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Original Research Article

Heterosis and Inbreeding Depression for Yield and Yield Components in Intraspecific Crosses of *Vigna*

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A B S T R A C T

An experiment was conducted on mung bean (*Vigna mungo* L.) and urdbean (*Vigna radiata* L.) to study the extent of heterosis over better parent (heterobeltiosis), mid parent and economic check as well as inbreeding depression in F2 generation. Four genotypes of each mungbean and urdbean were used to produce six crosses viz. HUM 16 x LGG 450(cross I), samrat x LGG 450 (cross II), TMB 37x LGG450 (cross III), shekhar × Barabanki (cross IV), PU 31 × Barabanki (cross V) and Uttara × Barabanki (crossVI) and their F2 populations. These populations were laid out in Random Block Design with three replications and SML 668 used as economic variety at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur. Range of hetrosis varied from 3.79 (HUM 16 x LGG 450) to 46.43 (Uttara x Barabanki) per cent over better parent; and five crosses showed significant positive value. All six crosses showed significant positive heterosis for yield and varied between 54.23 (HUM 16 x LGG 450) to 125.28 (Uttara x Barabanki) per cent over mid Parent. Out of all six significant crosses, five crosses had negative and cross I (Hum 16 x LGG450) had positive significant value over check variety (SML 668). Economic heterosis lies between -26.20 (Sekhar x Barabanki) to 7.42 (HUM 16 x LGG 450) per cent. Inbreeding depression (ID) range varied between 23.05 (HUM 16 x LGG 450) to 47.93 (Sekhar x Barabanki) per cent; whereas all six crosses showed positive and significant ID

Keywords

Heterobeltiosis, Inbreeding depression (ID), mid parent heterosis, Standard heterosis, Mungbean, Urdbean

Introduction

Pulses are known for their protein rich grain having two to three times more protein than cereal. Among pulses, mungbean and urdbean is the cheapest sources of plant protein, which contains about 22-27 per cent protein as well as a good source of minerals such as calcium and sodium. Mungbean and urdbean is an important short duration grain legume cultivated over a wide range of agro-climatic conditions. Dried mungbean seeds are rich in vitamin A and B, while the sprouted mungbean are rich in vitamin B and C. These qualities of pulses are sufficient to overcome the protein deficiency.

Variability is one of the main constraints which are responsible for the poor progress in breeding programme of pulse crop. The breeding approaches aimed for the development and isolation of superior homozygous lines or pure line varieties in

self-pollinated crop like mungbean and urdbean. It is very essential for the identification of highly heterotic crosses and selection of superior lines in advance segregating generations. Heterosis is a valuable expression that often results from genetic recombination (Lamkey and Edwards 1999). The exploitation of heterosis in mungbean and urdbean has not been commercialized due to limited extent of out crossing (Singh 1992, 2000). However, highly heterotic crosses can be used for development of high yielding pureline varieties in a self-pollinated crop like mungbean and urdbean. Therefore, the present study was undertaken to generate information on heterosis and inbreeding depression for yield and its component characters in mungbean as well as in urdbean. The magnitude of heterosis provides a basis for determining genetic diversity and also serves as a guide in selection of desirable parents.

Materials and Methods

Four genotypes/varieties of each mungbean and urdbean (HUM-16, TMB-37, Samrat, LGG 450, Pant U-31, Shekhar, Uttara, and barabanki) were crossed to produce six F1's namely. HUM 16 x LGG 450(cross I), samrat x LGG 450 (cross II), TMB 37x LGG450 (cross III), shekhar × Barabanki (cross IV), PU 31 × Barabanki (cross V) and Uttara × Barabanki (cross VI). The F1's were advanced to get F2 populations and simultaneously fresh F1's were also made in *Kharif* 2010. Thus, eight parents (SML 668 as check), six F1, and their F2 populations were evaluated in Randomized Block Design with three replications at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur. Seeds of parents and F1's were sown in a two row plot, whereas, ten rows constituted a plot for F2 generations, each row was 4 m long with a spacing of 30 cm between rows and 10 cm between plants. Observations were recorded on 10 plants from parents and F1's and 30 plants from F2 progenies selected randomly in each replication for thirteen quantitative traits *viz.* days to 50 per cent flowering, Plant height (cm), Number of primary branches, Number of cluster per plant, Pod per cluster, Number of pod per plant, days to maturity, pod length (cm), number of grains per pod, 100 seed weight (g), Harvest index (HI), Phenol content mg/g of fresh leaf and grain yield per plot (kg). Total phenol estimation was carried out with Folin-Ciocalteu Reagent (FCR). The method opted and protocol given by Bray and Thorpe (1954). The mean data on above traits were used to compute mean heterosis, heterobeltiosis, standard heterosis (Hays *et al.*, 1955) and inbreeding depression. The test of significance was carried out for the estimates of heterosis by adopting the t test as per the formula given by Sharma (1988). These calculated 't' values for relative heterosis, heterobeltiosis and standard heterosis were compared with table 't' value at error degrees of freedom at P=0.05 and 0.01 level of significance.

Results and Discussion

The analysis of variance of thirteen characters of twenty treatments including parents, F_1, F_2 and check presented in the table: 1 and revealed highly significant differences among genotypes for all the characters studied. The material taken under study was having comprising sufficient variability, which helps to the breeder for the identification of suitable high yielding genotypes to be used for the exploitation of heterosis to improve the yield of the crop. Variability provides the material resources to breeder for restructuring the plant genotype as well as provides wider genetic base for selection.

Table.1 Analysis of variance of design of experiments for thirteen character in Vigna species

Sl. No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to 50% flowering	0.188	20.02**	0.821
2.	Plant height	0.093	322.04**	4.61
3.	No. of Primary branches	0.197	4.62**	0.22
4.	No. of cluster per plant	3.078	106.13**	4.28
5.	Pod per cluster	1.807	1.56**	0.26
6.	No. of pod per plant	2.027	512.71**	8.56
7.	Days to maturity	5.906	58.39**	2.93
8.	Pod length	0.009	7.53**	0.16
9.	No. of grain per pod	0.469	7.90**	0.18
10.	100-seed weight	0.005	1.03**	0.004
11.	Harvest index	0.002	0.03**	0.001
12.	Phenol content	0.014	0.18**	0.001
13.	Grain yield/plot	0.003	0.07**	0.001

* Significant at P = 0.05
** Significant at P = 0.01

Table.2 Genetic variability study of thirteen characters in vigna species

S. No.	Crosses	PCV	GCV	Heritability	GA%
1.	Days to 50% flowering	8.72	8.21	0.886	15.91
2.	Plant height	32.11	31.42	0.958	63.36
3.	No. of Primary branches	31.11	29.02	0.869	55.75
4.	No. of cluster per plant	34.72	32.72	0.888	63.51
5.	Pod per cluster	26.40	20.89	0.626	34.07
6.	No. of pod per plant	29.29	28.57	0.952	57.42
7.	Days to maturity	6.45	5.99	0.863	11.47
8.	Pod length	26.97	26.15	0.940	52.23
9.	No. of grain per pod	24.05	23.25	0.934	46.30
10.	100-seed weight	15.99	15.90	0.988	32.56
11.	Harvest index	38.79	36.83	0.901	72.05
12.	Phenol content	26.16	25.96	0.985	53.09
13.	Grain yield/plot	30.91	30.56	0.978	62.26

Table.3 Mid Parent and Better Parent Hetrosis of six intraspecfic crosses of Vigna species for thirteen character

		Cross I		Cross II		Cross III		Cross IV		Cross V		Cross VI	
		MP	BP	MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
1.	Days to 50% flowering	15.25**	21.43**	0.59	10.26**	10.47**	20.25**	14.13**	20.69*	0	0	12.22**	16.09**
2.	Plant height	19.93**	35.80**	-12.45**	-11.88**	26.03**	46.27**	-14.38*	-6.04	-6.32**	0	15.913	27.69*
3.	No. of Primary branches	54.84**	75.61**	61.84**	86.36**	123.35**	105.61**	46.32*	40.14	21.66*	20	33.09**	29.29**
4.	No. of cluster per plant	73.51**	73.3	-19.29	-25.96*	89.39**	66.67**	41.87	26.09	20.00**	13.18**	51.58**	45.62**
5.	Pod per cluster	19.21**	12.5	39.33	26.53	75.42**	61.86**	41.94**	37.50*	-3.5	-17.65**	18.77**	4.51
6.	No. of pod per plant	107.48**	62.73	52.00**	25.22**	31.18**	17.19*	24.08**	14.92**	57.25**	48.67**	84.76**	75.90**
7.	Days to maturity	5.86	9.18	1.4	11.85**	11.16**	21.24**	3.57*	4.51*	13.04**	25.81	0.91	3.74*
8.	Pod length	-7.33	-24.52**	-6.667	-7.11	8.35	4.13	20.74*	18.98	1.33	-4.38*	26.50**	16.54**
9.	No. of grain / pod	4.21	-16.67**	37.17**	17.42**	40.43**	23.13*	30.81**	21.70**	16.02**	15.39**	43.59**	12.64
10.	100-seed weight	4.68*	-18.78**	0.46	-5.26**	-8.64**	-22.51**	1.14**	-18.42**	-2.44**	-11.64**	-17.99**	-23.78**
11.	Harvest index	75.87**	10.43**	55.71**	0.98	13.44	-17.79	-28.89**	-34.50**	69.05**	30.59**	52.43**	45.36
12.	Phenol content	18.06**	3.03	-6.24**	-10.85**	-17.17**	-34.62	4.78	-11.58	3.54	-13.77**	32.77**	22.35**
13.	Grain yield/plot	54.23**	3.79	55.65**	12.58**	58.43**	14.12**	68.16**	8.33*	91.74**	19.43**	125.28**	46.43**

Table.4 Heterosis over best check and Inbreeding Depression of intraspecific crosses of vigna species

Sl. No.	Characters	Intraspecfic Crosses (Best ChecK) Economic Heterosis						Intraspecific Crosses Inbreeding Depression					
		Cross I	Cross II	Cross III	Cross IV	Cross V	Cross VI	Cross I	Cross II	Cross III	Cross IV	Cross V	Cross VI
1.	Days to 50% flowering	25.93**	6.17	17.28**	29.63**	7.41*	24.69**	8.82*	1.63	4.21	12.38**	-5.75	7.92*
2.	Plant height	16.53**	1.59	27.71	-36.39**	-47.41**	-12.87**	4.16	-13.64*	50.72***	-5.38	-1.59	13.46
3.	No.of primary branches	122.89**	61.84**	189.47	161.84**	73.68**	138.16**	65.97***	-23.58	59.55**	15.58	19.7	16.02
4.	No. of cluster / plant	122.89**	15.96	174.10**	116.87**	86.15**	145.18**	61.36**	-52.21**	64.51**	20.55	13.92**	34.89**
5.	Pod per cluster	16.58*	60.62	103.37**	42.49**	8.81	38.08**	8.44**	1.61	22.93	20.91	27.74***	20.26**
6.	No. of pod / plant	156.61**	89.18**	90.14**	73.08**	94.95**	204.45**	68.71**	40.79*	43.74	-0.14	37.05**	40.47**
7.	Days to maturity	4.63	0.46	8.33**	7.41**	8.33**	2.78	11.06**	0.46	3.42	8.19**	0.86	0.9
8.	Pod length	-25.71**	-37.78**	-27.94**	-48.25**	-51.43	-53.02**	42.31**	3.57	-2.2	4.29	-15.03**	12.83*
9.	No. of grain / pod	-9.72*	7.64**	14.58*	-15.97**	-27.08**	-31.94**	33.85**	46.45	39.39**	12.4	10.48	11.22
10.	100-seed weight	-22.54**	-36.13**	-25.72**	-17.37**	-26.76**	-26.38**	-13.85**	-6.37***	-16.20***	-13.81**	9.94***	-21.89***
11.	Harvest index	-11.69*	-26.59**	-54.88**	-68.07**	15.61**	-37.42**	-3.47	67.67***	5.85	-111.83**	26.17**	34.40**
12.	Phenol content	13.33**	-17.60**	-8.33*	-16	-12.33*	-5.67**	34.12***	5.74**	-10.10**	19.05**	9.51**	19.44**
13.	Grain yield/plot	7.42**	-21.83	-11.79	-26.20**	-8.73**	-10.48**	28.05***	29.61**	31.19***	47.93***	43.06***	31.71***

Wide range of variability was observed amongst the available material for the characters taken under study. For all the character PCV was slightly higher than GCV, which indicated very meager effect of environment on the expression of the traits (table). This finding also get confirmed by the Konda *et al.,* (2009),Venkateswarle (2001), Reddy *et al.,* (2003) and Dikshit *et al.,* (2002).

High GCV along with PCV was observed for the traits viz. plant height, number of primary branches, number of cluster per plant, number of pod per plant, pod length, harvest index, phenol content and grain yield per plot(table:2). Similar result were also observed by Konda *et al.,* (2009), Venkateswarlu (2001), Reddy *et al.,* (2003), Prakash Singh and Khedar (2007), Dhananjay *et al.,* (2009) and Dikshit *et al.,* (2002). While moderate GCV followed by PCV was observed for pod per cluster and 100-seed we ight. It is also reported by Peerajade *et al.,* (2009), Sadiq and Abbas (2007). The estimates of GCV indicated that traits like grain yield, harvest index, number of cluster per plant and plant height may be used as selection criteria, because these traits showed comparatively very high GCV.

The main objective of heterosis was to search out the best cross combinations and degree of heterosis varied from cross to cross for all the traits. From the perusal of the table: 3&4, it is obvious that desirable heterosis would not be obtained for days to 50% flowering in any of the intra specific crosses; whereas, for the plant height desirable heterosis was obtained in crosses viz., Uttara x Barabanki (cross VI), PU 31 x Barabanki (cross V) and Sekhar x Barabanki (cross IV). In all the crosses, barabanki was involved as male parent and none of the crosses exhibited significant inbreeding depression. Thus it is evident that there is involvement of additive type of gene action, so barabanki may be used as one of the parent for developing the dwarfness in black gram and that could be fixable in nature.

For most of the yield attributing traits viz., number of primary branches, number of cluster per plant, pod per cluster, number of pod per plant and days to maturity in intraspecific crosses TMB 37 x LGG 450

(cross III) and Sekhar x Barabanki (cross IV) were found promising, so it is very much obvious that these cross combinations may be further exploited in *Vigna* improvement programme. This was in conformity with the results of the earlier worker Patil *et al.,* (1996), Sharma (2000), Jahagirdar (2001) and Singh and Dikshit (2003). Cross II (samrat x LGG 450) and III (TMB 37x LGG450) were showed positive significant over standard check SML 668. Khan *et al.,* (2005), Sohendi and Srinivas (2005) also reported the heterosis over mid and better parents in mungbean for number of seeds per pod. In case of harvest indexw character none of the crosses were found to be positive significant over EH. The range of inbreeding depression varied from -111.83 (cross IV) to 67.67 (cross II) however, the crosses II (samrat x LGG 450), III (TMB 37x LGG450) and IV (shekhar × Barabanki) were exhibited significant positive inbreeding depression for the harvest index.

Phenol content is one of the important characters related to disease resistance. Cross VI (Uttara x barabanki) exhibited highest positive significant positive heterosis over BP and MP, however cross I (Hum 16 x LGG450) also showed significant heterosis over MP and local check for phenol concentration. The inbreeding depression for phenol content was observed significantly positive in all cross combinations except cross III. Kosuage (1969),Thakur and Sohal (2013) and Singh *et al.,* (1975) reported earlier that phenols and sugars are responsible for disease resistance in different crops and resistant cultivar had more total phenols, flavonols and tannins as compared to those in the susceptible cultivar.

The breeder in autogamous crop is primarily interested in identifying parental combinations that are likely to prod.uce superior homozygous segregant, but identification of specific parental combinations capable of producing highest level of F_1, transgressive effects are of great value in the present context. The superiority of cross combination is of not availed unless it is economical. All the specific crosses exhibited significant and undesirable heterosis for pod length, number of grain per pod, 100-seed weight, harvest index (HI), Phenol content and grain yield per plot, whereas, only one cross HUM 16 x LGG 450 showed significant and desirable heterosis for phenol content and grain yield per plot along with the significant and high magnitude of inbreeding depression, suggesting that there is preponderance of non-additive type of gene action. Therefore, suitable breeding methodology may be used for hybridization and selection may be done in later generation for the improvement of phenol content to produce resistance against the MYMV along with the higher yield potential.

Abbreviation

Better Parent (BP), Mid Parent (MP), Economic heterosis (EH)

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