

Effect of irradiation, mating schemes and selection methods on nature of association of seed yield and its components in blackgram

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Abstract: Phenotypic correlation of seed yield and its component traits were studied in four selected irradiated F_3M_3 population, two three way and one double cross populations of blackgram advanced through bulk, individual plant selection (IPS) and single pod descent (SPD) method. All the twenty one populations exhibited significant positive correlation of plant height, number of clusters and pods per plant with seed yield per plant except three populations of bulk and one population of IPS method for plant height. Irradiated population of single cross 4 for pod length, single cross 1, 3 and three way cross 1 for number of seeds per pod exhibited significant positive correlation with seed yield per plant irrespective of the methods of advancement. The nature of association between pod length in three way cross 1 and number of seeds per pod in double cross advanced through bulk method was changed from negative to positive in IPS and SPD methods. Among the three methods of selection, single pod descent method showed a stronger magnitude and higher number of significant correlation in all the seven populations under study as compared to bulk and IPS methods. Most of the traits under study including pod length and number of seeds per pod contributed towards seed yield per plant in single cross $F_3 M_3$, three way and double cross populations.

Key words: *Blackgram, vigna mungo, selection methods, bulk, individual plant selection (IPS) and single pod descent method (SPD)*

Introduction

The natural variability for yield and its component traits are very narrow in a highly self pollinated crop like black gram and the scope of selection is very limited. Grafius (1959) opined that there may not be any genes for yield as such but operates only through its components. The nature of associations among yield and its components in advanced generations would be of practical value to the breeder for exercising selection. Blackgram is mostly grown on marginal lands, therefore it is possible that genes for high productivity could have been lost due to overriding role of natural selection. Induced mutations may compensate for such losses by creating variability and three way and double cross populations of selected lines for seed yield and component traits would increase the possibility of creation of desirable variability. However, when the segregating generations are

handled by different breeding methods, the nature and degree of character associations are likely to be changed. The information on the influence of different breeding methods on associations may be useful in planning a breeding programme and also in determining the efficiency of breeding methods. In view of this, the present study was conducted to determine relative shifts in the association brought about by different mating schemes and methods of generation advancement in blackgram.

Material and methods

The F_2M_2 progenies of four single crosses (TAU-1x169, TAU-Lx216, Mankyax169, Manikya x216). F_2 progenies of two three way crosses [(TAU1x169) x216] and [(Manikyax216) x169] and one double cross [(TAU1x169) x (Manikya x 216)] advanced through bulk, individual plant selection (IPS) and single pod descent - (SPD)

Table 1. Phenotypic correlations of different quantitative characters with seed yield per plant in F₃, M₃ and F₃ progenies of blackgram crosses

Population	Plant ht	No. of clusters/ plant	No. of pods/ plant	Pod length	No. of seeds/ pod	100-seed weight
<i>Bulk method</i>						
Single cross-1	0.270**	0.596**	0.682**	0.158	0.600**	0.010
Single cross-2	0.048	0.331**	0.692**	0.076	0.696**	0.266**
Single cross-3	0.124	0.777**	0.823**	0.081	0.106	0.037
Single cross-4	0.308**	0.838**	0.904**	0.321**	0.120	0.317**
TWC1	0.299**	0.732**	0.755**	-0.028	0.174*	0.144
TWC2	0.112	0.782**	0.862**	0.209**	0.024	0.105
DC	0.148*	0.645**	0.808**	0.096	-0.082	0.033
<i>IPS method</i>						
Single cross-1	0.316**	0.700**	0.926**	0.162*	0.445**	0.100
Single cross-2	0.336**	0.793**	0.923**	0.436**	0.431**	0.217*
Single cross-3	0.128	0.739**	0.791**	0.132	0.090	0.205
Single cross-4	0.202*	0.815**	0.854**	0.636**	0.682**	0.328**
TWC1	0.249**	0.582**	0.799**	0.447**	0.345**	0.138
TWC2	0.196*	0.737**	0.933**	0.029	0.090	0.236**
DC	0.280**	0.832**	0.718**	0.017	0.642**	0.250**
<i>SPD method</i>						
Single cross-1	0.264**	0.859**	0.850**	0.250*	0.675**	0.145
Single cross-2	0.381**	0.727**	0.880**	0.398**	0.496**	0.307**
Single cross-3	0.284**	0.632**	0.876**	0.380**	0.529**	0.209*
Single cross-4	0.214*	0.724**	0.826**	0.536**	0.646**	0.335**
TWC1	0.505**	0.819**	0.888**	0.406**	0.748**	0.272**
TWC2	0.331**	0.833**	0.850**	0.366**	0.199	0.423**
DC	0.191**	0.622**	0.919**	0.416**	0.520**	0.148*

** = Significant at 1% level

* = Significant at 5% level

Table 2. Phenotypic correlations of different quantitative characters with number of pods per plant in F₃ M₃ and F₃ progenies of blackgram crosses.

Populations	Plant ht	No. of clusters/plant	Pod length	No. of seeds/pod	100-seed weight
<i>Bulk method</i>					
Single cross-1	0.290**	0.850**	0.023	0.460**	0.030
Single cross-2	0.146	0.372**	0.020	0.612**	0.206*
Single cross-3	0.125	0.859**	0.057	0.101	0.047
Single cross-4	0.320**	0.937**	0.289**	0.101	0.203*
TWC1	0.136	0.625**	0.289**	0.547**	-0.101
TWC2	0.149	0.890**	0.220**	0.004	0.065
DC	0.132	0.814**	0.017	0.008	0.046
<i>IPS method</i>					
Single cross-1	0.261**	0.921**	0.159	0.437**	0.037
Single cross-2	0.389**	0.858**	0.215*	0.419**	0.148
Single cross-3	0.331**	0.887**	0.177	0.106	-0.071
Single cross-4	0.196*	0.890**	0.472**	0.493**	0.156
TWC1	0.299**	0.761**	0.410**	0.308**	0.036
TWC2	0.082	0.834**	0.024	0.217**	0.202*
DC	0.193*	0.875**	0.063	0.560**	0.090
<i>SPD Method</i>					
Single cross-1	0.427**	0.909**	0.170	0.452**	0.081
Single cross-2	0.289**	0.843**	0.443**	0.444**	0.281**
Single cross-3	0.174*	0.796**	0.384**	0.493**	0.164
Single cross-4	0.323**	0.887**	0.438**	0.550**	0.135
TWC1	0.435**	0.908**	0.027	0.215**	0.162*
TWC2	0.296**	0.911**	0.439**	0.268**	0.317**
DC	0.209**	0.843**	0.368**	0.446**	0.013

** = Significant at 1% level * = Significant at 5% level

methods were used for the present investigation. The parents for these crosses were carefully selected by identifying donor for pod number per plant (169), seed index (216) and two locally adopted varieties like TAU-1 and Manikya. The progenies of above crosses were evaluated by following recommended agronomic practices. Observations were recorded on individual plants and correlation was worked out among seed yield and its component traits viz., plant height, number of clusters per plant, pod length, number of seeds per pod, 100 seed weight and seed yield per plant by using the formulae given by Al. Jibouri *et al.* (1958).

Results and Discussion

The results of correlation analysis involving seed yield and its components are presented in Table 1 to 3.

Similar to the findings of Boomikumar and Rathinam (1981) and Malik *et al.* (1987) in greengram, the progenies of the seven cross combinations in the present study had significant association of number of pods per plant and number of clusters per plant with seed yield per plant in positive direction and this association was not affected by the selection methods in any of the seven populations. Correlation between number of clusters per plant and number of pods per plant with seed yield per plant showed consistency in magnitude and direction over different selection methods in all the seven crosses. The correlation should be fairly high (significant) and reasonably consistent over breeding methods in order to be a useful parameter and to have relevance in a crop improvement programme. Hence, selection for number of clusters per plant and number of pods per plant would definitely influence seed yield per plant, in desirable direction.

Change in association pattern

Out of the seven segregating populations, bulk method had significant inter character association between plant height and seed yield

in four populations compared to six and seven populations in IPS and SPD methods respectively. Between pod length and seed yield per plant significant associations in positive direction were exhibited by two populations under bulk method, four in IPS method and in all the seven populations under SPD method. Positive significant correlation between number of seeds per pod and seed yield per plant were observed in three, five and seven populations in bulk, IPS and SPD methods respectively. Similarly, hundred seed weight exhibited significant associations in two populations under bulk method, in four under IPS method and in six populations under SPD method. Similar results on associations with seed yield per plant were reported by Verma (1992) and Ram and Singh (1993) for plant height. Satyan *et al.* (1980) and Golasangi *et al.* (1996) for pod length. Raut *et al.* (1988) and Damodaran *et al.* ((1989) for number of seeds per pod and Sarker *et al.* (1984), Kumari and George (1985) and Mishra *et al.* (1995) for hundred seed weight.

Based on these results, SPD method appears to be superior over bulk and IPS methods on the basis of nature and magnitude of associations in desirable direction. To substantiate this, crosses like single cross 3 (Manikya x 169) exhibited non significant association for plant height and hundred seed weight with seed yield per plant under bulk and IPS methods but exhibited significant association under SPD method. Double cross [(TAU 1x169) x (Manikyax216)] and single cross 3 for pod length, three way cross 2 [(Manikyax216) x169)] for number of seeds per pod and single cross 1 (TAU1x169) and single cross 3 progenies for hundred seed weight exhibited non significant association with seed yield per plant under bulk and IPS methods but exhibited significant association under SPD method. The negative association of pod length in three way cross 1 [(TAU 1 x 169) x216] and number of seeds per pod in double cross [(TAU 1x169) x (Manikyax216)] population under bulk method was shifted to positive significant association under IPS and SPD methods.

Table 3. Phenotypic correlations of different quantitative characters with hundred seed weight in F_3 , M_3 and F_3 progenies of blackgram crosses.

Population	Plant ht	No. of clusters/plant	Pod length	No. of seeds/pod
Bulk method				
Single cross-1	0.070	0.037	0.005	0.087
Single cross-2	0.109	0.252**	0.087	0.092
Single cross-3	0.014	0.156*	0.053	0.102
Single cross-4	0.114	0.172*	0.064	0.399**
TWC 1	0.270**	0.098	0.068	0.097
TWC 2	0.105	0.044	-0.020	0.036
DC	0.056	0.058	0.065	0.018
IPS method				
Single cross-1	0.051	-0.139	0.037	0.105
Single cross-2	0.180	0.112	0.123	0.069
Single cross-3	0.044	0.100	0.080	0.049
Single cross-4	-0.029	0.180*	0.085	0.152*
TWC 1	0.109	-0.002	0.056	0.067
TWC 2	0.090	0.190*	0.430**	0.067
DC	0.287**	0.153*	0.065	0.178*
SPD method				
Single cross-1	0.101	0.050	0.260**	0.120
Single cross-2	0.239**	0.231**	0.310**	0.258**
Single cross-3	0.142	0.073	0.149*	0.241**
Single cross-4	0.214*	0.169	0.182*	0.340**
TWC 1	0.337**	0.244**	0.232**	0.231**
TWC 2	0.233**	0.324**	-0.053	0.215**
DC	0.426**	0.123	0.248**	0.194**

** = Significant at 1% level

* = Significant at 5% level.

Number of clusters per plant, number of seeds per pod, plant height and pod length exhibited higher degree of association with number of pods per plant in majority of the progenies under different selection methods (Table 2). Jiban Mitra and Mehra (1998) in grass pea also reported such results. These results reveal that increase in seed yield was not due to number of pods per plant alone but also due to increased clusters per plant, seeds per pod, plant height and pod length. However, hundred seed weight and number of pods per plant were not strongly associated in all the seven populations indicating increase in one character may result in decrease in other character.

The progenies of single cross 1 (TAU 1x169) for plant height, single cross 4 (Manikya x 216) for pod length, single cross 1, single cross 2 (TAU1 x 216) and TWC 1 [(TAU 1 x 169) x 216] for number of seeds per pod exhibited significant association in positive direction with number of pods per plant in all the three methods indicating that hybridization followed by irradiation might have changed undesirable linkages in the above populations.

It could be concluded that some of the desirable shifts in the association pattern occurred due to mutation of heterozygous genotypes, but there was no definite trend. In some cases the shift due to mutation was desirable like for number of clusters per plant and number of seeds per pod, while in other cases like hundred seed weight it was not desirable. However, by carefully selecting the parental genotypes and dosage of mutation it is possible to generate wider variability and hence desirable shifts in the character associations.

From table 3, it is clear that most of the progenies advanced through bulk and IPS methods have recorded non-significant association of plant height, clusters per plant, pod length and number of seeds per pod with hundred seed weight. However, comparatively large number of progenies advanced through SPD method exhibited

significant association of plant height, clusters per plant, pod length and number of seeds per pod with hundred seed weight. These results reveal that the improvement in seed yield has to be brought either with increased number of pods per plant or clusters per plant or with increased seeds per pod and not by improving test weight, as it has exhibited non significant association with majority of the characters. Hence, it is desirable to select genotypes with more number of pods per plant with optimum seed size for improvement of seed yield per plant.

Identification of best population

An attempt was made to score each population on the basis of significant correlation values as favourable or unfavourable association and non significant values as neutral association (Table 4).

Out of seven populations, irradiated single cross 2 population, TAU-1x216 recorded highest (33) number of favourable association values followed by TWC1 [(TAU-1x169)x216 and single cross 4 (Manikya x 216) populations. Among the different populations, Manikya x 169 scored lowest number of favourable significant correlations among the important seed yield, pod number and 100 seed weight contributing traits. All the populations exhibited one or two unfavourable correlation coefficients except TAU-1 x 216 population with highest number of favourable associations. The populations with highest number of associations could be considered as an ideal for further isolation of superior genotypes.

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Table 4. List of scores obtained by different populations on the basis of nature of correlation in F_2 , M_3 and F_3 generations of blackgram

Population	Favourable	Unfavourable	Neutral
<i>Single cross (Irradiated)</i>			
1) TAU-1 x 169	24	1	20
2) TAU-1x216	33	0	12
3) Manikya x 169	17	1	27
4) Manikya x 216	30	1	14
<i>Three way cross</i>			
5) [(TAU-1x169)x216]	31	3	11
6) [(Manikyax216)x169]	28	2	14
<i>Double cross</i>			
7) [(TAU-1 x 169) x (Manikya x 216)]	28	1	15

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