Combining ability analysis in Black gram (*Vigna mungo* L.)

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Abstract : A study was conducted in blackgram (*Vigna mungo* L. Hopper) to assess the combining ability of the parents as well as hybrids involving 5 lines and 5 testers crossed in LxT pattern. The GCA/SCA ratio has indicated that all the ten characters studied were found to be predominantly controlled by non-additive genes. The parents UH 80-9 and PDU 1 revealed high GCA effects for most of the characters, followed by COBG 302 and COBG 301. Among the hybrids PDU 1 x COBG 9 for days to 50 per cent flowering, Pant U-30 x COBG 301 for seed yield and PDU 1 x COBG 301 for seed protein exhibited the highest SCA effects coupled with high per se performance. *Key Words : SCA and GCA Variance SCA and GCA.*

Choice of the best parents is prerequisite in any crop breeding programmes. Evaluation of parents for their transmission potential for yield and yield components will pave a way for better selection. Since all available parents with high order of performance may not be able to transmit their superior traits into their progenies. Therefore, selection of desirable parents based on their combining ability is increasingly used now-a-days in crop improvement programmes. Much less reports on combining ability studies in black gram are available when compared to other pulses and cereals. Therefore, the present study of L x T analysis in blackgram was undertaken with 5 lines and 5 testers and the results are discussed.

Materials and Methods

A field experiment was conducted at National Pulses Research Centre, Vamban, Tamil Nadu with five diverse black gram lines viz. Vamban 1 (L_1), PDU 1 (L_2), WHBO 9 (L_3), UG 298 (L_4) and Pant U-30 (L_5), five well adopted testers viz. COBG 301 (T_1), COBG 302 (T_2), CO 5 (T_3), COBG 9 (T_4) and COBG 10 (T_5). 25 hybrids in a randomised block design which was replicated thrice. Recommended package of practices were followed. Observations on ten randomly selected plants from each replication for nine characters viz. plant height, days to 50 per cent flowering, primary branch number, cluster number, pod number, pod length, seed number per pod, hundred seed weight and seed yield were recorded and LxT analysis was done as suggested by Kempthrone (1957).

Results and Discussion

The analysis of variance revealed that differences due to genotypes were significant for all traits and variances due to general and specific combining ability (GCA and SCA) were also significant. The GCA/SCA ratio revealed the predominance of non-additive gene action for all characters (Table-1). This is in accordance with the findings of Sagar and Chandra (1977) for pod number and seed yield, Dasgupta and Dass (1987) for pod length and Haque *et al* (1988) for seed number per pod in black gram.

The highest *GCA* effects were recorded by the parents UH 80-9 (days to 50 per cent flowering, pod number and seed yield), Vamban 1 (seed protein), COBG 301 and Co 5 (both for seed yield) for the respective traits revealing the predominance. These additive gene action of on these characters utilising the parents in hybridization programme and transgressive segregants can also be obtained through pedigree method of breeding and selection made for the improvement of these traits.

High *SCA* effects coupled with high per se performance were expressed by the hybrids Vamban 1 x COBG 4 (primary branch number), PDU 1 x COBG 301 (Plant height and seed protein), PDU 1 x COBG 301 (Cluster number and seed yield), UH 80 x COBG 303 (pod number and seed number per pod) PDU 1x Co5 (pod length) and UG 298 x COBG 10 (days to 50 pr cent flowering) for the respective characters (Table 3). The high *sca* effects might be due to combination of favourable genes from both the parents or due to linkage at repulsion phase (Sarsan et al (1986).

The crosses PDU 1 x UH 809 (plant height, seed yield and seed protein), Vamban 1 x COBG 302 (days to 50 per cent flowering), PDU 1 x COBG 302 (cluster number and seed yield), UH 80-9 x COBG 9 (seed nuber per pod and seed yield), UH 80S-9 x COBG 9 (pod length) and PDU 1 x COBG 10 (hundred

seed weight) in which the parents had high *per se* and *GCA* effects exhibited high *sca* effects. This may be due to addition of favourable genes and additive x additive gene interaction.

In contrary to this the parents with high *GCA* effects also resulted in low *SCA* effects as in the case of Vamban 1 x COBG 10 (plant height and pod number), PDU 1 x COBG 9 (days to 50 per cent flowering), UG 298 x COBG 9 (cluster number, seed yield and seed protein), Pant U-30 x COBG 301 (hundred seed weight and seed number per pod) and Vamban 1 x COBG 9 (pod length) which may also involve additive gene effects and throw transgressive segregants in advanced generations for effective selection of elite progenies.

The hybrids such as Vamban 1 x COBG 9 (plant height and pod length), Pant U-30 x COBG 301 (pod number, seed yield and seed protein), UG 298 x COBG 10 and UG 80-9 x CO 5 (days to 50 per cent flowering), UH 80-9 x COBG 10 (cluster number, seed number per pod

and seed protein) and Plant U-30 x CO 5 (pod number and seed yield) exhibited high *SCA* effects with one of the parents having good general combining ability. Non-additive interallelic interaction like complementary gene interaction is suggested can be economically utilized either by exploiting hybrid vigour or by selecting elite segregants in the late regenerations.

A score chart was prepared by alloting + 1, 0, -1 scores to the parents with significant, non-significant and negative significant *SCA* effects respectively (Table-4). The parents UH 80-9 and PDU 2 scored the highest values of +9 and +8 respectively followed by COBG 301 and COBG 302 which scored +2 each. Since none of the parents had high *GCA* effects for all characters under study multiple crossing programme involving these parents to fix additive genetic variance and subsequent diallele mating system to increase the genetic variance in each generation is suggested for the improvement of blackgram for the economic traits.

From the present study it can be concluded that the

characters under study were predominantly controlled by both additive as well as non-additive gene action and breeding by pedigree method would result in partial exploitation of additive and additive x additive gene action in blackgram.

Table 1. Mangnitude of CCA amd SCA variances of yield and yield components

S.No.	Characters	CCA variance	SCA variance	CCA : SCA
1.	Plant height	0.0239	16.2323	0.0015:1
2.	Days to 50 per cent flowering	0.1243	9.0651	0.0137:1
3.	Primary branch number	0.0020	0.5278	0.0038:1
4.	Cluster number	0.0147	10.7848	0.0014:1
5.	Pod number	-1.3903*	133.3630	-
6.	Pod length	0.0044	0.2229	0.0197:1
7.	Seed number per pod	0.0023	0.2569	0.0090:1
8.	Hundred seed weight	-0.0005*	0.1144	-
9.	Seed yield	-0.0480*	13.0172	-
10.	seed protein	-0.0217*	3.3281	-

*Considered as zero.

Table 2. General combining abilaity effect of parents

Parents	Plant height	Days to 50% flo	Primary branch wering	Cluster number number	Pod number	Pod length	Seed number	Hundred seed per pod	Seed protein weight	Seed yield
Vamban 1	-2.03**	-1.47**	0.37	0.65	-4.00	-0.10	-0.21	0.04	-2.07	0.95
PDU 1	3.29	1.67	-0.27	0.79	1.76	0.17	0.16	0.10	1.95	0.40
UH 80-9	0.64	2.33	0.47	0.98	5.84	0.42	0.27	-0.03	1.72	0.60
UG 298	-0.97	-2.33	-0.24	0.74	-1.60	-0.07	0.05	0.18	--0.39	
Pant U 30	-0.94	0.40	0.31	-1.67	-1.99	-0.43	-0.28	-0.93	-1.56	
COBG 301	2.08	0.27	0.06	0.17	5.46	-0.01	-0.43	-0.16	0.72	0.71
COEG 302	-1.21	-0.93	0.42	0.79	0.02	-0.15	0.13	0.13	1.36	0.19
Co 5	-0.92	-1.00	-0.14	2.35	5.17	0.06	0.16	-0.05	0.56	-0.27
COBG 9	1.24	0.73	-0.35	-1.38	-3.29	-0.07	0.11	0.01	-0.54	-0.02
COBG 10	-1.18	0.93	0.02	-1.93	-7.36	0.17	0.03	0.08	-2.10	-0.60

*Significant of 1 per cnt level   **Significant at 5 per cent level

Table 3. Specific combining abilty effects

Hybrids	Plant height	Days to 50% flo wering	Primary branch	Cluster number number	Pod number	Pod length	Seed number	Hundred seed per pod	Seed yield weight	Seed protein
L1 x T1	-5.36**	-1.07	-0.49**	-2.47**	-14.40**	0.02	-0.84**	-4.29**	-2.03**	
L1 x T2	-4.36**	-2.20**	-0.85**	-4.12**	-12.43**	0.10	0.22*	-0.03	-3.17**	1.62**
L1 x T3	-0.11	1.87**	0.44**	2.83**	-4.48**	-0.06	0.13	0.16**	-0.81*	0.25
L1 x T4	8.34**	0.80	1.35**	5.49**	24.25**	0.25**	0.62**	0.36**	7.17**	-0.27
L1 x T5	1.49**	0.60	-0.45**	-1.73**	7.05**	-0.30**	-0.08	0.36**	1.09**	0.44
L2 x T1	6.79**	2.07**	-0.45**	0.33	12.88*	-0.15*	-0.27**	0.10*	3.32**	2.86**
L2 x T2	2.34**	-1.07	1.09**	4.85**	6.68**	0.51**	0.31**	0.16**	4.00**	2.42**
L2 x T3	-1.114*	-2.00*	-0.32*	-0.94	-9.64**	0.02	0.20**	-0.37**	-2.38**	-1.62**
L2 x T4	-5.08**	-4.07**	-0.41**	-2.81**	-12.78**	-0.10	-0.37**	-0.21**	-5.48**	-1.42**
L2 x T5	-2.90**	3.07**	0.09	-1.43*	1.86*	-0.27**	0.14**	0.32**	0.54	-2.24**
L3 x T1	-2.94**	1.47*	0.27	0.14	-0.68	0.19**	0.92	0.16**	-0.36	-0.31
L3 x T2	1.85**	-1.00	0.21	0.99	13.42**	-0.21**	0.24**	-0.28**	2.86**	-2.28**
L3 x T3	1.84**	-1.60**	-0.19	-2.60**	1.11	0.20**	-0.32**	0.10*	-0.02	2.15**
L3 x T4	-3.19**	1.67**	0.38*	-0.31	-11.143*	-0.34**	-0.17*	0.04	-2.98**	-0.93**
L3 x T5	2.44**	-0.53	0.15	1.77**	-2.43**	-0.15*	0.23**	-0.03	0.50	1.37**
L4 x T1	-1.37**	-1.53**	-0.09	-0.01	-11.06**	0.01	0.63**	0.17**	-3.24**	-1.80**
L4 x T2	0.86	2.00**	-0.05	-0.79	2.50**	0.52**	-0.52**	0.18**	0.31	-0.84*
L4 x T3	-0.22	-1.60**	-0.25	-1.98**	-1.18	-0.36**	0.08	-0.11(	1.069**	1.02*
L4 x T4	0.96	4.00**	01.53**	3.61**	12.38**	0.57**	.29**	0.11**	2.86**	2.57**
L4 x T5	-0.23	-2.87**	-0.15	-0.84	-2.65**	0.30**	-0.31**	-0.36**	-0.98**	-0.95*
L5 x T1	2.88**	-0.93	0.62**	1.99**	13.26**	-0.07	0.52**	0.42**	4.59**	1.28**
I5 X T2	-0.69	2.27**	-0.41**	-0.93	-10.18**	0.12*	-0.25	-0.04	-4.00**	-0.92*
L5 x T3	-0.37	1.33*	0.32**	2.69**	13.18**	0.20**	0.07	0.2188	2588	-1.80**
L5 x T4	-1.02	-2.40**	-1.10**	-5.99**	-12.43**	-0.38**	-0.37**	--0.30**	-1.57**	0.06
L5 x T5	-0.80	-0.27	-0.36*	2.23**	-3.83**	0.13*	0.02	-0.30**	-1.16**	1.35**

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Table 4. Score chart (based on gca effects of parents)

Parents	Plant height	Days to 50 % flowering	Primary branch number	Cluster number	Pod number	Pod length	seed number per pod	Hundred seed weight	Seed yield	Seed Protein	Total score
L1	-1	-1	+1	+1	-1	-1	-1	0	-1	+1	-3
L2	+1	+1	-1	+1	+1	+1	+1	+1	+1	+1	+8
L3	+1	+1	+1	+1	+1	+1	+1	0	+1	+1	+9
L4	-1	-1	-1	-1	-1	-1	0	+1	-1	-1	-7
L5	-1		-1	-1	-1	-1	-1	-1	-1	-1	-9
T1	+1	0	0	0	+1	0	-1	-1	+1	+1	+2
T2	-1	-1	+1	+1	0	-1	+1	+1	+1	0	+2
T3	-1	-1	-1	+1	+1	+1	+1	-1	0	+1	
T4	+1	+1	+-1	-1	-1	-1	+1	0	-1	0	-2
T5	-1	+1	0	-1	-1	+1	0	+1	-1	-1	-2

+1 = High status   0 = Moderate status   -1 = Low status

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Association analysis in black gram (*Vigna mungo* (L.) Hepper)

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Abstract : Correlation coefficient and path analysis studies conducted with ten parents and their twenty five hybrids revealed that primary branch number, cluster number, pod number, pod length and seed number per pod had strong positive association with yield. Besides, their inter correlations were positive and significant, indicating the possibility of improving these characters simultaneously. The path analysis indicated that the contribution of pod number followed by seed number per pod and primary branch number was much through direct effects and their indirect effects by way other traits were also much pronouncing. Seed protein had no association with any of the other characters and its direct effect on yield was also less. *(Key words : Correlation, Path analysis, Direct effects, Indirect effects)*

Yield is a complex Mentity and is associated with number of component characters which were themselves interrelated. Such inter dependence often affects their relationship with yield, thereby making correlation coefficient ineffective. So there is a need to partition the correlations into direct and indirect effects to get the information on actual contribution of each character to yield. Thus, correlation in conjunction with path analysis would give a better insight into cause and effect relationship between different pairs of characters.

Materials And Methods

Ten parents along with their twenty five hybrids were raised in a randomised block design, replicated thrice. Normal agronomic practices were followed throughout the crop period. Ten randomly selected plants were labelled for recording observations in each replication for the characters, plant height, days to 50 per cent flowering, primary branch number, cluster number, pod number, pod length, seed number per pod, hundred seed weight, seed yield and seed protein.