sandy loam.

Experimental Material

The experimental material consisting of ten genotypes (GM 2, GM 3, GM 4, K 851, Meha, Pusa Vishal, Vamban 2, Hum-1, SML-668 and COGG-192) were obtained from the Centre of Excellence for Research on Pulses, Sardarkrushinagar. The pedigree and source of the genotypes is given in Table 1.

Table 1: Paedigree of parental lines

Sr. No.	Genotypes	Pedigree	Source
1.	GM 4	GM 3 x Pusa Vishal 9933	SDAU, S.K. Nagar
2.	GM 2	Selection from local Germplasm	SDAU, S.K. Nagar
3.	GM 3	ML 9 x GM 2	SDAU, S.K. Nagar
4	K-851	4453-3 x T-44	CSAU, Kanpur
5.	Meha	Pant Mung 2 x AMP 36	IIPR, Kanpur
6.	Pusa Vishal	Selection from NK 92	IARI (New Delhi)
7.	Vamban-2	VGG 4 x MH 309	TNAU, Vamban
8.	Hum-1	BHUM1 x Pant U-30	BHU, Varanasi
9.	SML 668	Selection from 94	PAU, Ludhiana
10.	COGG-192	MGG-366 x CO GG902	TNAU, Coimbatore

The selfed seed for each of the ten parental lines was also produced simultaneously. Finally, the experimental material comprised of ten parental lines and their 45 hybrids.

Field Experiment

The plots of 55 genotypes comprising of 10 parents and their 45 F_1 were planted in a randomised block design with three replications in second week of July, 2012. The plot size for each genotype was 2.00m x 0.45 m keeping 45cm row to row and 10 cm plant to plant distance. All agronomical and plant protection practices were followed throughout the crop duration. The crossing in diallel fashion excluding reciprocals among the ten genotypes was carried out during summer 2012. The standard agronomical practices were followed to raise the parental plants under favourable field conditions for satisfactory emasculation, crossing and normal pod development. The seed of 45 crosses was produced through hand emasculation and hand pollination (Table 2).

Table 2: Diallel crosses

Sr. No.	Hybrid combinations	Sr. No.	Hybrid combinations
1.	GM 2 x GM 3	24.	GM 4 x COGG 192
2.	GM 2 x GM 4	25.	K-851 x Meha
3.	GM 2 x K 851	26.	K-851 x Pusa Vishal
4.	GM 2 x Meha	27.	K-851 x Vamban 2
5.	GM 2 x Pusa Vishal	28.	K-851 x Hum 1
6.	GM 2 x Vamban 2	29.	K-851 x SML668
7.	GM 2 x Hum 1	30.	K-851 x COGG 192
8.	GM 2 x SML 668	31.	Meha x Pusa Vishal
9.	GM 2 x COGG 192	32.	Meha x Vamban 2
10.	GM 3 x GM 4	33.	Meha x Hum 1
11.	GM 3 x K 851	34.	Meha x SML 668
12.	GM 3 x Meha	35.	Meha x COGG 192
13.	GM 3 x Pusa Vishal	36.	Pusa Vishal x Vamban 2
14.	GM 3 x Vamban 2	37.	Pusa Vishal x Hum
15.	GM 3 x Hum 1	38.	Pusa Vishal x SML 668
16.	GM 3 x SML 668	39.	Pusa Vishal x COGG 192
17.	GM 3 x COGG 192	40.	Vamban 2 x Hum 1
18.	GM 4 x K 851	41.	Vamban 2 x SML 668
19.	GM 4 x Meha	41.	Vamban 2 x COGG 192
20.	GM 4 x Pusa Vishal	43.	Hum 1 x SML 668
21.	GM 4 x Vamban 2	44.	Hum 1 x COGG 192
22.	GM 4 x Hum 1	45.	SML 668 x COGG 192
23.	GM 4 x SML 668		

Result and Discussion

Magnitude of Heterosis

The heterosis was estimated as per cent increase or decrease in F_1 value over mid parental values (Relative Heterosis) and over better parental values (Heterobeltiosis) for various traits. The Tables 3 to 7, show heterosis over mid parent and better parent for various characters, plant height, days to maturity, days to flowering, branches per plant, pods per plant, pod length, seed yield per plant, 100-seed weight and protein content. Negative heterosis is desirable for developmental traits like days to flowering and days to maturity.

1. Days to Flowering

The range of relative heterosis was observed from-8.96 per cent (GM 4 x Vamban-2) to 8.61 per cent (Vamban-2 x Hum-1). The heterobeltiosis among the hybrids varied between -0.81 (GM 4 x K-851) and 17.89 (Vamban-2 x Hum-1). Data revealed that out of 45 hybrids, 6 and 1 hybrids showed significant desirable heterosis over mid parent and better parent respectively.

2. Days to Maturity

The relative heterosis ranged from-4.30 (K-851 x Pusa Vishal) to 5.82 (Hum-1 x SML 668). Heterobeltiosis varied between -0.54 (GM 4 x Hum-1) and 9.14 (Vamban-2 x SML 668). Data showed that, 4 and 1 hybrids exhibited significant negative heterosis over mid parent and better parent, respectively.

3. Plant Height

The relative heterosis ranged from-43.31 (GM 4 x Vamban-2) to 60.00 (GM3 x Pusa Vishal). The heterobeltiosis varied between -34.64 (GM 4 x Vamban-2) and 89.09 (GM 3 x Pusa Vishal). Out of 45 hybrids, 12 and 5 hybrids exhibited significant desirable heterosis over mid parent and better parent, respectively.

The cross combination GM 4 x Vamban-2 registered the highest significant negative heterosis over mid parent (-43.31) and better parent (-34.64).

4. Branches per Plant

The relative heterosis varied between-20. 00 (GM 4 x COGG-192) and 17.86 (GM 2 x Meha). Heterobeltiosis ranged from-26.67 (GM 4 x COGG-192) to 13.33 (K-851 x Pusa Vishal). The data revealed that one cross registered significant positive heterosis over mid parent and one cross over better parent.

5. Pods per Plant

The relative heterosis varied between-78.06 (GM 2 x GM 4) and 61.15 (Meha x SML 668). The heterobeltiosis ranged from -62.16 (GM 3 x COGG-192) and 42.14 (K-851 x SML 668). The estimates of heterosis revealed that 20 and 12 hybrids exhibited significant desirable positive heterosis over mid-parent and better parent, respectively.

6. Pod Length

The relative heterosis varied between-19.01 (Meha x Vamban-2) and 25.24 (Pusa Vishal x Hum-1). The heterobeltiosis ranged from -19.75 (Meha x Vamban-2) to 23.76 (Pusa Vishal x Hum-1). The cross combination Pusa Vishal x Hum-1 registered significant positive heterosis over both mid parent value (25.24) and better parent (23.76).

Data showed that out of 45 hybrids, 6 and 2 hybrids showed significant positive heterosis over mid parent and better parent, respectively.

7. Seeds per Pods

The relative heterosis varied between -35.79 (GM 3 x Hum-1) and 58.97 (K-851 x Pusa Vishal). Heterobeltiosis ranged from -39.00 (GM 3 x Hum-1) to 50.30 (K-851 x Pusa Vishal). Data showed that out of 45 hybrids, one hybrid each showed significant positive heterosis over mid parent and one hybrid over better parent.

The cross combination K-851 x Pusa Vishal registered significant positive heterosis over mid parent (58.97) as well as over better parent (50.30).

8. Seed Yield per Plant

Most of the crosses registered significant negative heterosis and only one hybrid (K-851 x Meha) recorded significant positive heterosis for seed yield per plant. The range of relative heterosis varied between -66.67 (GM 3 x COGG-192) and 116 (K-851 x Meha). Heterobeltiosis ranged from -66.67 (GM 3 x COGG-192) to 68.75 (K-851 x Meha). The data revealed that the hybrid K-851 x Meha showed significant positive heterosis over mid parent and better parent.

9. 100-Seed Weight

The relative heterosis varied between -26.61 (GM 4 x SML 668) and 38.61 (GM 2 x Vamban-2). The heterobeltiosis ranged from -31.53 (GM 3 x SML 668) to 30.44 (GM 2 x Vamban-2). The data revealed that 12 and 6 hybrids showed significant positive heterosis over mid parents and better parent, respectively.

In cross combination GM 2 x Vamban-2 registered significant positive heterosis over mid parent (38. 61) and better parent (30.44).

10. Protein Content

The estimates of relative heterosis varied between-7.71 (Vamban-2 x Hum-1) and 10.31 (Pusa Vishal x SML 668). Heterobeltiosis ranged from -9.43 (GM 3 x Pusa Vishal) to 7.15 (Pusa Vishal x SML 668). A perusal of the results showed that 24 and 14 hybrids exhibited significant and positive heterosis over mid-parental and better parental values, respectively.

Thirteen cross combinations registered significant positive heterosis over mid parental values and better parents.

In autogamous crop like mungbean, the possibility of commercial exploitation of heterosis is rather remote, particularly because of floral biology and practical difficulties involved in seed production. The main objective of heterosis in the present study was to help in identifying superior cross combination and their exploitation to get better transgressive segregants. The knowledge of heterosis would help in elimination of poor crosses in early generation of testing. While reviewing the literature, it could be concluded that appreciable heterosis was present in pulse crops, including mungbean (Bhatnagar and Singh, 1964) [3]. The significance of mean sum of squares due to parents vs. hybrids for most of the traits indicated the presence of heterosis.

For seed yield per plant, only one cross (K 851 x Meha) registered significant positive heterosis and most other crosses (11 for relative heterosis and 18 for heterobeltiosis) registered negative heterosis. The hybrid K-851 x Meha, registered significant positive heterobeltiosis (68.75%) for seed yield per plant. This cross also manifested positive significant heterobeltiosis (31.21%) for pods per plant.

Maximum number of crosses expressed relative heterosis (24 crosses) and heterobeltiosis (14 crosses) for protein content followed by number of pods per plant (20 and 12 crosses, respectively) and 100-seed weight (12 and 6 crosses, respectively). The degree of heterosis varied from cross to cross for all the traits. Considerable heterosis in certain crosses and low in others revealed that nature of gene action varied with the genetic make-up of the parents. Heterobeltiosis for yield and components traits have been reported in mungbean by Patil *et al*. (1996) [9], Joseph and Santoshkumar (2000) [6], Aher *et al*. (2000) [1], Sawale *et al*. (2003) [12] and Barad *et al*. (2008) [2].

Summary and Conclusion

The observations were recorded as visual assessment for days to flowering and days to maturity and measurement on randomly selected five competitive individual plants for plant height (cm), branches per plant (No), pods per plant (No), pod length (cm), seeds per pod (No), seed yield per plant (g), 100-seed weight (g) and protein content (%) in seed.

The hybrid K-851 x Meha registered significant positive heterobeltiosis for seed yield per plant exhibiting high SCA effects with average to poor GCA effects of the parents indicated important role of dominance and epistatic gene effects in its phenotypic performance.

Table 3: Heterosis percentage in F_1 hybrid over mid parents [MP] and better parents [BP] for characters, days to flowering and day to maturity

Sr. No.	Hybrid	Days to flowering		Days to maturity	
		Mid Parent	Better Parent	Mid Parent	Better Parent
1.	GM 2 x GM 3	2.38*	2.38	1.31	2.12

2.	GM 2 x GM 4	4.03**	5.74**	1.87	2.69
3.	GM 2 x K-851	2.38*	2.38	1.87	2.69
4.	GM 2 x Meha	1.98	2.38	1.58	2.12
5.	GM 2 x Pusa Vishal	2.38*	2.39	1.87	2.69
6.	GM 2 x Vamban-2	-4.80**	2.38	-2.53*	2.12
7.	GM 2 x Hum-1	3.61**	4.88**	1.31	2.12
8.	GM 2 x SML 668	3.20**	4.03**	1.87	2.69
9.	GM 2 x COGG-192	3.61**	4.88**	2.93*	3.76*
10.	GM 3 x GM 4	4.84**	6.56**	3.17*	4.84*
11.	GM 3 x K-851	4.76**	4.76**	3.17*	4.84*
12.	GM 3 x Meha	4.35**	4.76**	1.83	2.09
13.	GM 3 x Pusa Vishal	4.76**	4.76**	3.70**	5.38**
14.	GM 3 x Vamban-2	-2.58**	4.76**	-2.76*	1.04
15.	GM 3 x Hum-1	-6.02*	7.32**	1.56	1.56
16.	GM 3 x SML 668	5.60**	6.45**	3.17*	4.84**
17.	GM 3 x COGG-192	4.42**	5.69**	3.17*	4.84**
18.	GM 4 x K-851	-2.01	-0.81**	2.69*	2.69
19.	GM 4 x Meha	-2.40	-0.81	2.39	3.76*
20.	GM 4 x Pusa Vishal	-2.01	-0.81	3.76**	3.76*
21.	GM-4 x Vamban-2	-8.96**	-0.81	-2.80*	2.69
22.	GM 4 x Hum-1	-0.81	-0.81	-2.12	-0.54*
23.	GM 4 x SML 668	-1.21	-0.81	0.54	0.54
24.	GM 4 x COGG- 192	-0.81	-0.81	4.30**	4.30**
25.	K-851 x Meha	1.98	2.38	2.92*	4.30**
26.	K-851 x Pusa Vishal	1.59	1.59	-4.30*	4.30**
27.	K-851 x Vamban-2	-7.01**	0.00	0.25	5.38**
28.	K-851 x Hum-1	1.20	2.44	2.65*	4.30**
29.	K-851 x SML 668	0.80	1.61	5.38**	5.38**
30.	K-851 x COGG-192	1.20	2.44	3.76**	3.76*
31.	Meha x Pusa Vishal	0.00	0.00	3.70**	5.38**
32.	Meha x Vamban-2	7.01**	0.00	-1.75	2.08
33.	Meha x Hum-1	1.20	2.44	2.08	2.08
34.	Meha x SML 668	0.80	1.61	2.12	3.76*
35.	Meha x COGG-192	1.20	2.44	3.17*	4.84**
36.	Pusa Vishal x Vamban-2	-7.01**	0.00	-1.78	3.76*
37.	Pusa Vishal x Hum-1	1.20	2.44	3.17*	4.84**
38.	Pusa Vishal x SML 668	0.80	1.61	2.69*	2.69
39.	Pusa Vishal x COGG-192	1.20	2.44	5.38**	5.38**
40.	Vamban-2 x Hum-1	8.61**	17.89**	1.75**	5.73**
41.	Vamban-2 x SML 668	8.21**	16.94**	3.31**	9.14**
42.	Vamban-2 x COGG-192	8.61**	17.89**	3. 31**	9.14**
43.	Hum-1 x SML 668	5.26**	5.69**	5.82**	7.53**
44.	Hum-1 x SML 668	5.69**	5.69**	4.76**	6.45**
45.	SML 668 x COGG-192	3.25**	3.25*	4.30**	4.30**
Range of heterosis		-8.96** to 8.61**	-0.81* to 17.89**	-4.30* to 5.82**	-0.54* to 9.14**
Number of crosses showing significant desirable heterosis		6	1	4	1
S.Em.$_{(ij.)}$ ±		0.48	0.55	0.80	0.93

*, ** = Significant at P = 0.05 and P = 0.01 per cent levels, respectively.

Table 4: Heterosis percentage in F_1 hybrid over mid parents [MP] and better parent [BP] for characters, plant height and branches per plant

Sr. No.	**Hybrid**	**Plant height (cm)**		**Branches per plant**	
		Mid Parent	**Better Parent**	**Mid Parent**	**Better Parent**
1.	GM 2 x GM 3	-27.22**	-24.85**	-10.34	-13.33
2.	GM 2 x GM 4	-5.73	-3.90	-14.29*	-20.00*
3.	GM 2 x K-851	-12.22	2.41	5.45	-3.33
4.	GM 2 x Meha	3.86	27.16**	17.86*	10.00
5.	GM 2 x Pusa Vishal	1.73	24.85*	0.00	-6.67
6.	GM 2 x Vamban-2	-30.66**	-21.94**	-11.11	-20.00*
7.	GM 2 x Hum-1	-6.15	-0.77	-7.41	-16.67*
8.	GM 2 x SML 668	7.12	37.39**	-1.89	-13.33*
9.	GM 2 x COGG-192	-27.33**	-24.96**	-12.73	-20.00*
10.	GM 3 x GM 4	26.32**	28.00**	10.71	-16.67*
11.	GM 3 x K-851	53.42**	72.59**	-12.73	-20.00*
12.	GM 3 x Meha	17.75*	38.83**	-10.71	-16.67*
13.	GM 3 x Pusa Vishal	60.00**	89.09**	-14.29*	-20.00*
14.	GM 3 x Vamban-2	-3.49	12.67	0.00	-10.00

15.	GM 3 x Hum-1	21.57**	24.30**	3.70	-6.67
16.	GM 3 x SML 668	47.49**	81.96**	-1.89	-13.33
17.	GM 3 x COGG-192	-4.72	1.78	--5.45	-13.33
18.	GM 4 x K-851	-18.86*	-7.59	-12.73	-20.00*
19.	GM 4 x Meha	-9.18	8.45	-3.57	-10.00
20.	GM 4 x Pusa Vishal	-12.07	5.25	0.00	-6.67
21.	GM-4 x Vamban-2	-43.31**	-34.64**	7.41	-3.33
22.	GM 4 x Hum-1	-26.35**	-23.84**	-3.70	-13.33
23.	GM 4 x SML 668	-29.91	-12.39	-1.89	-13.33
24.	GM 4 x COGG- 192	-25.33**	-21.16**	-20.00**	-26.67**
25.	K-851 x Meha	-7.33	-3.32	-17.86*	-23.33**
26.	K-851 x Pusa Vishal	0.10	4.65	-7.14	13.33**
27.	K-851 x Vamban-2	-30.60**	7.41	-14.81*	-23.33**
28.	K-851 x Hum-1	-18.72*	-10.74	7.41	-16.67*
29.	K-851 x SML 668	-4.80	3.47	-16.98*	-26.67*
30.	K-851 x COGG-192	-17.52*	-0.19	-12.73	-20.00*
31.	Meha x Pusa Vishal	5.45	5.45	-10.71	-16.67**
32.	Meha x Vamban-2	-15.76*	18.79	-18.52*	-26.67**
33.	Meha x Hum-1	-13.94	-0.81	-14.81*	-23.33**
34.	Meha x SML 668	19.37*	23.91*	-5.66	-16.67*
35.	Meha x COGG-192	3.17	31.52**	-20.00**	-26.67**
36.	Pusa Vishal x Vamban-2	2.58	44.65**	-18.52*	-26.67**
37.	Pusa Vishal x Hum-1	-4.65	9.90	0.00	-10.00
38.	Pusa Vishal x SML 668	20.63*	25.22*	13.21	0.00
39.	Pusa Vishal x COGG-192	-21.24**	0.40	-12.73	-20.00*
40.	Vamban-2 x Hum-1	17.24**	40.29**	3.70	-6.67
41.	Vamban-2 x SML 668	20.44**	78.04**	1.89	-10.00
42.	Vamban-2 x COGG-192	-8.82	-0.91	-9.09	-16.67*
43.	Hum-1 x SML 668	-1.18	18.70	1.89	-10.00
44.	Hum-1 x SML 668	-1.27	8.06	-5.45	-13.33
45.	SML 668 x COGG-192	5.44	39.68**	-9.09	-16.67
Range of heterosis		-43.31** to 60.00**	-34.64** to 89.09**	-20.00** to 17.86**	-26.67** to 13.33**
Number of crosses showing significant desirable heterosis		12	6	1	1
S.Em.$_{(ij.)}$ ±		2.95	3.41	0.31	0.13

*, **= Significant at P = 0.05 and P = 0.01 per cent levels, respectively.

Table 5: Heterosis percentage in F_1 hybrid over mid parents [MP] and better parents [BP] for characters, pods per plant and pod length

Sr. No.	Hybrid	Pods per plant		Pod length (cm)	
		Mid Parent	Better Parent	Mid Parent	Better Parent
1.	GM 2 x GM 3	33.27**	15.81**	20.20**	9.86
2.	GM 2 x GM 4	-78.06**	-57.52**	12.63	6.96
3.	GM 2 x K-851	-32.92**	-49.28**	5.08	4.20
4.	GM 2 x Meha	17.81**	6.21**	13.28	7.94
5.	GM 2 x Pusa Vishal	-37.09**	-46.74**	10.55	5.01
6.	GM 2 x Vamban-2	-32.31**	-32.79**	17.36*	8.47
7.	GM 2 x Hum-1	-37.05**	-37.5**	3.91	-1.80
8.	GM 2 x SML 668	25.15**	17.39**	5.83	4.10
9.	GM 2 x COGG-192	22.06*	8.43**	-3.35	-3.55
10.	GM 3 x GM 4	-36.74**	-43.44**	3.05	1.36
11.	GM 3 x K-851	-20.53**	-45.32**	12.57	6.01
12.	GM 3 x Meha	8.10**	13.91**	2.57	0.56
13.	GM 3 x Pusa Vishal	-22.22**	-36.36**	-1.90	-3.54
14.	GM 3 x Vamban-2	-42.66**	-33.04**	4.27	3.32
15.	GM 3 x Hum-1	8.45**	26.66**	0.00	-1.18
16.	GM 3 x SML 668	35.27**	-22.76**	12.38	3.06
17.	GM 3 x COGG-192	-61.19**	-62.16**	4.95	-1.83
18.	GM 4 x K-851	28.28**	2.65	-4.24	-9.82
19.	GM 4 x Meha	-29.44**	-46.95**	2.29	0.28
20.	GM 4 x Pusa Vishal	20.58*	8.98**	6.38	4.61
21.	GM-4 x Vamban-2	-40.19**	22.04**	16.88*	15.81*
22.	GM 4 x Hum-1	17.74**	20.83**	-3.81	-4.94
23.	GM 4 x SML 668	-7.54**	-27.67**	-0.29	-8.56
24.	GM 4 x COGG- 192	7.21	-1.93**	4.76	-2.00
25.	K-851 x Meha	53.74**	31.21**	10.81	5.58
26.	K-851 x Pusa Vishal	-8.85	-24.85**	-0.05	-5.05

27.	K-851 x Vamban-2	16.66**	-12.20**	5.24	-2.73
28.	K-851 x Hum-1	4.48	-21.37**	1.86	-3.74
29.	K-851 x SML 668	53.67**	42.14**	-12.08	-13.52*
30.	K-851 x COGG-192	-18.21**	-13.10**	-7.28	-7.47
31.	Meha x Pusa Vishal	11.31**	7.50**	-5.33	-6.91
32.	Meha x Vamban-2	-24.83*	-32.66**	-19.01*	-19.75**
33.	Meha x Hum-1	-29.30**	-36.66**	-7.14	-8.24
34.	Meha x SML 668	61.15**	41.05**	-7.14	-14.85*
35.	Meha x COGG-192	30.48**	5.94**	-2.86	-9.13
36.	Pusa Vishal x Vamban-2	-7.96**	-6.12**	3.88	2.93
37.	Pusa Vishal x Hum-1	-43.26**	-42.79**	25.24**	23.76**
38.	Pusa Vishal x SML 668	-15.15	19.60	20.95**	10.92
39.	Pusa Vishal x COGG-192	-48.32**	-53.80**	15.71*	8.24
40.	Vamban-2 x Hum-1	-21.37**	-21.37**	-1.81	-2.96
41.	Vamban-2 x SML 668	-37.64**	4.45	4.29	-4.37
42.	Vamban-2 x COGG-192	10.40**	25.29	-6.19	-12.25*
43.	Hum-1 x SML 668	-63.41**	-38.62**	2.38	-6.11
44.	Hum-1 x SML 668	-7.71**	4.70**	9.05	2.00
45.	SML 668 x COGG-192	25.80*	-7.64**	-12.55	-12.73*
Range of heterosis		-78.06** to 61. 15**	-62.16** to 42.14**	-19.01* to 25.24**	-19.75* to 23.76**
Number of crosses showing significant desirable heterosis		20	12	6	2
S.Em.$_{(ij.)}$ ±		0.41	2.83	0.44	0.51

*, **= Significant at P = 0.05 and P = 0.01 per cent levels, respectively.

Table 6: Heterosis percentage in F_1 hybrid over mid parents [MP] and better parents [BP] for character, seeds per pod and seed yield per plant

Sr. No.	Hybrid	Seeds per pod		Seed yield per plant (Kg / ha)	
		Mid Parent	Better Parent	Mid Parent	Better Parent
1.	GM 2 x GM 3	-25.16	-33.89*	25.42	23.33
2.	GM 2 x GM 4	-2.87	-6.11	-58.73**	-60.61**
3.	GM 2 x K-851	-6.61	-11.67	-50.00**	-66.67**
4.	GM 2 x Meha	-6.49	-9.67	21.74	-6.67
5.	GM 2 x Pusa Vishal	-13.64	-21.56	-60.00**	-66.67**
6.	GM 2 x Vamban-2	9.03	-2.78	-36.84*	-40.00*
7.	GM 2 x Hum-1	-17.58	-24.44	-55.56**	-60.00**
8.	GM 2 x SML 668	19.33	18.33	-11.11	-20.00
9.	GM 2 x COGG-192	-4.76	-5.56	16.67	-16.67
10.	GM 3 x GM 4	-7.26	-16.37	-46.03**	-48.48**
11.	GM 3 x K-851	-2.54	-10.28	-25.00	-50.00*
12.	GM 3 x Meha	0.99	-8.93	-13.04	-33.33
13.	GM 3 x Pusa Vishal	19.50	14.63	-32.00	-43.33*
14.	GM 3 x Vamban-2	-8.50	-10.64	-50.88**	-53.33**
15.	GM 3 x Hum-1	-35.79*	-39.00*	-11.11	-20.00
16.	GM 3 x SML 668	15.38	-25.42	-7.41	-16.67
17.	GM 3 x COGG-192	-7.05	-18.08	-66.67**	-66.68**
18.	GM 4 x K-851	-7.22	-8.48	-2.33	-36.36*
19.	GM 4 x Meha	-35.74*	-36.31*	-55.10**	-66.67**
20.	GM 4 x Pusa Vishal	-5.77	-10.91	-32.08	-45.45**
21.	GM-4 x Vamban-2	-12.42	-18.79	-46.67**	-51.52**
22.	GM 4 x Hum-1	-2.86	-7.27	5.26	-18.18
23.	GM 4 x SML 668	-28.65*	-31.07*	-57.89**	-63.64**
24.	GM 4 x COGG- 192	0.00	-3.39	-4.76	-9.09
25.	K-851 x Meha	-15.32	-16.07	116.00**	68.75**
26.	K-851 x Pusa Vishal	58.97**	50.30**	-10.34	-35.00
27.	K-851 x Vamban-2	0.65	-6.67	5.56	-29.63
28.	K-851 x Hum-1	-4.76	-9.09	3.03	-29.17
29.	K-851 x SML 668	-25.73	-28.25	-9.09	-37.50
30.	K-851 x COGG-192	-4.68	-7.91	-7.69	-40.00*
31.	Meha x Pusa Vishal	-9.62	-14.55	-2.86	-15.00
32.	Meha x Vamban-2	-6.54	-13.33	-38.10	-51.85*
33.	Meha x Hum-1	-25.08	-28.48	-38.46	-50.00*
34.	Meha x SML 668	-17.54	-20.34	7.69	-12.50
35.	Meha x COGG-192	-16.37	-19.21	6.67	-20.00
36.	Pusa Vishal x Vamban-2	0.34	-2.67	-20.83	-29.63
37.	Pusa Vishal x Hum-1	0.67	0.67	-2.22	-8.33
38.	Pusa Vishal x SML 668	-15.60	-22.03	20.00	12.50

39.	Pusa Vishal x COGG-192	0.92	-6.78	-1.96	-16.67
40.	Vamban-2 x Hum-1	-9.47	-14.00	-17.65	-22.22
41.	Vamban-2 x SML 668	-5.13	-16.38	29.41	22.22
42.	Vamban-2 x COGG-192	-7.69	-18.64	5.26	0.00
43.	Hum-1 x SML 668	0.92	- 6.78	-12.50	-12.51
44.	Hum-1 x SML 668	8.87	0.56	-29.63	-36..67
45.	SML 668 x COGG-192	-23.25	-23.29	-29.63	-36.67
Range of heterosis		-35.79** to 58.97**	-39.00** to 50.30**	-66.67** to 116.00**	-66.68** to 68.03**
Number of crosses showing significant desirable heterosis		1	1	1	1
S.Em.$_{(ij.)}$ ±		1.51	1.75	1.64	1.89

*, **= Significant at P = 0.05 and P = 0.01 per cent levels, respectively.

Table 7: Heterosis percentage in F_1 hybrid over mid parent [MP] and better parents [BP] for character, 100-seed weight and protein content.

Sr. No.	Hybrid	100-seed weight (g)		Protein content (%)	
		Mid Parent	**Better Parent**	**Mid Parent**	**Better Parent**
1.	GM 2 x GM 3	23.12**	18.50**	-3.80**	-6.31**
2.	GM 2 x GM 4	-3.56	-13.63**	-0.08	-0.80
3.	GM 2 x K-851	1.19	-2.89	6.78**	5.89**
4.	GM 2 x Meha	12.87**	5.50	0.57**	-2.09*
5.	GM 2 x Pusa Vishal	-2.36	-6.64*	9.35**	5.24**
6.	GM 2 x Vamban-2	38.61**	30.44**	-3.15**	-3.99**
7.	GM 2 x Hum-1	-26.20	-5.94	-1.38	-1.85*
8.	GM 2 x SML 668	-5.89*	-16.01**	2.41**	0.59
9.	GM 2 x COGG-192	6.18	1.67	3.13**	1.53
10.	GM 3 x GM 4	-21.23**	-29.45**	0.60	-2.29**
11.	GM 3 x K-851	-14.50**	-17.94**	-0.54	-3.49**
12.	GM 3 x Meha	3.30	-3.44	-1.83*	-5.41**
13.	GM 3 x Pusa Vishal	2.15	-2.33	-3.89**	-9.43**
14.	GM 3 x Vamban-2	23.26**	-27.78**	1.70*	0.35
15.	GM 3 x Hum-1	-2.62	-5.94	-1.25	-2.94**
16.	GM 3 x SML 668	23.28**	-31.53**	2.66**	-1.32
17.	GM 3 x COGG-192	-6.70*	-10.67**	-0.65	-4.29**
18.	GM 4 x K-851	-17.19**	-30.04**	3.70**	2.83**
19.	GM 4 x Meha	-2.04	-19.08**	3.19**	1.61
20.	GM 4 x Pusa Vishal	21.20**	-28.21**	9.87**	5.74**
21.	GM-4 x Vamban-2	-15.55**	-29.83**	2.42**	1.53
22.	GM 4 x Hum-1	-2.72	-17.37**	6.13**	5.63**
23.	GM 4 x SML 668	-26.61**	-28.25**	7.47**	5.56**
24.	GM 4 x COGG- 192	-2.99	-18.21**	-0.61	-2.15*
25.	K-851 x Meha	18.81**	-11.06*	2.89**	1.32
26.	K-851 x Pusa Vishal	-12.43**	-16.27*	9.34**	5.23**
27.	K-851 x Vamban-2	5.25	-0.94	0.15	-0.71
28.	K-851 x Hum-1	7.39*	3.72	0.82	0.35
29.	K-851 x SML 668	-12.58**	-21.98**	4.31**	0.24**
30.	K-851 x COGG-192	-0.32	4.56	2.19**	0.61
31.	Meha x Pusa Vishal	-0.09	-12.06**	7.93**	6.25**
32.	Meha x Vamban-2	7.71*	4.72	-0.32	-3.41**
33.	Meha x Hum-1	24.46**	17.89**	-0.47	-3.18**
34.	Meha x SML 668	-16.90**	-31.27**	4.65**	4.12**
35.	Meha x COGG-192	-14.01**	-17.85**	-2.34**	-3.06**
36.	Pusa Vishal x Vamban-2	2.17	10.29**	2.44**	-3.02**
37.	Pusa Vishal x Hum-1	2.99	-7.38*	1.70*	-3.36**
38.	Pusa Vishal x SML 668	0.48	-3.75	10.31**	7.15**
39.	Pusa Vishal x COGG-192	31.63**	17.43**	9.90**	6.51**
40.	Vamban-2 x Hum-1	-10.10**	-14.85**	-7.71**	-8.15**
41.	Vamban-2 x SML 668	-15.58**	-30.18**	-4.45**	-6.15**
42.	Vamban-2 x COGG-192	6.26	1.52	-1.15	-2.68**
43.	Hum-1 x SML 668	-20.79**	-29.31**	-2.61**	-4.35**
44.	Hum-1 x SML 668	30.14**	24.61**	3.13**	1.53
45.	SML 668 x COGG-192	-5.86*	-20. 63	4.18**	3.41**
Range of heterosis		-26.61** to 38.61**	-31.53** to 30.44**	-7.71** to 10.31**	-9.43** to 6.51 **
Number of crosses showing significant desirable heterosis		12	6	24	14
S.Em.$_{(ij.)}$ ±		0.18	0.21	0.16	0.18

*, ** = Significant at P = 0.05 and P = 0.01 per cent levels, respectively.

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