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Research Article

Combining ability, heterosis and inbreeding depression in inter specific hybrids involving greengram [*Vigna radiata* (L.) Wilczek] and blackgram [*Vigna mungo* (L.) Hepper]

Yashpal*, M. N. Singh, N. Pathak and S. K. Saroj
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences
Banaras Hindu University, Varanasi-221005, India
Email: yashpaltaak@gmail.com

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Abstract

A line x tester analysis of interspecific hybrids involving greengram (female) and blackgram (male) was carried out for 11 quantitative traits. As expected in wide crosses, none of the parent was found to be good general combiner for yield. However, PDM-11, HUM-26 Azad-U-1 and KUG-427 were spotted out as superior general combiners for 2-5 yield traits. Likewise, hybrids, PDM-11 × KUG-427, HUM-26 × Azad-U-1, HUM-6 × BHU-U-1 and HUM-26 × BHU-U-1 were identified as best specific cross combinations for few yield components only. Further, economic heterosis for seed yield and few important yield traits such as, pod length, seeds per pod and 100-seed weight, was significantly negative, while it was mostly positive for days to first flowering, days to maturity, plant height, number of primary and secondary branches including pods per plant. All the crosses showing negative yield heterosis reflected positive inbreeding depression. Non-additive gene action was of prime importance for all the characters except for days to 50% flowering.

Key words:
Greengram, Blackgram, Combining ability, Heterosis, Inbreeding depression

Introduction

Greengram and blackgram are the two most important short duration pulse crops in India. Due to narrow genetic variability in primary gene pool, inter-varietal hybridization have not proven much successful in breaking yield barriers in these two important grain legumes (Sharma *et al.* 2013). Genetic improvement mainly depends upon the amount of genetic variability present in the base population and serves as a valuable source of base population for providing wide variability (Gokulakrishnan *et al.* 2012). For observing high yield potential and resistance to diseases and pests, widening of gene pool through interspecific crosses are inevitable. The alien gene transfer has paid rich dividends for creating novel genetic variability for desirable characters including disease resistance in several crop plants (Stalker, 1980). Combining ability analysis is an important tool in assessing the usefulness of parents and understanding the magnitude of gene action involved in the inheritance of quantitative traits of economic importance. The magnitude of heterosis enable to select the desirable parents for developing superior F_1 hybrids that may be exploited for hybrid vigour and /or for building better gene pool to be employed in population improvement. The main objective of present investigation was to identify desirable general combiners as well as specific cross combinations for yield and yield attributing traits besides, observing the extent of heterosis and inbreeding depression in interspecific hybrids involving greengram and blackgram.

Material and methods

Three diverse genotypes/varieties of each of greengram *viz.*, PDM-11, HUM-6 and HUM-26 (as line) and blackgram, namely, Azad-U-1, BHU-U-1 and KUG-427 (as tester) were crossed in line x tester fashion during *Kharif*, 2010 to obtain nine interspecific crosses. All the $F_{1's}$ were selfed to procure seeds for F_2 generation. The final experiment comprising of nine each of F_1s and F_2s along with the parents were grown in randomized block design with two replications at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, during *Kharif*, 2011. Each plot consisted of 2 meter row length with inter and intra row spacing of 30 x 10 cm, respectively. The parents and F_1s were grown as single row each; whereas, each $F_{2'}$s had 3-5 rows. The observations were recorded on five randomly selected competent plants from each row for 11 quantitative traits (Table 1). The analysis of variance, heterosis and inbreeding depression were calculated as per Panse and Sakhatme (1964), Meredith and Bridge (1972) and Meghji *et al.*,(1984), respectively while combining ability analysis was done following Kempthorne (1957).

Results and discussion

Combining ability: The analysis of variance (data not shown) for combining ability in respect of 11 characters clearly revealed that line x tester variances were highly significant for all the characters except for number of primary branches, seeds per pod and yield per plant, indicating thereby that parents involved were highly divergent for most of the characters studied.

Further, estimates of components of variance (Table 1), indicated that SCA variance was highly significant for all the traits except for number of primary branches, seed per pod and seed yield per plant, indicating the importance of non-additive gene action for the expression of most of the yield traits. As reported earlier by Singh (2005) and Singh (2012), degree of dominance was also greater than one for all the traits except for days to first flowering, further suggesting the prevalence of non-additive genetic variance for the expression of almost all the traits studied. Under such circumstances, selection should be delayed in early segregating generation till maximum homozygosity is achieved in advanced generation.

Estimate of GCA effect (Table 2) exhibited that none of the parent recorded significant GCA effect for yield *per se*. However, among lines PDM-11 showed significant and desirable GCA effects for maximum number of other traits *viz*. days to maturity, pods per plant, pod length, cluster per plant and 100-seed weight; followed by HUM-26 (days to first flowering, days to maturity) and HUM-6 (number of secondary branches). Similarly, among testers Azad-U-1 showed significant and desirable GCA effect for days to first flowering, plant height, cluster per plant and 100-seed weight; KUG-427 for days to first flowering, days to maturity and pods per plant and BHU-1 for pod length. Such a poor expression of GCA for yield and other traits might be due to chromosomal anomalies causing sterility as well as greater allelic difference over a larger number of loci between the two species involved in the crosses.

Estimate of SCA effect (Table 3) revealed that none of cross combination recorded significantly desirable SCA effect for yield *per se*. However, PDM-11 × KUG-427 observed significant SCA effect for maximum number of other traits *viz.* days to first flowering, days to maturity , number of secondary branches, pods per plant, pod length, clusters per plant, followed by HUM-6 × BHU-U-1 (days to first flowering, days to maturity , pod length, number of clusters per plant); HUM-26 × Azad-U-1 (days to maturity , plant height, pods per plant, pod length); HUM-26 × BHU-U-1 (plant height, pod length, clusters per plant); PDM-11 × Azad-U-1 (clusters per plant); PDM-11 × BHU-U-1 (pods per plant) and HUM-6 × Azad-U-1 (number of secondary branches). The above mentined trend for GCA and SCA effect was also noted earliear by Singh (2005). In the present study, the crosses exhibiting significant SCA effect for traits under investigation involved parents with high × high (PDM-11 × KUG-427 for days to maturity and pods per plant; PDM-11 × Azad-U-1 for clusters per plant), high × low (PDM-11 × BHU-U-1 for pods per plant and HUM-6 × BHU-U-1 for pod length) and low × low (HUM-6 × BHU-U-1 for days to first flowering and days to maturity; PDM-11 × KUG-427 for number of secondary branches; HUM-26 × BHU-U-1 for clusters per plant and HUM-6 × KUG-427 for 100-seed weight) combiners indicating the presence of allelic as well as non-allelic interaction in the expression of these traits. Cross combinations involving high × high combiners indicate the significance of additive and/or additive × additive gene action in the expression of traits that can be exploited easily by simple conventional breeding methods like pedigree method. However, the crosses involving either good or poor combiners as one of the parents, will yield desirable segregants in advance generations, provided additive genetic system present in the good combiners and epistatic effects also act in the same direction to maximize the yield attributes.

Heterosis and inbreeding depression: Heterosis over mid parent, better parent and check variety i.e. PDM-11 as well as inbreeding depression of inter-specific hybrids showed negative trends for usually post mating traits *viz.*, pod length, seeds per pod and 100-seed weight including seed yield per plant whereas, significantly positive values could be perceived for number of primary branches, number of secondary branches, clusters per plant and pods per plant (Table 4) which are in conformity with earlier reports of Pandiyan *et al.* (2010). Hybrids showing heterosis over check variety also showed heterosis over mid parent and better parent (data not shown).

The reasons behind poor performance of the F_1 hybrids in relation to yield and related traits in wide crosses might be due to meiotic irregularities leading to poor pollen and/or ovule fertility as the parents involved were distantly related and have qualitative differences in genomes (Brink and Cooper, 1947). Further, reduction in pod length and seeds per pod including 100-seed weight provides an opportunity to plants for the diversion of photosynthates towards other traits like increased plant height and fruiting nodes resulting more clusters and ultimately enhanced club shaped pods per plant.

Few heterotic crosses, such as PDM-11× KUG-427, followed by HUM-26 × Azad-U-1 and HUM- 6 × BHU-U-1 were observed to be desirable for maximum number of four traits (Table 4). High and significant heterosis in negative direction for yield and yield components such as pod length, seeds per pod and 100-seed weight was also noted by earlier workers (Singh, 1999; Singh, 2005; Singh and Singh, 2006 and Singh, 2012). Poor performance of the inter-specific F_1 hybrids has been the common feature in majority of crop plants (Stalker, 1980), which in turn resulted in poor or even negative yield heterosis. Interestingly enough, most of the crosses showing poor yield heterosis usually exhibited negative inbreeding depression. Significant negative inbreeding depression could be attributed due to accumulation of favourable genes in homozygous condition, including their favourable interaction with alien cytoplasm and/or high magnitude of additive gene action. Higher F_2 mean might also be due to sampling error, as in present case, observations were recorded only on those F_2 plants which survived up to maturity and/or bore some pods. The plants which died during vegetative growth or produced negligible pods were excluded from the observation. Higher F_2 mean for fertility (Singh *et al.* 1996), pods per plant (Singh, 1990) and other yield contributing traits (Singh, 1999; Singh, 2005 and Singh, 2012) are reported earlier.

From the present study it is quite obvious that, PDM-11(mungbean) and Azad-U-1 (urdbean), being good combiners for important yield traits, may be utilized in future breeding programme to recover the rare transgressive segregate(s) for breaking the yield plateau in these two important pulse crops.

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Table 1. Estimate of component of variance and genetic parameters

SV	DFF	DM	PH	PB	SB	PD/P	PL	SD/P	CL/P	SW	SY/P
σ² GCA	13.65	27.63	19.91	0.23	0.46	9.82	0.04	-0.004	6.31	0.10	-0.01
σ² SCA	13.09**	83.63**	176.66**	0.47	2.50**	25.93**	0.16**	0.16	15.34**	0.22**	0.16
σ² A	54.60	110.51	79.66	0.92	1.85	39.28	0.16	-0.02	25.22	0.38	-0.05
σ² D	52.36	334.52	706.65	1.89	9.99	103.71	0.62	0.62	61.34	0.88	0.65
Degree of dominance	0.98	1.74	2.98	1.44	2.33	1.62	1.95	6.22	1.56	1.52	3.70

* , ** significant at 5% and 1% respectively; SV-Source of variation, DFF-Days to first flowering, DM-Days to maturity, PH-Plant height (cm), PB-Number of primary branches, SB-Number of secondary branches, PD/P-Pods per plant, PL-Pod length (cm), SD/P-Seeds per pod, CL/P-Clusters per plant, SW-100-Seed weight (gm), SY/P-Seed yield per plant (gm)

Table 2. Estimate of general combining ability effects for six parents from a line × tester design in respect of 11 characters

Parents	DFF	DM	PH	PB	SB	PD/P	PL	SD/P	CL/P	SW	SY/P
PDM-11	0.64	-4.05**	2.16	-0.32	-0.52*	0.86*	0.23**	-0.08	2.64**	0.42**	0.16
HUM-6	3.19**	5.57**	0.82	0.63	0.98**	0.01	-0.17**	0.27	-0.56	-0.28*	0.11
HUM-26	-3.84**	-1.52*	-2.98	-0.31	-0.46	-0.86**	-0.06	-0.19	-2.08**	-0.14	-0.27
Azad-U-1	-3.07**	0.98	-4.18*	0.23	0.31	-3.54**	-0.19**	0.02	2.76**	0.26*	-0.07
BHU-U-1	4.33**	5.00**	-2.88	0.48	0.33	-1.33**	0.21**	0.22	-2.58**	0.01	0.18
KUG-427	-1.26**	-5.98**	7.06**	-0.71	-0.64*	4.87**	-0.02	-0.24	-0.18	-0.26*	-0.11
SE line	0.36	0.49	1.58	0.34	0.22	0.26	0.03	0.25	0.40	0.09	0.23
SE tester	0.36	0.49	1.58	0.34	0.22	0.26	0.03	0.25	0.40	0.09	0.23

* , ** significant at 5% and 1% respectively; DFF-Days to first flowering, DM-Days to maturity, PH-Plant height (cm), PB-Number of primary branches, SB-Number of secondary branches, PD/P-Pods per plant, PL-Pod length (cm), SD/P-Seeds per pod, CL/P-Clusters per plant, SW-100-Seed weight (gm), SY/P-Seed yield per plant (gm)

Table3. Estimate of specific combining ability effects of nine crosses for 11 characters in inter-specific crosses involving greengram and blackgram

Crosses	DFF	DM	PH	PB	SB	PD/P	PL	SD/P	CL/P	SW	SY/P
PDM-11 × Azad-U-1	1.51*	6.00**	-5.09	-0.24	-1.38**	-6.32**	-0.08	0.44	3.36**	-0.01	-0.01
PDM-11 × BHU-U-1	2.11**	5.03**	9.41**	0.51	-0.14	3.16**	-0.38**	-0.21	-5.11**	-0.01	0.04
PDM-11 × KUG-427	-3.61**	-11.03**	-4.32	-0.26	1.52**	3.16**	0.46**	-0.24	1.74*	0.01	-0.03
HUM-6 × Azad-U-1	-0.69	-1.62	12.64**	0.66	1.77**	1.03*	-0.13*	-0.41	-2.14*	-0.56**	-0.56
HUM-6 × BHU-U-1	-3.54**	-6.98**	-2.16	-1.19	-0.04	-0.99	0.22**	0.64	3.49**	0.19	0.54
HUM-6 × KUG-427	4.24**	8.60**	-10.49**	0.54	-1.73**	-0.04	-0.09	-0.24	-1.36	0.36*	0.02
HUM-26 × Azad-U-1	-0.81	-4.38**	-7.56*	-0.41	-0.39	5.29**	0.21**	-0.04	-1.22	0.56**	0.57
HUM-26 × BHU-U-1	1.44*	1.95*	-7.26*	0.69	0.19	-2.17**	0.16**	-0.44	1.61*	-0.19	-0.58
HUM-26 × KUG-427	-0.63	2.43*	14.81**	-0.28	0.21	-3.12**	-0.36**	0.48	-0.39	-0.37*	0.01
SE	0.62	0.84	2.75	0.58	0.39	0.44	0.04	0.43	0.69	0.15	0.39

* , ** significant at 5% and 1% respectively; DFF-Days to first flowering, DM-Days to maturity, PH-Plant height (cm), PB-Number of primary branches, SB-Number of secondary branches, PD/P-Pods per plant, PL-Pod length (cm), SD/P-Seeds per pod, CL/P-Clusters per plant, SW-100-Seed weight (gm), SY/P-Seed yield per plant (gm)

Table 4. Estimation of economic heterosis (EH) over check variety (PDM-11) and inbreeding depression (ID) for 11 characters

Crosses	Days to first flowering		Days to maturity		Plant height (cm)		Number of primary branches		Number of secondary branches		Pods per plant	
	EH	ID	EH	ID	EH	ID	EH	ID	EH	ID	EH	ID
PDM-11 × Azad-U-1	25.08**	25.09**	45.13**	6.15*	42.57**	13.45**	23.64	10.29	11.54	-20.69	-27.76**	-54.89**
PDM-11 × BHU-U-1	49.69**	18.09**	49.67**	14.95*	72.87**	26.79**	41.82*	25.00*	43.59*	18.75	12.59**	27.41**
PDM-11 × KUG-427	14.92**	-10.04*	9.44**	-12.43**	65.58**	21.60**	6.36	-12.82	61.54**	14.29	33.97**	32.30**
HUM-6 X×Azad-U-1	26.15**	9.39*	48.10**	25.10**	74.02**	7.60	57.27**	45.67*	130.77**	36.11	-5.34*	24.95*
HUM-6 × BHU-U-1	40.15**	10.87*	46.10**	26.41**	48.13**	11.46**	28.18	17.73*	84.62**	48.61**	-4.66	17.18**
HUM-6 × KUG-427	46.92**	15.29*	52.94**	12.69**	51.20**	17.95**	38.18*	31.58*	16.67	36.26*	20.00**	23.42**
HUM-26 × Azad-U-1	4.15	-22.16**	33.46**	-12.65**	28.00**	10.34	20.91	10.53	38.46*	18.52	6.38*	63.21**
HUM-26 × BHU-U-1	33.85**	5.75	48.85**	5.05*	31.06**	10.32	45.45*	25.63	53.85**	20.83	-11.72**	42.97**
HUM-26 × KUG-427	10.31**	-34.87**	33.23**	5.58	92.43**	25.76**	6.36	4.27	29.49	11.88	6.38*	41.65**
SE	0.87	-	1.19	-	3.88	-	0.83	-	0.55	-	0.63	-
CD 5%	2.01	-	2.74	-	8.95	-	1.90	-	1.27	-	1.44	-
CD 1%	2.92	-	3.99	-	13.03	-	2.77	-	1.83	-	2.10	-

Table 4 Contd…

Crosses	Pod length (cm)		Seeds per pod		Clusters per plant		100-Seed weight (gm)		Seed yield per plant (gm)	
	EH	ID	EH	ID	EH	ID	EH	ID	EH	ID
PDM-11 × Azad-U-1	-58.67**	-61.29**	-74.59**	-23.40	93.46**	23.86**	-12.79*	-6.67	-83.84**	-102.70*
PDM-11 × BHU-U-1	-57.33**	-46.88*	-79.46**	-139.47*	-12.69	-40.97**	-18.60**	-14.28	-81.22**	-100.00*
PDM-11 × KUG-427	-49.33**	-25.00	-84.86**	-32.14	58.46**	30.83**	-24.42**	-12.31	-84.28**	0.00
HUM-6 X×Azad-U-1	-64.67**	-50.94**	-80.00**	-70.27*	26.54**	6.38	-41.86**	-62.00*	-89.08**	-112.00
HUM-6 × BHU-U-1	-54.67**	-19.12	-66.49**	-56.45*	28.85**	27.46**	-30.23**	-40.00*	-77.29**	-78.85**
HUM-6 × KUG-427	-62.00**	-31.58	-81.08**	-177.14*	10.00	30.77**	-32.56**	-12.07	-84.28**	-133.33
HUM-26 × Azad-U-1	-58.67**	-9.68	-81.08**	-22.85	21.92*	34.70**	-12.79*	-18.67	-82.53**	45.00
HUM-26 × BHU-U-1	-54.00**	-11.59	-83.24**	-96.77*	2.69	22.10**	-36.05**	-47.27*	-90.39**	-63.64
HUM-26 × KUG-427	-64.00**	-33.33	-78.38**	7.50	5.77	-32.00**	-46.51**	0.00	-87.77**	25.00
SE	0.06	-	0.60	-	0.98	-	0.21	-	0.56	-
CD 5%	0.14	-	1.39	-	2.26	-	0.49	-	1.29	-
CD 1%	0.21	-	2.03	-	3.30	-	0.71	-	1.87	-

*, ** significant at 5% and 1% respectively