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Character association and variability studies in black gram advanced breeding lines

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Abstract

Black gram is an important pulse crop grown for its high protein content. The production in black gram is mainly hindered due to heavy losses caused by Yellow Mosaic Virus (YMV) disease. For black gram improvement, knowledge on genetic variability and disease free genotypes is a prerequisite. Hence, the present study includes evolution of 15 black gram genotypes yield and its compact traits along with YMV and leaf crinkle scoring. ANOVA revealed significant variations for days to 50% flowering, plant height, No. of pods/plant and grain yield. PU 31 and TBG 129 recorded nil incidence of YMV and very low incidence of leaf crinkle which can be used as a source of disease resistance. PCV ranged from low (8.37) to high (23.52). High heritability was recorded for days to 50% flowering while remaining all traits recorded moderate heritability. Based on heritability and GAM values, none of the traits were controlled by additive gene action alone. Grain yield is expressed by both additive and non additive gene action and it is negatively significantly correlated with YMV and leaf crinkle. Hence selection against diseases is rewarding.

Keywords: Character association, variability studies, black gram advanced breeding lines

Introduction

Black gram is one of the important multipurpose legume pulse crop grown in arid and semi arid tropics. It is photo insensitive and can be grown throughout the year. The relative drought tolerance and short duration of this crop makes it fit into any cropping system. (Gandi *et al.*, 2018) [6]. India is the major producer and consumer of black gram. It is considered as poor man's source of protein. The grain is highly value because it contains 25% protein, 2% fat, 50% carbohydrate, 4% minerals, and 0.4% vitamins. The main constraint in production of black gram is Yellow Mosaic Virus (YMV) disease as it causes yield losses up to 85% (Nene, 1973) [9]. That too it is cultivated in poor and marginal soils and more over there is not much variability available in this crop because in developing superior genotypes same parents were chosen as source material. The enhancement of crop productivity mainly depends on the genetic variability and heritability of yield and its dependent traits. Correlation of various characters gives an insight into the strategy of selection for developing productive genotypes. Hence, keeping in view of the above points the present investigation was undertaken with an aim to assess the significance of variability present among black gram genotypes and to identify potential genotypes for direct use or for future use with less incidence of YMV

Materials and Methods:

In the present investigation, 15 black gram genotypes including one local check variety, were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2018. Genotypes were sown in a randomized complete block design (RCBD) in three replications with a spacing of 30 × 10 cm per each entry. Each genotype was grown in 8 lines of 3 m length. Fertilizers and need based plant protection measures were taken to raise a healthy crop. Observations were recorded on plant height (cm), pod length (cm), No. of branches, No. of pods/plant, No. of grains/pod, days to 50% flowering, grain yield (q/ha), YMV and leaf crinkle disease incidence.

Analysis of variance and summary statistics was calculated as per Panse and Sukathme (1967). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953) [4]. Heritability in broad sense was computed as per Allard (1960) [1]. Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955) [7]. Phenotypic correlations were calculated according to Falconer (1981) [5].

Results and Discussions

Analysis of variance helps us to know about the significant differences existing among genotypes for a trait and in the present investigation, days to 50 % flowering, No. of branches/plant, No. of pods/plant and grain yield are highly significant while pod length and No. of branches/plant recorded significance among replications (Table 1). Significance of replications indicates that the blocking was quiet effective in removing the variation caused due to factors like soil fertility, water holding capacity of soil etc and only the real variations among the genotypes was reflected as variation between genotypes.

Very wide range was recorded for plant height (Table 2) from 22.7cm (PU 31) to 41.9 cm (GBG 58) while other traits days to 50% flowering, No. of pods/plant and grain yield also recorded wide range of variation. Early flowering was observed in PU 31 (34days) while higher grain yield was recorded for LBG 952 (10.1q/ha). YMV ranged from 0.0 % (LBG 922, PU 31, TBG 129) to 66.6 % (GBG 58) while leaf crinkle ranged from 3.3 (PU 31, TBG 129) to 43.36 (GBG 58). Hence PU 31 and TBG 129 are the best sources for resistance breeding.

The variation (Table 3) for PCV ranged from low (8.37 for days to 50% flowering) to high (23.52 for No. of pods/plant). Similar results were recorded by Kumar *et al.*, 2015^[8], Anuradha *et al.*, 2017, 2018^[2, 3], Gandi *et al.*, 2018^[6], Sushmitharaj *et al.*, 2018^[11]. GCV ranged from 5.80 (pod length) to 16.09 (grain yield). Though days 50% flowering was highly significant ($P = 4 \times 10^{-12}$) it recorded low GCV and PCV indicating low variability for the trait, the narrow difference between GCV & PCV and very low environmental coefficient of variation (2.79) indicates that it is almost not effected by the environmental fluctuations. It is also reflected in terms of its high heritability value (88.84%). High significance among genotypes in ANOVA for days to 50% flowering ultimately reflected in high heritability of the trait. Hence, for days to 50% flowering even the slightest variation is heritable or is due to genetic factors rather than environmental factors. But it recorded medium GAM value (15.31) indicating that it is governed by both additive and non additive gene action.

Hence, days to 50% flowering in the present population if selected will result in improvement up to some extent only.

Plant height also recorded high significance ($P = 1.3 \times 10^{-4}$) with a CV of 10.9% and variability was moderate with moderate heritability (57.47%). The GAM was also moderate indicating that this trait had moderate genetic variation and the genetic cause is due to both additive and non additive gene action. Hence, this trait also cannot be improved through simple selection easily. Earlier workers (Kumar *et al.*, 2015^[8], Gandi *et al.*, 2018^[6] and Sushmitharaj *et al.*, 2018^[11]) reported high heritability and high GAM for plant height.

No. of branches/plant didn't show significance between genotypes and also GCV (8.21) was low with medium (25.61) heritability values and low GAM (8.50) values. In this case the variation is quiet low and the genetic variation is masked

by the environmental variation and moreover the non additive nature of gene action further hinders the selection process. Hence, no chance of improvement for this traits through simple selection procedures.

Pod length recorded significance between replications but not among genotypes. Hence there is no need to study further GCV and PCV values are also indicating low differences among genotypes along with low hereditary of the trait with very low GAM which collectively indicate that this trait can't be improved further through selection. It is because the variation was non significant, very low, wider difference of GCV & PCV and more over the prevalence of non additive gene action renders selection difficult.

No. of pods/plant recorded moderate GCV, high PCV and moderate ECV which indicates that the trait has variability which is of genetic cause and was also influenced by environment, whereas Kumar *et al.*, (2015)^[8], Gandi *et al.*, (2018)^[6] and Sushmitharaj *et al.*, (2018)^[11] reported high GCV for No. of pods/plant. The heritability of the trait was moderate (46.40%) with high GAM (22.48) indicating that the genetic variation is due to both additive and non additive gene action. Hence selection may be possible to some extent as there were significant differences between genotypes and additive genes respond to it.

No. of grains/pod recorded non significance among genotypes and also low GCV (6.49) with medium heritability (24.07) and low GAM (6.56). Hence, this trait can't be improved further in the present population.

Grain yield recorded high significance ($P = 0.001$) among 15 black gram genotypes with moderate to high GCV (16.09) and PCV (22.97) whereas Kumar *et al.*, (2015)^[8], Gandi *et al.*, (2018)^[6] and Sushmitharaj *et al.*, (2018)^[11] reported high GCV for yield. The ECV was also moderate. Hence genotypes are significantly differing for grain yield and there existed enough genetic variation among genotypes which helps in improvement of the trait. It is also moderately influenced by environment as observed from moderate difference between GCV and PCV. The heritability of the trait was medium (49.04%) with high GAM (23.21) which tells us that this traits expression is due to both additive and non additive component of genetic variation. Hence, grain yield cannot be improved through selection alone. Correlation with other traits plays on important role.

Since none of the traits recorded high heritability with high GAM, purely additive gene action is not present among 15 black gram genotypes for any of the traits. Improvement of traits like grain yield which is complex in nature is difficult to achieve through simple selection hence to improve such traits where both additive and non-additive gene action is present, hybridization followed by selection at later stages is required. From correlation table (Table No.4) it is evident that grain yield is negatively significantly correlated with YMV and leaf crinkle while YMV and leaf crinkle were positively correlated. Hence selection against diseases is important to increase the grain yield.

Table 1: Anova of 15 black gram genotypes

Source of Variations	df	Mean Squares						
		Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)
Treatments	14	28.99***	60.09**	2.31	0.45	20.47**	1.12	5.62**
Replications	2	2.02	23.58	17.50**	0.85*	0.39	0.33	0.04
Error	28	1.17	11.89	1.14	0.24	5.69	0.58	1.45
P value for treatments		4.0E-12	1.3E-04	0.054	0.06	0.002	0.06	0.001
P value for replications		0.19	0.16	0.00	0.04	0.93	0.57	0.97

Table 2: Mean values of 15 black gram entries for yield and its component traits

S. No	Entry Name	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)	YMV (%)	Leaf crinkle (%)
1	LBG 918	39.0	30.4	7.5	4.5	14.0	7.0	6.4	0.8	18.3
2	LBG 904	40.0	34.3	7.2	4.5	11.3	6.2	9.2	1.0	15.0
3	LBG 932	42.7	32.4	8.2	4.5	16.2	6.0	10.1	0.8	4.0
4	LBG 922	39.0	27.1	7.5	4.6	15.0	6.9	8.2	0.0	13.6
5	LBG 787	35.0	29.1	6.5	4.4	11.3	5.9	6.9	8.3	30.0
6	PU 31	34.3	22.7	5.7	3.6	13.1	6.4	7.1	0.0	3.3
7	GBG 55	34.7	29.9	8.1	4.6	14.7	5.5	6.1	50.0	28.3
8	GBG 58	42.0	41.9	8.7	5.1	7.1	6.6	4.7	66.6	43.3
9	GBG 63	38.0	31.0	6.4	5.1	14.2	6.3	7.0	23.3	11.6
10	GBG 81	42.0	33.7	8.6	5.0	13.3	7.7	8.7	3.6	15.0
11	GBG 99	41.0	33.2	8.5	5.0	13.3	7.3	6.3	10.0	11.6
12	TBG 129	37.0	33.3	8.1	4.7	14.7	6.4	7.6	0.0	3.3
13	ABF BG 3	38.0	33.7	8.0	5.0	14.2	7.2	8.2	5.0	5.0
14	ABF BG 4	42.7	35.2	7.9	4.7	17.1	7.1	6.3	6.6	33.3
15	Local	34.0	26.3	7.5	4.4	18.0	6.1	7.2	2.6	6.6
	Mean	38.62	31.62	7.62	4.64	13.85	6.58	7.33	11.9	16.1
	Minimum	34.0	22.7	5.7	3.6	7.1	5.5	4.7		
	Maximum	42.7	41.9	8.7	5.1	18.0	7.7	10.1		
	CD (0.05)	1.81	5.77	1.78	0.81	3.99	1.27	2.01		
	CD (0.01)	2.43	7.78	2.41	1.1	5.38	1.71	2.71		
	CV (%)	2.79	10.9	14	10.48	17.22	11.54	16.4		

Table 3: Summary statistics of genetic parameters for 15 black gram genotypes

S. No	Parameter	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)
1	GCV	7.89	12.68	8.21	5.80	16.02	6.49	16.09
2	PCV	8.37	16.72	16.23	11.97	23.52	13.24	22.97
3	ECV	2.79	10.90	14.00	10.48	17.22	11.54	16.40
4	H ² (Broad Sense)	88.84	57.47	25.61	23.44	46.40	24.07	49.04
5	Genetic Advance	5.91	6.26	0.65	0.27	3.11	0.43	1.70
6	GAM	15.31	19.80	8.56	5.78	22.48	6.56	23.21

Table 4: Phenotypic correlation of yield and other characters in 15 black gram genotypes

S. No.	Traits	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)	YMV (%)
1	Plant height (cm)	0.72**							
2	No. of Branches/pl	0.60*	0.69**						
3	Pod length (cm)	0.54*	0.74**	0.65**					
4	No. of pods/pl	-0.16	-0.48	-0.03	-0.19				
5	No. of grain/pod	0.56*	0.29	0.37	0.41	-0.02			
6	Grain Yield (q/ha)	0.17	-0.19	-0.04	-0.15	0.34	0.01		
7	YMV (%)	0.04	0.49	0.30	0.39	-0.53*	-0.28	-0.66**	
8	Leaf crinkle (%)	0.24	0.51	0.23	0.27	-0.50	-0.06	-0.65**	0.70**

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