Breeding Potential of Crosses Derived from Parents Differing in Overall GCA Status for Productivity *per se* Traits and Powdery Mildew Disease Response in Blackgram [*Vigna mungo* (L.) Hepper]

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ABSTRACT

Background: Predicting the breeding potential of crosses in terms traits means, genetic variability and frequency of desirable transgressive segregants in early segregating generations is crucial in breeding programme. Therefore, an experiment was carried out to assess breeding potential of crosses involved parents with varying overall GCA status and contrasting responses to powdery mildew disease (PMD) in blackgram.

Methods: Total of 40 F_1s developed by following Line × Tester design; among, nine crosses were selected based on gca status of parents and responses to PMD. F_1, F_2 and F_3 along with parents of six and three crosses were evaluated for 10 productivity *per se* traits and responses to PMD separately during *kharif*, 2016 and *rabi*, 2016-17 respectively. The traits means, absolute and standardized range, PCV and frequency of transgressive segregants in F_2 and F_3 were compared to assess the breeding potential of the crosses.

Result: F_2 and F_3 generations derived from six crosses (for productivity traits) and three crosses (for PDI) were differed for means, absolute and standardized range, PCV and the frequency of transgressive segregants. This is may be due to the contribution of diverse genes from female and male parent. Though considerable number of transgressive segregants were also identified in F_2 and F_3 of all the crosses, high frequency of desirable transgressive segregants was observed in crosses involved parents with overall high GCA status.

Key words: Blackgram, Combining ability, Genetic variability, Transgressive segregants.

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is an important pulse crop grown in India. It accounts 10% of total pulse production (3.06 MT) from 13% of total area (5.60 M ha) in India (Sakila and Pandiyan, 2018) with productivity of 546 kg ha^{-1} (Singh *et al.*, 2020). The productivity of blackgram is very low and mainly attributed to narrow genetic base of breeding material used, poor plant type, non-availability of high yielding cultivars, cultivation in marginal land and susceptibility to biotic and abiotic stresses. Among the biotic stresses powdery mildew disease (PMD) caused by *Erysiphe polygoni* DC, is the most destructive disease and most prevalent in late sown *kharif* crop or *rabi* blackgram crop (Boraiah *et al.*, 2017). Which causes potential yield loses up to 90% depending on crop stage and severity. Development of resistant cultivars is an effective and eco-friendly approach to mitigate losses due to the disease and it depends on availability and utilization of diverse genetic resources. An ample of resistance sources has been identified in blackgram for PMD by several researches and reported genetic variation in responses to PMD (Prashanthi *et al.,* 2010; Boraiah *et al.*, 2017).

Besides, biotic stresses, low genetic variability, handling and selection of large number of early segregating population results in vague selection of early segregating population are the major bottlenecks. Plant breeders often face the problem of selecting parents and subsequently a

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few potential crosses out of a large number of crosses in early segregating generations. The traits mean and variance of early segregating generations serve as useful statistical estimates for predicting the breeding potential of crosses. Further, it is desirable to practice selection for economically important and yield attributing traits in segregating populations derived from crosses which exhibits high

breeding potential in terms of recovering high frequencies of high yielding pure lines in advanced generations (Suresh, 2016). It depends on identification and isolation of transgressive sergeants for yield contributing traits.

Although several studies reported genetic variability and transgressive segregants for productivity *per se* traits (Basamma, 2011; Boraiah, 2017) in blackgram. However, few studies predicted the parental attributes contributing for genetic variability and transgressive segregants in early segregating generations and selection of potential crosses thereof. Thus, in the present study, the crosses involved parents with varying overall GCA status were compared in terms of mean values, absolute and standardized range, PCV and frequency of transgressive segregants for productivity traits and PMD reaction to frame a selection criteria for identification of potential crosses.

MATERIALS AND METHODS
Development of experimental materials

Forty F_1s developed by crossing 10 diverse genotypes with the four genotypes contrasting for PMD response following L × T mating design (Kempthorne, 1957) during 2014. The seed materials of parental lines were obtained from ZARS, UAS, GKVK, Bengaluru. Among 40 F_1 s, six crosses (C1: VBN 4 × LBG 17; C2: COBG 653 × LBG 17; C3: VBG 10-024 × DBGV 5; C4: DU 1 × TAU 1; C5: LBG 752 × DBGV 5 and C6: T 9 × LBG 685) were selected based on overall general combining ability and specific combining ability for productivity *per se* traits (Boraiah *et al*., 2019). Of these six crosses, C1, C2 involved both the parents with overall high gca status (H × H); C3 involved both the parents with overall low gca status (L × L) and the remaining three crosses were contrasting for overall gca status (H × L/L × H). The selfed seeds from these six F_1 s harvested and bulked separately and were sown to raise F_2 populations during 2015 *rabi* season. From each F_2 population, 60 plants were selected randomly and selfed to generate F_3 populations. Further, three crosses (C5: LBG 752 × DBGV 5; C6: VBN 6 × LBG 17 and C7: LBG 625 × LBG 17) were selected based on contrasting for responses to PM disease (Supplementary Table 1). Similarly, the selfed seeds from these three F_1s harvested and bulked separately and were sown to raise F_2 populations during 2016 *Kharif* season. From each F_2 population, 60 plants were selected randomly and selfed to generate F_3 populations.

Evaluation for productivity *per se* traits and PMD response

The seeds of 10 parents, six F_1 s (C1, C2, C3, C4, C5 and C6) and their F_2 and F_3 generations were planted in a single row of 2 m length with a spacing of 30×10 cm in randomized block design with two replications during 2016 *kharif*. A total of 20 parental plants, 20 plants in each F_1, 200 F_2 plants and 60 F_3 progenies of each of the six crosses were maintained. Recommended agronomic and plant protection practices were followed to raise a healthy crop. Data was recorded on five randomly selected plants in each replication of the P_1, P_2 and F_1, all F_2 plants and 10 randomly selected plants from each F_3 progenies on eight productivity *per se* traits *viz*., days to 50% flowering (DFF), plant height (PH), branches plant[-1] (BRP), days to maturity (DTM), clusters plant[-1] (CLP), pods plant[-1] (PDP), seed yield plant[-1] (YLD) and 100 seed weight (SW).

Similarly, the seeds of the five parents, three F_1s (C5, C7 and C8) and their F_2 and F_3 generations were sown during 2016 *rabi* to assess reaction to PMD under natural condition. Data on PMD severity was recorded on ten randomly selected plants in each replication of the P_1, P_2 and F_1, all F_2 plants and 10 randomly selected plants from each F_3 progenies. The PMD severity was recorded as per the method described by Gawande and Patil (2003). The per cent disease severity was converted into per cent disease index (PDI).

Statistical analysis

The data recorded on 10 productivity *per se* traits and PDI was used for statistical analysis to compute QTs mean, absolute range (AR) and standardized range (SR). The phenotypic coefficient of variation (PCV) was estimated according to Burton and Devane (1953). The data recorded for productivity traits and PMD responses under study were analysed by using Windowstat 8.0 (developed by Indostat services 18.0, Ameerpet, Hyderabad, India).

Estimating breeding potential of the crosses

The crosses with high QT mean, range, PCV and frequency of transgressive segregants in F_2 and F_3 generations were considered as better breeding potential crosses to produce high frequency of desirable recombinant inbred lines (RIL) in advanced generations.

Identification of transgressive segregants

In F_2 and F_3 progenies, the number of plants scoring lower than lower scoring parent and higher than higher scoring parent for each of the 10 productivity traits and PDI were counted and designated as transgressive segregants.

RESULTS AND DISCUSSION

The six crosses (C1, C2, C3, C4, C5 and C6) involved parents with varying overall gca status (Supplementary Table 2 and 3) and three crosses (C5: LBG 752 × DBGV 5; C6: VBN 6 × LBG 17 and C7: LBG 625 × LBG 17) contrasting for responses to PM disease (Supplementary Table 1) were compared in terms of quantitative traits (QTs) mean values, absolute and standardized range, PCV (Table 1 and 2) and frequency of transgressive segregants in F_2 and F_3 generations (Table 3). The mean values of the most of the traits were higher in F_2 generation compared to F_3 generation in all the crosses. However, *per se* performance of F_2 generations were higher in C1 and C6 for plant height (63.16 cm and 58.95 cm), branches plant[-1] (4.29 and 3.83) and seed yield plant[-1] (14.38 and 14.39). Similarly, absolute range for the most of the traits were higher in C1 and C4 in F_2 and

Table 1: Estimates productivity traits means, absolute range (AR) and standardized range (SR) and phenotypic coefficient of variation (PCV) in F_2 and F_3 generations derived from six crosses in blackgram.

Cross	Generations	Variables	DFF (days)	PH (cm)	BRP	DTM (days)	CLP	PDP	YLD (gm)	SW (gm)
C1	F_2	Mean	40.66	63.16	4.29	80.98	13.53	41.77	14.38	5.8
(H × H)		PCV	4.45	20.14	26.82	3.21	31.06	45.96	50.2	9.01
		AR	36-46	38-94	2-7	75-90	5-25	12-108	2.1-41	4.5-6.88
		SR	0.25	0.89	1.17	0.19	1.48	2.3	2.71	0.41
	F_3	Mean	42.34	49.26	3.47	82.17	8.69	28.27	8.04	5.51
		PCV	4.79	19.97	22.58	2.32	38.58	51.68	60.47	9.73
		AR	40.1-44.9	30.6-63.6	2.9-4.5	79.9-84.4	5.3-11.8	16.2-44	4.24-13.0	4.99-5.95
		SR	0.11	0.67	0.46	0.05	0.75	0.98	1.09	0.17
C2	F_2	Mean	37.52	43.16	3.8	77.66	10.61	34.03	11.73	5.74
(H × H)		PCV	4.47	28.39	24.4	2.36	29.61	42.09	43.77	10.79
		AR	35-42	20-83	2-7	75-82	5-20	11-90	2.5-26.5	4.28-7.02
		SR	0.19	1.46	1.32	0.09	1.41	2.32	2.05	0.48
	F_3	Mean	37.9	33.67	3.31	78.01	9.1	34.81	10.59	5.86
		PCV	4.41	36.75	23.75	2.11	33.61	50.35	52.63	9.94
		AR	35.9-40.2	17.8-50	2.7-4.2	76.2-80.2	6.4-13.7	19.2-71.5	5.52-20.2	5.36-6.32
		SR	0.11	0.96	0.45	0.05	0.8	1.5	1.39	0.16
C3	F_2	Mean	39.71	55.81	4.02	78.13	13.1	35.06	10.56	5.72
(L × L)		PCV	4.42	21.67	32.02	2.6	31.42	37.05	40.93	10.1
		AR	35-43	28-78	2-9	73-83	6-24	13-70	2.2-22.5	4.5-6.85
		SR	0.2	0.9	1.74	0.13	1.37	1.63	1.92	0.41
	F_3	Mean	38.34	39.94	3.6	78.4	11.46	38.12	11.42	5.66
		PCV	4.71	27.97	23.26	2.25	35.52	50.62	51.55	9.03
		AR	35.4-40.3	23.2-61.3	2.7-5	75.7-80.2	7-18.9	21.4-73.9	5.87-18.7	5.18-6.08
		SR	0.13	0.95	0.64	0.06	1.04	1.38	1.13	0.16
C4	F_2	Mean	38.4	54.74	4.21	77.77	11.8	36.13	12.01	5.77
(H × L)		PCV	3.87	18.69	24.7	2.32	25.94	40.93	47.66	10.64
		AR	35-42	30-83	3-7	75-83	5-20	12-98	1.2-30.6	4.12-7
		SR	0.18	0.97	0.95	0.1	1.27	2.38	2.45	0.5
	F_3	Mean	38.23	36.99	3.43	78.3	10.09	31.24	11.86	5.95
		PCV	3.8	27.87	23.08	1.81	35.61	55.72	52.64	9.39
		AR	36.2-40.3	22-51.2	2.6-4.5	76.5-80	5.7-15.5	9.5-68	5.15-21.9	5.27-6.44
		SR	0.11	0.79	0.55	0.04	0.97	1.87	1.42	0.2
C5	F_2	Mean	39.73	57.05	3.47	79.73	10.94	31.5	10.1	5.72
(H × L)		PCV	4.46	18.94	25.53	2.22	27.5	42.46	48.43	8.09
		AR	36-43	32-78	2-7	76-83	5-20	12-90	2.3-27.8	4.8-6.81
		SR	0.18	0.81	1.44	0.09	1.37	2.48	2.52	0.35
	F_3	Mean	40.73	45.16	3.47	80.65	10.57	33.21	10.88	5.71
		PCV	3.46	22.5	22.7	1.71	29.9	44.35	51.25	8.52
		AR	38.8-42.6	31.3-58.9	2.7-4.5	79.1-82.3	7.1-14.2	14.8-54.6	3.55-16.4	5.13-6.18
		SR	38.8	31.3	2.7	79.1	7.1	14.8	3.55	5.13
C6	F_2	Mean	40.56	58.95	3.83	80.9	14.15	42.47	14.39	5.95
(L × H)		PCV	4.68	22.45	26.53	3.46	32.69	43.64	45.03	7.58
		AR	36-43	28-98	2-9	75-89	5-28	12-109	2.8-38.8	4.85-6.8
		SR	0.17	1.19	1.83	0.17	1.63	2.28	2.5	0.33
	F_3	Mean	42.34	43.25	3.4	81.89	10.59	35.36	11.58	5.79
		PCV	4.79	20.28	24.14	4.32	34.34	43.69	48.55	8.56
		AR	40.1-44.9	29.2-54.7	2.2-4.5	74.1-84.2	5.1-14.4	15.3-61.5	4.53-20.6	5.15-6.16
		SR	0.11	0.59	0.68	0.12	0.88	1.31	1.39	0.17

H: High overall GCA status; L: Low overall GCA status.

F_3 generations than other crosses suggesting the presence of extreme phenotypes in these two crosses. The estimates of standardized range decreased from F_2 to F_3 generations for most of the traits derived from all the six crosses. However, the magnitudes of standardized range were relatively larger in F_2 and comparable in F_3 generations derived from C1 and C6 than those in the other crosses for seed yield plant[-1] and clusters plant[-1]. The estimates of PCV were higher in both F_2 and F_3 generations derived from C1 and C6 for most of the productivity *per se* traits. Further, the estimates of PCV increased from F_2 to F_3 generations derived from C1 for DFF, CLP, PDP, seeds pod[-1], seed yield plant[-1] and 100 seed weight. These results are in agreement with the observations of Veeramani *et al.* (2005); Konda *et al.* (2009) and Neelavathi and Govindarasu (2010) in blackgram. However, the findings of present study are more comparable with findings of Basamma *et al.* (2013) withrespect to wide range of variation for most of the yield attributing traits in F_2 and F_3 and it may due to some common parents used in both the study.

The sergeants in all the crosses transgressed in both the direction (lower parent and higher parent) across all the productivity *per se* traits (Table 3). The sergeants that transgressed desirable parent were more frequent in both F_2 and F_3 generations derived from C3, C4 and C5 for branches plant[-1], plant height, days to maturity, pods plant[-1],

clusters plant[-1] and seed weight than those derived from the other three crosses. However, considerable frequency of transgressive segregants were also observed in C1 and C6 for major yield contributing traits such as pods plant[-1] and seed yield plant[-1] in F_2 generation and for branches plant[-1] (95%), clusters plant[-1] (95%), pods plant[-1] (93%), seeds pod[-1] (93%), 100 seed weight (100%) and seed yield plant[-1] (92%) in C1 in F_3 generation. In accordance with present study Basamma (2011) also reported more number of transgressive segregants for seeds per pod, seed weight and seed yield per plant in two blackgram segregating populations (LBG 17 × TAU 1 and BDU 4 × TAU 1) where two parents (LBG 17 and TAU 1) were common for both studies.

With respect to PMD resistance, the estimates of average PDI was lower for cross derived from C7 followed by C5 in both the segregating generations. While, the estimates of absolute range and estimates of PCV were higher in C7 followed by C5 and C7 in both F_2 and F_3 generations (Table 3). These results suggested the potential utility of C5 and C7 to derive promising RILs in advanced generations based on lower estimates of mean PDI and higher estimates of range and PCV. Similarly, segregants that transgressed resistant parent were more frequent in both F_2 and F_3 generations derived from C5 and C7. Hence, the crosses, C5 and C7 were found to have better breeding potential to derive superior RILs for PMD resistance.

Table 2: Estimates of frequency (%) of transgressive segregants for productivity *per se* traits in F_2 and F_3 populations derived from six crosses in blackgram.

Crosses	Generation	Direction	DFF (days)	PH (cm)	BRP	DTM (days)	CLP	PDP	YLD (gm)	SW (gm)
C1	F_2	> HP	0.00	0.00	4.50	0.00	4.50	41.00	42.00	13.00
(H × H)		< LP	27.50	26.00	63.50	2.50	33.00	45.50	40.50	71.00
	F_3	> HP	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		< LP	0.00	71.67	95.00	0.00	95.00	93.33	91.67	100.00
C2	F_2	> HP	0.00	0.00	0.50	0.00	0.00	16.50	21.50	13.50
(H × H)		< LP	4.50	75.50	79.00	7.00	72.50	57.00	40.50	57.50
	F_3	> HP	0.00	0.00	0.00	0.00	0.00	11.67	8.33	0.00
		< LP	0.00	100.00	95.00	0.00	95.00	56.67	43.33	68.33
C3	F_2	> HP	90.00	66.50	32.00	66.00	66.00	44.50	35.00	29.00
(L × L)		< LP	4.50	26.50	47.00	9.50	25.50	33.50	42.50	61.00
	F_3	> HP	81.67	10.00	3.33	73.33	76.67	43.33	21.67	0.00
		< LP	1.67	80.00	80.00	0.00	20.00	18.33	33.33	83.33
C4	F_2	> HP	44.50	27.50	33.50	34.50	41.50	34.00	38.00	18.50
(H × L)		< LP	2.50	49.00	66.50	27.50	37.50	49.50	48.00	17.50
	F_3	> HP	20.00	0.00	5.00	28.33	10.00	20.00	50.00	6.67
		< LP	0.00	100.00	90.00	3.33	65.00	60.00	35.00	0.00
C5	F_2	> HP	18.50	2.50	12.00	18.50	31.50	22.00	26.50	18.50
(H × L)		< LP	9.00	29.00	88.00	9.00	34.50	65.00	71.50	62.00
	F_3	> HP	13.33	0.00	0.00	15.00	20.00	20.00	25.00	3.33
		< LP	0.00	81.67	98.33	0.00	41.67	65.00	75.00	86.67
C6	F_2	> HP	0.00	1.50	1.50	2.50	8.00	33.00	51.50	26.00
(L × H)		< LP	10.00	34.00	76.00	19.00	25.00	32.00	35.50	28.00
	F_3	> HP	6.67	0.00	0.00	0.00	0.00	6.67	18.33	0.00
		< LP	0.00	95.00	98.33	1.67	56.67	38.33	45.00	58.33

H: High overall GCA status; L: Low overall GCA status; HP: Higher parent; LP: Lower parent.

The frequency of transgressive segregants for productivity *per se* traits and PDI in all the crosses in the present investigation varied from 0 to 100%. This is mainly attributed to genetic variability of parents spread across different traits (Table 1 and 2). In general the crosses involved genetically diverse parents produce ample number transgressive segregants. For instance, Jambormias *et al.* (2015) observed the multiple trait transgressive segregants (18.90%) in F_3 families derived from cross Gelatik × MamasaLereButsiwin mungbean. Though several studies reported fair number of transgressive segregants in interspecific crosses, but it depends on cross compatibility and genetic architecture of diverse parents. The genetic studies indicated that transgressive segregation in desirable direction mostly results from the combinations of alleles from both the parents that have complimentary gene effects dispersed between parents. The individuals that receive 'plus' alleles from both the parents or 'minus' alleles from both the parents are likely to exhibit extreme phenotypes. The present study indicated higher probability of isolating genotypes with maximum number of desirable genes from segregating populations derived from C3, C4 and C5 along with ample of number in C1 and C6 (for productivity traits) and C5 and C7 (for PDI).

The increasing trend and higher magnitude of estimates of QTs means, absolute and standardized range, PCV and ample number of transgressive segregant in desirable directions in F_2 and F_3 generations suggested better breeding potential of C1 and C6 (for productivity traits) and, C5 and C7 (for PDI). Thus, it implies that selecting F_2's and F_3's with higher trait variances and higher means, on the other hand rejecting F_2's and F_3's with different combinations of variances and means, such as low variance and high mean, high variance and low mean or low variance and low mean could be a best criteria for predicting the breeding potential of crosses.

Further, it was observed from present study that the F_2 and F_3 generations derived from six crosses for productivity traits and three crosses for PDI differed across QTs means, absolute and standardized range, PCV and frequency of transgressive segregants due to the contribution of diverse genes from female and male parent. In a study of Boraiah *et al.* (2018) reported that the crosses derived from parents contrasting for overall gca status and/or those derived from parents with intermediate genetic divergence were more frequently heterotic than those derived from comparable gca status and with extreme genetic divergence. Similarly, from findings of the present study concluded that generally the crosses involving parents with high overall GCA status produce more number of desired transgressive segregants and thus such crosses can be selected as potential crosses in breeding programmes.

In the present investigation deliberately selected the crosses involved parents varying overall GCA status to know the consequence and importance of the parent selection in segregating generations. The findings from the current study, it can be concluded that the inclusion of parents with high overall GCA status during hybridization in breeding programme is desirable for recovery of high frequency of transgressive segregants with desirable combinations of

Table 3: Estimates of absolute range, standardized range, mean, PCV for per cent PM disease index in F_2 and F_3 generation of the three crosses in blackgram.

Genetic parameters	C5 (LGB 752 × DBGV 5)		C6 (VBN 6 × LBG 17)		C7 (LBG 625 × LBG 17)	
	F_2	F_3	F_2	F_3	F_2	F_3
Absolute range	0.00-90.48	0.00-52.21	0.00-90.48	0.00-86.77	0.00-53.41	0.00-42.27
Standardized Range	12.69	4.62	8.98	6.21	9.03	5.73
Mean	7.13	11.30	10.07	13.98	5.92	7.37
PCV (%)	131.16	147.96	267.48	305.51	162.18	100.66
Frequency of transgressive segregants (%)	RP 82.0 SP 0.0	RP 20.5 SP 0.0	RP 60.5 SP 0.0	RP 11.0 SP 0.0	RP 78.0 SP 9.0	RP 17.0 SP 1.5

RP: Resistant parent; SP: Susceptible parent.

Supplementary Table 1: Mean *per cent* PM disease index (PDI) of parents and F_1 s of the three crosses in blackgram.

Parent/generation	PDI	Reaction
LGB 752	9.02	Resistant
DBGV 5	90.48	Highly susceptible
LGB 752 × DBGV 5 (F_1)	10.00	Resistant
VBN 6	90.48	Highly susceptible
LBG 17	2.32	Resistant
VBN 6 × LBG 17 (F_1)	9.50	Resistant
LBG 625	30.38	Moderately susceptible
LBG 17	2.32	Resistant
LBG 625 × LBG 17 (F_1)	8.12	Resistant

Supplementary Table 2: Estimates of general combining ability effects for productivity *per se* traits and per cent PM disease index (PDI) in blackgram.

Parents	Days to 50% flowering	Plant height (cm)	Branches plant^{-1}	Days to maturity	Clusters plant^{-1}	Pods plant^{-1}	Seed yield plant^{-1} (g)	100 seed weight (g)	PDI
Lines									
VBN 4	1.89**	3.01**	0.40**	1.01**	0.24	5.00**	2.40**	0.10	-28.53**
VBN 5	-0.61**	-0.85	-0.14	-0.55*	-0.02	-1.56	-0.50	-0.19*	-0.27
VBN 6	-2.05**	-3.21**	-0.14	-0.30	-0.13	0.44	-0.18	-0.12	3.98**
DU 1	-0.86**	-1.07	-0.14	-1.43**	-0.90*	-3.33**	-0.24	0.28**	17.00**
T 9	0.70**	-1.63**	-0.58**	-1.11**	-1.87**	-5.88**	-2.66**	-0.23**	13.84**
LBG 625	1.33**	4.94**	-0.03	1.26**	-0.22	-2.66*	-0.27	0.07	-13.53**
LGB 752	2.01**	12.77**	0.70**	4.20**	2.36**	4.53**	0.81	0.01	-35.77**
VBG 10-010	-1.11**	-3.84**	-0.23*	-0.49*	-0.01	-0.06	-0.54	-0.02	13.28**
VBG 10-024	-0.68**	-5.27**	-0.38**	-0.61*	-0.45	-0.18	-0.97	-0.23**	14.88**
COBG 653	-0.61**	-4.85**	0.52**	-1.99**	0.99*	3.72**	2.14**	0.32**	15.10**
SEm±	0.22	0.61	0.10	0.23	0.44	1.08	0.60	0.08	0.82
CD @ P = 0.05	0.44	1.21	0.21	0.47	0.87	2.16	1.19	0.17	1.64
CD @ P = 0.01	0.58	1.61	0.28	0.62	1.15	2.87	1.57	0.22	2.17
Testers									
DBGV 5	-0.56**	-1.63**	0.07	-3.03**	-0.38	-1.76*	-1.34**	0.16**	12.64**
LBG 685	0.89**	4.34**	0.21**	0.03	1.60**	0.79	-0.63	-0.12*	-8.57**
LBG 17	0.14	0.31	-0.10	2.13**	0.11	2.46**	2.32**	-0.03	-21.36**
TAU 1	-0.46**	-3.01**	-0.18**	0.88**	-1.33**	-1.49*	-0.35	-0.01	17.28**
SEm±	0.14	0.76	0.07	0.15	0.28	0.68	0.37	0.05	0.52
CD @ P = 0.05	0.28	0.77	0.13	0.29	0.55	1.37	0.75	0.10	1.04
CD @ P = 0.01	0.37	1.02	0.18	0.39	0.73	1.81	1.00	0.14	1.37

Supplementary Table 3: Overall *sca* status of crosses across productivity *per se* traits in blackgram.

Lines \ Testers	DBGV 5 (L)		LBG 685 (H)		LBG 17 (H)		TAU 1 (L)	
	Total score	Status	Total score	Status	Total score	Status	Total score	Status
VBN 4 (H)	181	H	312	L	90	H	245	L
VBN 5 (L)	145	H	278	L	168	H	189	H
VBN 6 (H)	173	H	236	L	255	L	131	H
DU 1 (H)	262	L	150	H	249	L	115	H
T 9 (L)	305	L	50	H	256	L	195	H
LBG 625 (L)	237	L	175	H	163	H	236	L
LGB 752 (H)	96	H	242	L	220	L	242	L
VBG 10-010 (L)	157	H	252	L	191	H	176	H
VBG 10-024 (L)	89	H	131	H	304	L	249	L
COBG 653 (H)	332	L	155	H	101	H	203	L
Final Norm			198.40					

H = High overall sca status; L = Low overall *sca* status; (H) = High overall GCA status of parents; (L) = Low overall GCA status of parents.

target traits in blackgram. This may be due to the recombination of genes from both the parents with positive effects, indicating that the parents involved in developing early segregating generations (F_2 and F_3) derived were differed for many genes which causes large amount of genetic variability for the traits associated with productivity and PMD resistance.

CONCLUSION

The identification and isolation of superior pure lines in self-pollinated crops like blackgram depends on the breeding methodology and selection criteria used in during early segregating generations. The present study indicated the utility of the quantitative traits means, range, PCV and frequency of transgressive segregants in early segregating generations for predicting the breeding potential of crosses to maximize the frequency of desirable RILs in advanced generations in blackgram. From the findings of the present study it is concluded that prevalence of higher trait means and variances in early segregating generations could be an ideal criteria for selecting potential crosses. Further to recover high frequency of desirable transgressive

segregantsit desirable toselect crosses involved parents with high overall GCA status.

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Conflict of interest

All authors affirm that they have no conflict of interest.

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